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(74) **Agents:** POTTER, Jane, E., R.; Seed Intellectual Property Law Group PLLC, Suite 6300, 701 Fifth Avenue, Seattle, WA 98104-7092 et al. (US).

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COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF OVARIAN CANCER

Technical Field

The present invention relates generally to ovarian cancer therapy. The invention is more specifically related to polypeptides comprising at least a portion of an ovarian carcinoma protein, and to polynucleotides encoding such polypeptides, as well as antibodies and immune system cells that specifically recognize such polypeptides. Such polypeptides, polynucleotides, antibodies and cells may be used in vaccines and pharmaceutical compositions for treatment of ovarian cancer.

10 Background of the Invention

Ovarian cancer is a significant health problem for women in the United States and throughout the world. Although advances have been made in detection and therapy of this cancer, no vaccine or other universally successful method for prevention or treatment is currently available. Management of the disease currently relies on a combination of early diagnosis and aggressive treatment, which may include one or more of a variety of treatments such as surgery, radiotherapy, chemotherapy and hormone therapy. The course of treatment for a particular cancer is often selected based on a variety of prognostic parameters, including an analysis of specific tumor markers. However, the use of established markers often leads to a result that is difficult to interpret, and high mortality continues to be observed in many cancer patients.

Immunotherapies have the potential to substantially improve cancer treatment and survival. Such therapies may involve the generation or enhancement of an immune response to an ovarian carcinoma antigen. However, to date, relatively few ovarian carcinoma antigens are known and the generation of an immune response against such antigens has not been shown to be therapeutically beneficial.

Accordingly, there is a need in the art for improved methods for identifying ovarian tumor antigens and for using such antigens in the therapy of ovarian cancer. The present invention fulfills these needs and further provides other related advantages.

SUMMARY OF THE INVENTION

Briefly stated, this invention provides compositions and methods for the therapy of cancer, such as ovarian cancer. In one aspect, the present invention provides polypeptides comprising an immunogenic portion of an ovarian carcinoma protein, or a
5 variant thereof that differs in one or more substitutions, deletions, additions and/or insertions such that the ability of the variant to react with ovarian carcinoma protein-specific antisera is not substantially diminished. Within certain embodiments, the ovarian carcinoma protein comprises a sequence that is encoded by a polynucleotide sequence selected from the group consisting of SEQ ID NO:456-457, 460-477 and 512-
10 570 and complements of such polynucleotides.

The present invention further provides polynucleotides that encode a polypeptide as described above or a portion thereof, expression vectors comprising such polynucleotides and host cells transformed or transfected with such expression vectors.

The present invention further provides polypeptide compositions
15 comprising an amino acid sequence selected from the group consisting of sequences recited in SEQ ID Nos:394-455, 458-459, 478-511, and 571-596.

Within other aspects, the present invention provides pharmaceutical compositions and vaccines. Pharmaceutical compositions may comprise a physiologically acceptable carrier or excipient in combination with one or more of: (i) a
20 polypeptide comprising an immunogenic portion of an ovarian carcinoma protein, or a variant thereof that differs in one or more substitutions, deletions, additions and/or insertions such that the ability of the variant to react with ovarian carcinoma protein-specific antisera is not substantially diminished, wherein the ovarian carcinoma protein comprises an amino acid sequence encoded by a polynucleotide that comprises a
25 sequence recited in any one of SEQ ID NO: 456-457, 460-477 and 512-570 or (ii) a polynucleotide encoding such a polypeptide; (iii) an antibody that specifically binds to such a polypeptide; (iv) an antigen-presenting cell that expresses such a polypeptide and/or (v) a T cell that specifically reacts with such a polypeptide. Vaccines may comprise a non-specific immune response enhancer in combination with one or more
30 of: (i) a polypeptide comprising an immunogenic portion of an ovarian carcinoma protein, or a variant thereof that differs in one or more substitutions, deletions, additions

and/or insertions such that the ability of the variant to react with ovarian carcinoma protein-specific antisera is not substantially diminished, wherein the ovarian carcinoma protein comprises an amino acid sequence set forth in SEQ ID Nos:394-455, 458-459, 478-511, and 571-596 or an amino acid sequence encoded by a polynucleotide that
5 comprises a sequence recited in any one of SEQ ID NO: 456-457, 460-477 and 512-570 or (ii) a polynucleotide encoding such a polypeptide; (iii) an anti-idiotypic antibody that is specifically bound by an antibody that specifically binds to such a polypeptide; (iv) an antigen-presenting cell that expresses such a polypeptide and/or (v) a T cell that specifically reacts with such a polypeptide.

10 The present invention further provides, in other aspects, fusion proteins that comprise at least one polypeptide as described above, as well as polynucleotides encoding such fusion proteins.

 Within related aspects, pharmaceutical compositions comprising a fusion protein or polynucleotide encoding a fusion protein in combination with a
15 physiologically acceptable carrier are provided.

 Vaccines are further provided, within other aspects, comprising a fusion protein or polynucleotide encoding a fusion protein in combination with a non-specific immune response enhancer.

 Within further aspects, the present invention provides methods for
20 inhibiting the development of a cancer in a patient, comprising administering to a patient a pharmaceutical composition or vaccine as recited above.

 The present invention further provides, within other aspects, methods for stimulating and/or expanding T cells, comprising contacting T cells with (a) a polypeptide comprising an immunogenic portion of an ovarian carcinoma protein, or a
25 variant thereof that differs in one or more substitutions, deletions, additions and/or insertions such that the ability of the variant to react with ovarian carcinoma protein-specific antisera is not substantially diminished, wherein the ovarian carcinoma protein comprises an amino acid sequence set forth in SEQ ID Nos:394-455, 458-459, 478-511, and 571-596 or an amino acid sequence encoded by a polynucleotide that comprises a
30 sequence recited in any one of SEQ ID NO: 456-457, 460-477 and 512-570; (b) a polynucleotide encoding such a polypeptide and/or (c) an antigen presenting cell that

expresses such a polypeptide under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells. Such polypeptide, polynucleotide and/or antigen presenting cell(s) may be present within a pharmaceutical composition or vaccine, for use in stimulating and/or expanding T cells in a mammal.

5 Within other aspects, the present invention provides methods for inhibiting the development of ovarian cancer in a patient, comprising administering to a patient T cells prepared as described above.

 Within further aspects, the present invention provides methods for inhibiting the development of ovarian cancer in a patient, comprising the steps of: (a)
10 incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with one or more of: (i) a polypeptide comprising an immunogenic portion of an ovarian carcinoma protein, or a variant thereof that differs in one or more substitutions, deletions, additions and/or insertions such that the ability of the variant to react with ovarian carcinoma protein-specific antisera is not substantially diminished, wherein the ovarian carcinoma protein
15 comprises an amino acid sequence encoded by a polynucleotide that comprises a sequence recited in any one of SEQ ID NO: 456-457, 460-477 and 512-570; (ii) a polynucleotide encoding such a polypeptide; or (iii) an antigen-presenting cell that expresses such a polypeptide; such that T cells proliferate; and (b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the
20 development of ovarian cancer in the patient. The proliferated cells may be cloned prior to administration to the patient.

 The present invention also provides, within other aspects, methods for identifying secreted tumor antigens. Such methods comprise the steps of: (a) implanting tumor cells in an immunodeficient mammal; (b) obtaining serum from the
25 immunodeficient mammal after a time sufficient to permit secretion of tumor antigens into the serum; (c) immunizing an immunocompetent mammal with the serum; (d) obtaining antiserum from the immunocompetent mammal; and (e) screening a tumor expression library with the antiserum, and therefrom identifying a secreted tumor antigen. A preferred method for identifying a secreted ovarian carcinoma antigen
30 comprises the steps of: (a) implanting ovarian carcinoma cells in a SCID mouse; (b) obtaining serum from the SCID mouse after a time sufficient to permit secretion of

ovarian carcinoma antigens into the serum; (c) immunizing an immunocompetent mouse with the serum; (d) obtaining antiserum from the immunocompetent mouse; and (e) screening an ovarian carcinoma expression library with the antiserum, and therefrom identifying a secreted ovarian carcinoma antigen.

5 The present invention also discloses antibody epitopes recognized by the O8E polyclonal anti-sera which epitopes are presented herein as SEQ ID NO: 394-415.

Further disclosed by the present invention are 10-mer and 9-mer peptides predicted to bind HLA-0201 which peptides are disclosed herein as SEQ ID NO:416-435 and SEQ ID NO:436-455, respectively.

10 These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

In another aspect of the present invention, the applicants have
15 unexpectedly identified a series of novel repeating sequence elements in the 5' end of the gene encoding O772P. Therefore, the present invention provides O772P polypeptides having structures represented by X_n -Y, wherein X comprises a sequence having at least 50% identity, preferably at least 70% identity, and more preferably at least 90% identity with an O772P repeat sequence set forth in SEQ ID NO: 596. Y will
20 typically comprise a sequence having at least 80% identity, preferably at least 90% identity and more preferably at least 95% identity with the O772P constant region sequence set forth in SEQ ID NO: 594. According to this embodiment, n will generally be an integer from 1 to 35, preferably an integer from 15 to 25, and X can be the same or different.

25 In one preferred embodiment, X comprises a sequence selected from the group consisting of any one of SEQ ID NOs: 574-593 and Y comprises the sequence set forth in SEQ ID NO: 594.

In another preferred embodiment, an illustrative O772P polypeptide comprises the sequence set forth in SEQ ID NO: 595, containing 20 repeating sequence
30 elements (i.e., X_{20}) wherein the X elements are arranged in the following order (moving from N-terminal to C-terminal in the O772P repeat region): SEQ ID NO: 574 - SEQ ID

NO: 575 - SEQ ID NO: 576 - SEQ ID NO: 577 - SEQ ID NO: 578 - SEQ ID NO: 579 -
SEQ ID NO: 580 - SEQ ID NO: 581 - SEQ ID NO: 582 - SEQ ID NO: 583 - SEQ ID
NO: 584 - SEQ ID NO: 585 - SEQ ID NO: 586 - SEQ ID NO: 587 - SEQ ID NO: 588 -
SEQ ID NO: 589 - SEQ ID NO: 590 - SEQ ID NO: 591 - SEQ ID NO: 592 - SEQ ID
5 NO: 593.

According to another aspect of the present invention, an O772P polynucleotide is provided having the structure X_n -Y, wherein X comprises an O772P repeat sequence element selected from the group consisting of any one of SEQ ID NOs: 512-540, 542-546 and 548-567. Y will generally comprise a sequence having at least
10 80% identity, preferably at least 90% identity, and more preferably at least 95% identity with the O772P constant region sequence set forth in SEQ ID NO: 568. In this embodiment, n is typically an integer from 1 to 35, preferably from 15 to 25 and X can be the same or different.

In another embodiment, an illustrative O772P polynucleotide comprises
15 the sequence set forth in SEQ ID NO: 569, containing 20 repeating sequence elements (i.e., X_{20}).

According to another aspect of the present invention, O772 polypeptides are provided comprising at least an antibody epitope sequence set forth in any one of SEQ ID NOs: 490-511.

20 According to another aspect of the present invention, O8E polypeptides are provided comprising at least an antibody epitope sequence set forth in any one of SEQ ID NOs: 394-415.

BRIEF DESCRIPTION OF THE SEQUENCE IDENTIFIERS AND DRAWINGS

SEQ ID NO:1-71 are ovarian carcinoma antigen polynucleotides shown
25 in Figures 1A-1S.

SEQ ID NO:72-74 are ovarian carcinoma antigen polynucleotides shown in Figures 2A-2C.

SEQ ID NO:75 is the ovarian carcinoma polynucleotide 3g (Figure 4).

SEQ ID NO:76 is the ovarian carcinoma polynucleotide 3f (Figure 5).

30 SEQ ID NO:77 is the ovarian carcinoma polynucleotide 6b (Figure 6).

SEQ ID NO:78 is the ovarian carcinoma polynucleotide 8e (Figure 7A).

SEQ ID NO:79 is the ovarian carcinoma polynucleotide 8h (Figure 7B).

SEQ ID NO:80 is the ovarian carcinoma polynucleotide 12e (Figure 8).

SEQ ID NO:81 is the ovarian carcinoma polynucleotide 12h (Figure 9).

5 SEQ ID NO:82-310 are ovarian carcinoma antigen polynucleotides shown in Figures 15A-15EEE.

SEQ ID NO:311 is a full length sequence of ovarian carcinoma polynucleotide O772P.

SEQ ID NO:312 is the O772P amino acid sequence.

10 SEQ ID NO:313-384 are ovarian carcinoma antigen polynucleotides.

SEQ ID NO:385 represents the cDNA sequence of a form of the clone O772P, designated 21013.

SEQ ID NO:386 represents the cDNA sequence of a form of the clone O772P, designated 21003.

15 SEQ ID NO:387 represents the cDNA sequence of a form of the clone O772P, designated 21008.

SEQ ID NOs:388 is the amino acid sequence corresponding to SEQ ID NO:385.

SEQ ID NOs:389 is the amino acid sequence corresponding to SEQ ID NO:386. SEQ ID NOs:390 is the amino acid sequence corresponding to SEQ ID NO:387.

20 SEQ ID NO:391 is a full length sequence of ovarian carcinoma polynucleotide O8E.

SEQ ID NO:392-393 are protein sequences encoded by O8E.

25 SEQ ID NO:394-415 are peptide sequences corresponding to the OE8 antibody epitopes.

SEQ ID NO:416-435 are potential HLA-A2 10-mer binding peptides predicted using the full length open-reading frame from OE8.

30 SEQ ID NO:436-455 are potential HLA-A2 9-mer binding peptides predicted using the full length open-reading frame from OE8.

SEQ ID NO:456 is a truncated nucleotide sequence of the full length Genbank sequence showing homology to O772P

SEQ ID NO:457 is the full length Genbank sequence showing significant homology to O772P

5 SEQ ID NO:458 is a protein encoding a truncated version of the full length Genbank sequence showing homology to O772P

SEQ ID NO:459 is the full length protein sequence from Genbank showing significant homology to the protein sequence for O772P

10 SEQ ID NO:460 encodes a unique N-terminal portion of O772P contained in residues 1-70.

SEQ ID NO:461 contains unique sequence and encodes residues 1-313 of SEQ ID NO: 456.

SEQ ID NO:462 is the hypothetical sequence for clone O772P.

SEQ ID NO:463 is the cDNA sequence for clone FLJ14303.

15 SEQ ID NO:464 is a partial cDNA sequence for clone O772P.

SEQ ID NO:465 is a partial cDNA sequence for clone O772P.

SEQ ID NO:466 is a partial cDNA sequence for clone O772P.

SEQ ID NO:467 is a partial cDNA sequence for clone O772P.

SEQ ID NO:468 is a partial cDNA sequence for clone O772P.

20 SEQ ID NO:469 is a partial cDNA sequence for clone O772P.

SEQ ID NO:470 is a partial cDNA sequence for clone O772P.

SEQ ID NO:471 is a partial cDNA sequence for clone O772P.

SEQ ID NO:472 is a partial cDNA sequence for clone O772P.

SEQ ID NO:473 is a partial cDNA sequence for clone O772P.

25 SEQ ID NO:474 is a partial cDNA sequence for clone O772P.

SEQ ID NO:475 is a partial cDNA sequence for clone O772P.

SEQ ID NO:476 is a partial cDNA sequence for clone O772P.

SEQ ID NO:477 represents the novel 5'-end of the ovarian tumor antigen O772P.

30 SEQ ID NO:478 is the amino acid sequence encoded by SEQ ID NO:462.

SEQ ID NO:479 is the amino acid sequence encoded by SEQ ID NO:463.

SEQ ID NO:480 is a partial amino acid sequence encoded by SEQ ID NO:472.

5 SEQ ID NO:481 is a partial amino acid sequence encoded by a possible open reading frame of SEQ ID NO:471.

SEQ ID NO:482 is a partial amino acid sequence encoded by a second possible open reading frame of SEQ ID NO:471.

10 SEQ ID NO:483 is a partial amino acid sequence encoded by SEQ ID NO:467.

SEQ ID NO:484 is a partial amino acid sequence encoded by a possible open reading frame of SEQ ID NO:466.

SEQ ID NO:485 is a partial amino acid sequence encoded by a second possible open reading frame of SEQ ID NO:466.

15 SEQ ID NO:486 is a partial amino acid sequence encoded by SEQ ID NO:465.

SEQ ID NO:487 is a partial amino acid sequence encoded by SEQ ID NO:464.

20 SEQ ID NO:488 represents the extracellular, transmembrane and cytoplasmic regions of O772P.

SEQ ID NO:489 represents the predicted extracellular domain of O772P.

SEQ ID NO:490 represents the amino acid sequence of peptide #2 which corresponds to an O772P specific antibody epitope.

25 SEQ ID NO:491 represents the amino acid sequence of peptide #6 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:492 represents the amino acid sequence of peptide #7 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:493 represents the amino acid sequence of peptide #8 which corresponds to an O772P specific antibody epitope.

30 SEQ ID NO:494 represents the amino acid sequence of peptide #9 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:495 represents the amino acid sequence of peptide #11, which corresponds to an O772P specific antibody epitope.

SEQ ID NO:496 represents the amino acid sequence of peptide #13 which corresponds to an O772P specific antibody epitope.

5 SEQ ID NO:497 represents the amino acid sequence of peptide #22 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:498 represents the amino acid sequence of peptide #24 which corresponds to an O772P specific antibody epitope.

10 SEQ ID NO:499 represents the amino acid sequence of peptide #27 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:500 represents the amino acid sequence of peptide #40 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:501 represents the amino acid sequence of peptide #41 which corresponds to an O772P specific antibody epitope.

15 SEQ ID NO:502 represents the amino acid sequence of peptide #47 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:503 represents the amino acid sequence of peptide #50 which corresponds to an O772P specific antibody epitope.

20 SEQ ID NO:504 represents the amino acid sequence of peptide #51 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:505 represents the amino acid sequence of peptide #52 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:506 represents the amino acid sequence of peptide #53 which corresponds to an O772P specific antibody epitope.

25 SEQ ID NO:507 represents the amino acid sequence of peptide #58 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:508 represents the amino acid sequence of peptide #59 which corresponds to an O772P specific antibody epitope.

30 SEQ ID NO:509 represents the amino acid sequence of peptide #60 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:510 represents the amino acid sequence of peptide #61 which corresponds to an O772P specific antibody epitope.

SEQ ID NO:511 represents the amino acid sequence of peptide #71 which corresponds to an O772P specific antibody epitope.

5 SEQ ID NO:512 (O772P repeat1) represents an example of a cDNA sequence corresponding to repeat number 21 from the 5' variable region of O772P.

SEQ ID NO:513 (O772P repeat2) represents an example of a cDNA sequence corresponding to repeat number 20 from the 5' variable region of O772P.

10 SEQ ID NO:514 (O772P repeat3) represents an example of a cDNA sequence corresponding to repeat number 19 from the 5' variable region of O772P.

SEQ ID NO:515 (O772P repeat4) represents an example of a cDNA sequence corresponding to repeat number 18 from the 5' variable region of O772P.

SEQ ID NO:516 (O772P repeat5) represents an example of a cDNA sequence corresponding to repeat number 17 from the 5' variable region of O772P.

15 SEQ ID NO:517 (HB repeat1) represents an example of a cDNA sequence corresponding to repeat number 21 from the 5' variable region of O772P.

SEQ ID NO:518 (HB repeat2) represents an example of a cDNA sequence corresponding to repeat number 20 from the 5' variable region of O772P.

20 SEQ ID NO:519 (HB repeat3) represents an example of a cDNA sequence corresponding to repeat number 19 from the 5' variable region of O772P.

SEQ ID NO:520 (HB repeat4) represents an example of a cDNA sequence corresponding to repeat number 18 from the 5' variable region of O772P.

SEQ ID NO:521 (HB repeat5) represents an example of a cDNA sequence corresponding to repeat number 17 from the 5' variable region of O772P.

25 SEQ ID NO:522 (HB repeat6 5'-end) represents an example of a cDNA sequence corresponding to repeat number 16 from the 5' variable region of O772P.

SEQ ID NO:523 (1043400.1 repeat1) represents an example of a cDNA sequence corresponding to repeat number 9 from the 5' variable region of O772P.

30 SEQ ID NO:524 (1043400.1 repeat2) represents an example of a cDNA sequence corresponding to repeat number 10 from the 5' variable region of O772P.

SEQ ID NO:525 (1043400.1 repeat3) represents an example of a cDNA sequence corresponding to repeat number 10/11 from the 5' variable region of O772P.

SEQ ID NO:526 (1043400.1 repeat4) represents an example of a cDNA sequence corresponding to repeat number 11 from the 5' variable region of O772P.

5 SEQ ID NO:527 (1043400.1 repeat5) represents an example of a cDNA sequence corresponding to repeat number 14 from the 5' variable region of O772P.

SEQ ID NO:528 (1043400.1 repeat6) represents an example of a cDNA sequence corresponding to repeat number 17 from the 5' variable region of O772P.

10 SEQ ID NO:529 (1043400.3 repeat1) represents an example of a cDNA sequence corresponding to repeat number 20 from the 5' variable region of O772P.

SEQ ID NO:530 (1043400.3 repeat2) represents an example of a cDNA sequence corresponding to repeat number 21 from the 5' variable region of O772P.

15 SEQ ID NO:531 (1043400.5 repeat1) represents an example of a cDNA sequence corresponding to repeat number 8 from the 5' variable region of O772P.

SEQ ID NO:532 (1043400.5 repeat2) represents an example of a cDNA sequence corresponding to repeat number 9 from the 5' variable region of O772P, in addition containing intron sequence.

SEQ ID NO:533 (1043400.5 repeat2) represents an example of a cDNA sequence corresponding to repeat number 9 from the 5' variable region of O772P.

20 SEQ ID NO:534 (1043400.8 repeat1) represents an example of a cDNA sequence corresponding to repeat number 17 from the 5' variable region of O772P.

SEQ ID NO:535 (1043400.8 repeat2) represents an example of a cDNA sequence corresponding to repeat number 18 from the 5' variable region of O772P.

25 SEQ ID NO:536 (1043400.8 repeat3) represents an example of a cDNA sequence corresponding to repeat number 19 from the 5' variable region of O772P.

SEQ ID NO:537 (1043400.9 repeat1) represents an example of a cDNA sequence corresponding to repeat number 4 from the 5' variable region of O772P.

SEQ ID NO:538 (1043400.9 repeat2) represents an example of a cDNA sequence corresponding to repeat number 5 from the 5' variable region of O772P.

30 SEQ ID NO:539 (1043400.9 repeat3) represents an example of a cDNA sequence corresponding to repeat number 7 from the 5' variable region of O772P.

SEQ ID NO:540 (1043400.9 repeat4) represents an example of a cDNA sequence corresponding to repeat number 8 from the 5' variable region of O772P.

SEQ ID NO:541 (1043400.11 repeat1) represents an example of a cDNA sequence corresponding to repeat number 1 from the 5' variable region of O772P.

5 SEQ ID NO:542 (1043400.11 repeat2) represents an example of a cDNA sequence corresponding to repeat number 2 from the 5' variable region of O772P.

SEQ ID NO:543 (1043400.11 repeat3) represents an example of a cDNA sequence corresponding to repeat number 3 from the 5' variable region of O772P.

10 SEQ ID NO:544 (1043400.11 repeat4) represents an example of a cDNA sequence corresponding to repeat number 11 from the 5' variable region of O772P.

SEQ ID NO:545 (1043400.11 repeat5) represents an example of a cDNA sequence corresponding to repeat number 12 from the 5' variable region of O772P.

SEQ ID NO:546 (1043400.12 repeat1) represents an example of a cDNA sequence corresponding to repeat number 20 from the 5' variable region of O772P.

15 SEQ ID NO:547 (PB repeatA) represents an example of a cDNA sequence corresponding to repeat number 1 from the 5' variable region of O772P.

SEQ ID NO:548 (PB repeatB) represents an example of a cDNA sequence corresponding to repeat number 2 from the 5' variable region of O772P.

20 SEQ ID NO:549 (PB repeatE) represents an example of a cDNA sequence corresponding to repeat number 3 from the 5' variable region of O772P.

SEQ ID NO:550 (PB repeatG) represents an example of a cDNA sequence corresponding to repeat number 4 from the 5' variable region of O772P.

SEQ ID NO:551 (PB repeatC) represents an example of a cDNA sequence corresponding to repeat number 4 from the 5' variable region of O772P.

25 SEQ ID NO:552 (PB repeatH) represents an example of a cDNA sequence corresponding to repeat number 6 from the 5' variable region of O772P.

SEQ ID NO:553 (PB repeatJ) represents an example of a cDNA sequence corresponding to repeat number 7 from the 5' variable region of O772P.

30 SEQ ID NO:554 (PB repeatK) represents an example of a cDNA sequence corresponding to repeat number 8 from the 5' variable region of O772P.

SEQ ID NO:555 (PB repeatD) represents an example of a cDNA sequence corresponding to repeat number 9 from the 5' variable region of O772P.

SEQ ID NO:556 (PB repeatI) represents an example of a cDNA sequence corresponding to repeat number 10 from the 5' variable region of O772P.

5 SEQ ID NO:557 (PB repeatM) represents an example of a cDNA sequence corresponding to repeat number 11 from the 5' variable region of O772P.

SEQ ID NO:558 (PB repeat9) represents an example of a cDNA sequence corresponding to repeat number 12 from the 5' variable region of O772P.

10 SEQ ID NO:559 (PB repeat8.5) represents an example of a cDNA sequence corresponding to repeat number 13 from the 5' variable region of O772P.

SEQ ID NO:560 (PB repeat8) represents an example of a cDNA sequence corresponding to repeat number 14 from the 5' variable region of O772P.

SEQ ID NO:561 (PB repeat7) represents an example of a cDNA sequence corresponding to repeat number 15 from the 5' variable region of O772P.

15 SEQ ID NO:562 (PB repeat6) represents an example of a cDNA sequence corresponding to repeat number 16 from the 5' variable region of O772P.

SEQ ID NO:563 (PB repeat5) represents an example of a cDNA sequence corresponding to repeat number 17 from the 5' variable region of O772P.

20 SEQ ID NO:564 (PB repeat4) represents an example of a cDNA sequence corresponding to repeat number 18 from the 5' variable region of O772P.

SEQ ID NO:565 (PB repeat3) represents an example of a cDNA sequence corresponding to repeat number 19 from the 5' variable region of O772P.

SEQ ID NO:566 (PB repeat2) represents an example of a cDNA sequence corresponding to repeat number 20 from the 5' variable region of O772P.

25 SEQ ID NO:567 (PB repeat1) represents an example of a cDNA sequence corresponding to repeat number 21 from the 5' variable region of O772P.

SEQ ID NO:568 represents the cDNA sequence form the 3' constant region.

30 SEQ ID NO:569 represents a cDNA sequence containing the consensus sequences of the 21 repeats, the 3' constant region and the 3' untranslated region.

SEQ ID NO:570 represents the cDNA sequence of the consensus repeat sequence.

SEQ ID NO:571 represents the consensus amino acid sequence of one potential open reading frame of repeat number 1 from the 5' variable region of O772P.

5 SEQ ID NO:572 represents the consensus amino acid sequence of a second potential open reading frame of repeat number 1 from the 5' variable region of O772P.

SEQ ID NO:573 represents the consensus amino acid sequence of a third potential open reading frame of repeat number 1 from the 5' variable region of O772P.

10 SEQ ID NO:574 represents the consensus amino acid sequence of repeat number 2 from the 5' variable region of O772P.

SEQ ID NO:575 represents the consensus amino acid sequence of repeat number 3 from the 5' variable region of O772P.

15 SEQ ID NO:576 represents the consensus amino acid sequence of repeat number 4 from the 5' variable region of O772P.

SEQ ID NO:577 represents the consensus amino acid sequence of repeat number 5 from the 5' variable region of O772P.

SEQ ID NO:578 represents the consensus amino acid sequence of repeat number 6 from the 5' variable region of O772P.

20 SEQ ID NO:579 represents the consensus amino acid sequence of repeat number 7 from the 5' variable region of O772P.

SEQ ID NO:580 represents the consensus amino acid sequence of repeat number 8 from the 5' variable region of O772P.

25 SEQ ID NO:581 represents the consensus amino acid sequence of repeat number 9 from the 5' variable region of O772P.

SEQ ID NO:582 represents the consensus amino acid sequence of repeat number 10 from the 5' variable region of O772P.

SEQ ID NO:583 represents the consensus amino acid sequence of repeat number 11 from the 5' variable region of O772P.

30 SEQ ID NO:584 represents the consensus amino acid sequence of repeat number 12 from the 5' variable region of O772P.

SEQ ID NO:585 represents the consensus amino acid sequence of repeat number 13 from the 5' variable region of O772P.

SEQ ID NO:586 represents the consensus amino acid sequence of repeat number 14 from the 5' variable region of O772P.

5 SEQ ID NO:587 represents the consensus amino acid sequence of repeat number 15 from the 5' variable region of O772P.

SEQ ID NO:588 represents the consensus amino acid sequence of repeat number 16 from the 5' variable region of O772P.

10 SEQ ID NO:589 represents the consensus amino acid sequence of repeat number 17 from the 5' variable region of O772P.

SEQ ID NO:590 represents the consensus amino acid sequence of repeat number 18 from the 5' variable region of O772P.

SEQ ID NO:591 represents the consensus amino acid sequence of repeat number 19 from the 5' variable region of O772P.

15 SEQ ID NO:592 represents the consensus amino acid sequence of repeat number 20 from the 5' variable region of O772P.

SEQ ID NO:593 represents the consensus amino acid sequence of repeat number 21 from the 5' variable region of O772P.

20 SEQ ID NO:594 represents the amino acid sequence of the 3' constant region.

SEQ ID NO:595 represents an amino acid sequence containing the consensus sequences of the 21 repeats and the 3' constant region.

SEQ ID NO:596 represents the amino acid sequence of the consensus repeat sequence.

25 Figures 1A-1S (SEQ ID NO:1-71) depict partial sequences of polynucleotides encoding representative secreted ovarian carcinoma antigens.

Figures 2A-2C depict full insert sequences for three of the clones of Figure 1. Figure 2A shows the sequence designated O7E (11731; SEQ ID NO:72), Figure 2B shows the sequence designated O9E (11785; SEQ ID NO:73) and Figure 2C
30 shows the sequence designated O8E (13695; SEQ ID NO:74).

Figure 3 presents results of microarray expression analysis of the ovarian carcinoma sequence designated O8E.

Figure 4 presents a partial sequence of a polynucleotide (designated 3g; SEQ ID NO:75) encoding an ovarian carcinoma sequence that is a splice fusion
5 between the human T-cell leukemia virus type I oncoprotein TAX and osteonectin.

Figure 5 presents the ovarian carcinoma polynucleotide designated 3f (SEQ ID NO:76).

Figure 6 presents the ovarian carcinoma polynucleotide designated 6b (SEQ ID NO:77).

10 Figures 7A and 7B present the ovarian carcinoma polynucleotides designated 8e (SEQ ID NO:78) and 8h (SEQ ID NO:79).

Figure 8 presents the ovarian carcinoma polynucleotide designated 12c (SEQ ID NO:80).

15 Figure 9 presents the ovarian carcinoma polynucleotide designated 12h (SEQ ID NO:81).

Figure 10 depicts results of microarray expression analysis of the ovarian carcinoma sequence designated 3f.

Figure 11 depicts results of microarray expression analysis of the ovarian carcinoma sequence designated 6b.

20 Figure 12 depicts results of microarray expression analysis of the ovarian carcinoma sequence designated 8e.

Figure 13 depicts results of microarray expression analysis of the ovarian carcinoma sequence designated 12c.

25 Figure 14 depicts results of microarray expression analysis of the ovarian carcinoma sequence designated 12h.

Figures 15A-15EEE depict partial sequences of additional polynucleotides encoding representative secreted ovarian carcinoma antigens (SEQ ID NO:82-310).

30 Figure 16 is a diagram illustrating the location of various partial O8E sequences within the full length sequence.

Figure 17 is a graph illustrating the results of epitope mapping studies on O8E protein.

Figure 18 is graph of a fluorescence activated cell sorting (FACS) analysis of O8E cell surface expression.

5 Figure 19 is graph of a FACS analysis of O8E cell surface expression.

Figure 20 shows FACS analysis results for O8E transfected HEK293 cells demonstrating cell surface expression of O8E.

Figure 21 shows FACS analysis results for SKBR3 breast tumor cells demonstrating cell surface expression of O8E.

10 Figure 22 shows O8E expression in HEK 293 cells. The cells were probed with anti-O8E rabbit polyclonal antisera #2333L.

Figure 23 shows the ELISA analysis of anti-O8E rabbit sera.

Figure 24 shows the ELISA analysis of affinity purified rabbit anti-O8E polyclonal antibody.

15 Figure 25 is a graph determining antibody internalization of anti-O8E mAb showing that mAbs against amino acids 61-80 induces ligand internalization.

DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the therapy of cancer, such as ovarian cancer. The compositions described herein may include immunogenic polypeptides, polynucleotides encoding such polypeptides, binding agents such as antibodies that bind to a polypeptide, antigen presenting cells (APCs) and/or immune system cells (*e.g.*, T cells).

Polypeptides of the present invention generally comprise at least an immunogenic portion of an ovarian carcinoma protein or a variant thereof. Certain ovarian carcinoma proteins have been identified using an immunoassay technique, and are referred to herein as ovarian carcinoma antigens. An "ovarian carcinoma antigen" is a protein that is expressed by ovarian tumor cells (preferably human cells) at a level that is at least two fold higher than the level in normal ovarian cells. Certain ovarian carcinoma antigens react detectably (within an immunoassay, such as an ELISA or Western blot) with antisera generated against serum from an immunodeficient animal

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implanted with a human ovarian tumor. Such ovarian carcinoma antigens are shed or secreted from an ovarian tumor into the sera of the immunodeficient animal. Accordingly, certain ovarian carcinoma antigens provided herein are secreted antigens. Certain nucleic acid sequences of the subject invention generally comprise a DNA or
5 RNA sequence that encodes all or a portion of such a polypeptide, or that is complementary to such a sequence.

The present invention further provides ovarian carcinoma sequences that are identified using techniques to evaluate altered expression within an ovarian tumor. Such sequences may be polynucleotide or protein sequences. Ovarian carcinoma
10 sequences are generally expressed in an ovarian tumor at a level that is at least two fold, and preferably at least five fold, greater than the level of expression in normal ovarian tissue, as determined using a representative assay provided herein. Certain partial ovarian carcinoma polynucleotide sequences are presented herein. Proteins encoded by genes comprising such polynucleotide sequences (or complements thereof) are also
15 considered ovarian carcinoma proteins.

Antibodies are generally immune system proteins, or antigen-binding fragments thereof, that are capable of binding to at least a portion of an ovarian carcinoma polypeptide as described herein. T cells that may be employed within the compositions provided herein are generally T cells (*e.g.*, CD4⁺ and/or CD8⁺) that are
20 specific for such a polypeptide. Certain methods described herein further employ antigen-presenting cells (such as dendritic cells or macrophages) that express an ovarian carcinoma polypeptide as provided herein.

Ovarian Carcinoma Polynucleotides

Any polynucleotide that encodes an ovarian carcinoma protein or a
25 portion or other variant thereof as described herein is encompassed by the present invention. Preferred polynucleotides comprise at least 15 consecutive nucleotides, preferably at least 30 consecutive nucleotides, and more preferably at least 45 consecutive nucleotides, that encode a portion of an ovarian carcinoma protein. More preferably, a polynucleotide encodes an immunogenic portion of an ovarian carcinoma
30 protein, such as an ovarian carcinoma antigen. Polynucleotides complementary to any

such sequences are also encompassed by the present invention. Polynucleotides may be single-stranded (coding or antisense) or double-stranded, and may be DNA (genomic, cDNA or synthetic) or RNA molecules. Additional coding or non-coding sequences may, but need not, be present within a polynucleotide of the present invention, and a
5 polynucleotide may, but need not, be linked to other molecules and/or support materials.

Polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes an ovarian carcinoma protein or a portion thereof) or may comprise a variant of such a sequence. Polynucleotide variants may contain one or more substitutions, additions, deletions and/or insertions such that the immunogenicity
10 of the encoded polypeptide is not diminished, relative to a native ovarian carcinoma protein. The effect on the immunogenicity of the encoded polypeptide may generally be assessed as described herein. Variants preferably exhibit at least about 70% identity, more preferably at least about 80% identity and most preferably at least about 90% identity to a polynucleotide sequence that encodes a native ovarian carcinoma protein or
15 a portion thereof.

The percent identity for two polynucleotide or polypeptide sequences may be readily determined by comparing sequences using computer algorithms well known to those of ordinary skill in the art, such as Megalign, using default parameters. Comparisons between two sequences are typically performed by comparing the
20 sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, or 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Optimal alignment of sequences for
25 comparison may be conducted, for example, using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. Preferably, the percentage of sequence identity is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide or polypeptide sequence in the
30 window may comprise additions or deletions (*i.e.*, gaps) of 20 % or less, usually 5 to 15 %, or 10 to 12%, relative to the reference sequence (which does not contain additions or

deletions). The percent identity may be calculated by determining the number of positions at which the identical nucleic acid bases or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (*i.e.*, the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

Variants may also, or alternatively, be substantially homologous to a native gene, or a portion or complement thereof. Such polynucleotide variants are capable of hybridizing under moderately stringent conditions to a naturally occurring DNA sequence encoding a native ovarian carcinoma protein (or a complementary sequence). Suitable moderately stringent conditions include prewashing in a solution of 5 X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-65°C, 5 X SSC, overnight; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS.

It will be appreciated by those of ordinary skill in the art that, as a result of the degeneracy of the genetic code, there are many nucleotide sequences that encode a polypeptide as described herein. Some of these polynucleotides bear minimal homology to the nucleotide sequence of any native gene. Nonetheless, polynucleotides that vary due to differences in codon usage are specifically contemplated by the present invention. Further, alleles of the genes comprising the polynucleotide sequences provided herein are within the scope of the present invention. Alleles are endogenous genes that are altered as a result of one or more mutations, such as deletions, additions and/or substitutions of nucleotides. The resulting mRNA and protein may, but need not, have an altered structure or function. Alleles may be identified using standard techniques (such as hybridization, amplification and/or database sequence comparison).

Polynucleotides may be prepared using any of a variety of techniques. For example, an ovarian carcinoma polynucleotide may be identified, as described in more detail below, by screening a late passage ovarian tumor expression library with antisera generated against sera of immunocompetent mice after injection of such mice with sera from SCID mice implanted with late passage ovarian tumors. Ovarian carcinoma polynucleotides may also be identified using any of a variety of techniques designed to evaluate differential gene expression. Alternatively, polynucleotides may

be amplified from cDNA prepared from ovarian tumor cells. Such polynucleotides may be amplified via polymerase chain reaction (PCR). For this approach, sequence-specific primers may be designed based on the sequences provided herein, and may be purchased or synthesized.

- 5 An amplified portion may be used to isolate a full length gene from a suitable library (e.g., an ovarian carcinoma cDNA library) using well known techniques. Within such techniques, a library (cDNA or genomic) is screened using one or more polynucleotide probes or primers suitable for amplification. Preferably, a library is size-selected to include larger molecules. Random primed libraries may also be preferred for
10 identifying 5' and upstream regions of genes. Genomic libraries are preferred for obtaining introns and extending 5' sequences.

- For hybridization techniques, a partial sequence may be labeled (e.g., by nick-translation or end-labeling with ^{32}P) using well known techniques. A bacterial or bacteriophage library is then screened by hybridizing filters containing denatured
15 bacterial colonies (or lawns containing phage plaques) with the labeled probe (see Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989). Hybridizing colonies or plaques are selected and expanded, and the DNA is isolated for further analysis. cDNA clones may be analyzed to determine the amount of additional sequence by, for example, PCR using
20 a primer from the partial sequence and a primer from the vector. Restriction maps and partial sequences may be generated to identify one or more overlapping clones. The complete sequence may then be determined using standard techniques, which may involve generating a series of deletion clones. The resulting overlapping sequences are then assembled into a single contiguous sequence. A full length cDNA molecule can be
25 generated by ligating suitable fragments, using well known techniques.

- Alternatively, there are numerous amplification techniques for obtaining a full length coding sequence from a partial cDNA sequence. Within such techniques, amplification is generally performed via PCR. Any of a variety of commercially available kits may be used to perform the amplification step. Primers may be designed
30 using, for example, software well known in the art. Primers are preferably 22-30 nucleotides in length, have a GC content of at least 50% and anneal to the target

sequence at temperatures of about 68°C to 72°C. The amplified region may be sequenced as described above, and overlapping sequences assembled into a contiguous sequence.

One such amplification technique is inverse PCR (*see* Triglia et al., *Nucl. Acids Res.* 16:8186, 1988), which uses restriction enzymes to generate a fragment in the known region of the gene. The fragment is then circularized by intramolecular ligation and used as a template for PCR with divergent primers derived from the known region. Within an alternative approach, sequences adjacent to a partial sequence may be retrieved by amplification with a primer to a linker sequence and a primer specific to a known region. The amplified sequences are typically subjected to a second round of amplification with the same linker primer and a second primer specific to the known region. A variation on this procedure, which employs two primers that initiate extension in opposite directions from the known sequence, is described in WO 96/38591. Additional techniques include capture PCR (Lagerstrom et al., *PCR Methods Applic.* 1:111-19, 1991) and walking PCR (Parker et al., *Nucl. Acids. Res.* 19:3055-60, 1991). Other methods employing amplification may also be employed to obtain a full length cDNA sequence.

In certain instances, it is possible to obtain a full length cDNA sequence by analysis of sequences provided in an expressed sequence tag (EST) database, such as that available from GenBank. Searches for overlapping ESTs may generally be performed using well known programs (*e.g.*, NCBI BLAST searches), and such ESTs may be used to generate a contiguous full length sequence.

Certain nucleic acid sequences of cDNA molecules encoding portions of ovarian carcinoma antigens are provided in Figures 1A-1S (SEQ ID NO:1 to 71) and Figures 15A to 15EEE (SEQ ID NO:82 to 310). The sequences provided in Figures 1A-1S appear to be novel. For sequences in Figures 15A-15EEE, database searches revealed matches having substantial identity. These polynucleotides were isolated by serological screening of an ovarian tumor cDNA expression library, using a technique designed to identify secreted tumor antigens. Briefly, a late passage ovarian tumor expression library was prepared from a SCID-derived human ovarian tumor (OV9334) in the vector λ -screen (Novagen). The sera used for screening were obtained by

injecting immunocompetent mice with sera from SCID mice implanted with one late passage ovarian tumors. This technique permits the identification of cDNA molecules that encode immunogenic portions of secreted tumor antigens.

The polynucleotides recited herein, as well as full length polynucleotides comprising such sequences, other portions of such full length polynucleotides, and sequences complementary to all or a portion of such full length molecules, are specifically encompassed by the present invention. It will be apparent to those of ordinary skill in the art that this technique can also be applied to the identification of antigens that are secreted from other types of tumors.

Other nucleic acid sequences of cDNA molecules encoding portions of ovarian carcinoma proteins are provided in Figures 4-9 (SEQ ID NO:75-81), as well as SEQ ID NO:313-384. These sequences were identified by screening a microarray of cDNAs for tumor-associated expression (*i.e.*, expression that is at least five fold greater in an ovarian tumor than in normal ovarian tissue, as determined using a representative assay provided herein). Such screens were performed using a Synteni microarray (Palo Alto, CA) according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). SEQ ID NO:311 and 391 provide full length sequences incorporating certain of these nucleic acid sequences.

Any of a variety of well known techniques may be used to evaluate tumor-associated expression of a cDNA. For example, hybridization techniques using labeled polynucleotide probes may be employed. Alternatively, or in addition, amplification techniques such as real-time PCR may be used (*see* Gibson et al., *Genome Research* 6:995-1001, 1996; Heid et al., *Genome Research* 6:986-994, 1996). Real-time PCR is a technique that evaluates the level of PCR product accumulation during amplification. This technique permits quantitative evaluation of mRNA levels in multiple samples. Briefly, mRNA is extracted from tumor and normal tissue and cDNA is prepared using standard techniques. Real-time PCR may be performed, for example, using a Perkin Elmer/Applied Biosystems (Foster City, CA) 7700 Prism instrument. Matching primers and fluorescent probes may be designed for genes of interest using, for example, the primer express program provided by Perkin Elmer/Applied Biosystems

(Foster City, CA). Optimal concentrations of primers and probes may be initially determined by those of ordinary skill in the art, and control (e.g., β -actin) primers and probes may be obtained commercially from, for example, Perkin Elmer/Applied Biosystems (Foster City, CA). To quantitate the amount of specific RNA in a sample, a
5 standard curve is generated alongside using a plasmid containing the gene of interest. Standard curves may be generated using the Ct values determined in the real-time PCR, which are related to the initial cDNA concentration used in the assay. Standard dilutions ranging from 10^{-10} to 10^{-6} copies of the gene of interest are generally sufficient. In addition, a standard curve is generated for the control sequence. This permits
10 standardization of initial RNA content of a tissue sample to the amount of control for comparison purposes.

Polynucleotide variants may generally be prepared by any method known in the art, including chemical synthesis by, for example, solid phase phosphoramidite chemical synthesis. Modifications in a polynucleotide sequence may also be introduced
15 using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis (see Adelman et al., *DNA* 2:183, 1983). Alternatively, RNA molecules may be generated by *in vitro* or *in vivo* transcription of DNA sequences encoding an ovarian carcinoma antigen, or portion thereof, provided that the DNA is incorporated into a vector with a suitable RNA polymerase promoter (such as T7 or SP6). Certain
20 portions may be used to prepare an encoded polypeptide, as described herein. In addition, or alternatively, a portion may be administered to a patient such that the encoded polypeptide is generated *in vivo*.

A portion of a sequence complementary to a coding sequence (i.e., an antisense polynucleotide) may also be used as a probe or to modulate gene expression.
25 cDNA constructs that can be transcribed into antisense RNA may also be introduced into cells or tissues to facilitate the production of antisense RNA. An antisense polynucleotide may be used, as described herein, to inhibit expression of an ovarian carcinoma protein. Antisense technology can be used to control gene expression through triple-helix formation, which compromises the ability of the double helix to
30 open sufficiently for the binding of polymerases, transcription factors or regulatory molecules (see Gee et al., In Huber and Carr, *Molecular and Immunologic Approaches*,

Futura Publishing Co. (Mt. Kisco, NY; 1994). Alternatively, an antisense molecule may be designed to hybridize with a control region of a gene (e.g., promoter, enhancer or transcription initiation site), and block transcription of the gene; or to block translation by inhibiting binding of a transcript to ribosomes.

- 5 Any polynucleotide may be further modified to increase stability *in vivo*. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends; the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages in the backbone; and/or the inclusion of nontraditional bases such as inosine, queosine and wybutosine, as well as acetyl-, methyl-, thio- and
10 other modified forms of adenine, cytidine, guanine, thymine and uridine.

- Nucleotide sequences as described herein may be joined to a variety of other nucleotide sequences using established recombinant DNA techniques. For example, a polynucleotide may be cloned into any of a variety of cloning vectors, including plasmids, phagemids, lambda phage derivatives and cosmids. Vectors of
15 particular interest include expression vectors, replication vectors, probe generation vectors and sequencing vectors. In general, a vector will contain an origin of replication functional in at least one organism, convenient restriction endonuclease sites and one or more selectable markers. Other elements will depend upon the desired use, and will be apparent to those of ordinary skill in the art.

- 20 Within certain embodiments, polynucleotides may be formulated so as to permit entry into a cell of a mammal, and expression therein. Such formulations are particularly useful for therapeutic purposes, as described below. Those of ordinary skill in the art will appreciate that there are many ways to achieve expression of a polynucleotide in a target cell, and any suitable method may be employed. For
25 example, a polynucleotide may be incorporated into a viral vector such as, but not limited to, adenovirus, adeno-associated virus, retrovirus, or vaccinia or other pox virus (e.g., avian pox virus). Techniques for incorporating DNA into such vectors are well known to those of ordinary skill in the art. A retroviral vector may additionally transfer or incorporate a gene for a selectable marker (to aid in the identification or selection of
30 transduced cells) and/or a targeting moiety, such as a gene that encodes a ligand for a receptor on a specific target cell, to render the vector target specific. Targeting may also

be accomplished using an antibody, by methods known to those of ordinary skill in the art.

Other formulations for therapeutic purposes include colloidal dispersion systems, such as macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. A preferred colloidal system for use as a delivery vehicle *in vitro* and *in vivo* is a liposome (*i.e.*, an artificial membrane vesicle). The preparation and use of such systems is well known in the art.

Ovarian Carcinoma Polypeptides

Within the context of the present invention, polypeptides may comprise at least an immunogenic portion of an ovarian carcinoma protein or a variant thereof, as described herein. As noted above, certain ovarian carcinoma proteins are ovarian carcinoma antigens that are expressed by ovarian tumor cells and react detectably within an immunoassay (such as an ELISA) with antisera generated against serum from an immunodeficient animal implanted with an ovarian tumor. Other ovarian carcinoma proteins are encoded by ovarian carcinoma polynucleotides recited herein. Polypeptides as described herein may be of any length. Additional sequences derived from the native protein and/or heterologous sequences may be present, and such sequences may (but need not) possess further immunogenic or antigenic properties.

An "immunogenic portion," as used herein is a portion of an antigen that is recognized (*i.e.*, specifically bound) by a B-cell and/or T-cell surface antigen receptor. Such immunogenic portions generally comprise at least 5 amino acid residues, more preferably at least 10, and still more preferably at least 20 amino acid residues of an ovarian carcinoma protein or a variant thereof. Preferred immunogenic portions are encoded by cDNA molecules isolated as described herein. Further immunogenic portions may generally be identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3rd ed., 243-247 (Raven Press, 1993) and references cited therein. Such techniques include screening polypeptides for the ability to react with ovarian carcinoma protein-specific antibodies, antisera and/or T-cell lines or clones. As used herein, antisera and antibodies are "ovarian carcinoma protein-

specific" if they specifically bind to an ovarian carcinoma protein (*i.e.*, they react with the ovarian carcinoma protein in an ELISA or other immunoassay, and do not react detectably with unrelated proteins). Such antisera, antibodies and T cells may be prepared as described herein, and using well known techniques. An immunogenic
5 portion of a native ovarian carcinoma protein is a portion that reacts with such antisera, antibodies and/or T-cells at a level that is not substantially less than the reactivity of the full length polypeptide (*e.g.*, in an ELISA and/or T-cell reactivity assay). Such immunogenic portions may react within such assays at a level that is similar to or greater than the reactivity of the full length protein. Such screens may generally be
10 performed using methods well known to those of ordinary skill in the art, such as those described in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. For example, a polypeptide may be immobilized on a solid support and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies
15 detected using, for example, ¹²⁵I-labeled Protein A.

As noted above, a composition may comprise a variant of a native ovarian carcinoma protein. A polypeptide "variant," as used herein, is a polypeptide that differs from a native ovarian carcinoma protein in one or more substitutions, deletions, additions and/or insertions, such that the immunogenicity of the polypeptide
20 is not substantially diminished. In other words, the ability of a variant to react with ovarian carcinoma protein-specific antisera may be enhanced or unchanged, relative to the native ovarian carcinoma protein, or may be diminished by less than 50%, and preferably less than 20%, relative to the native ovarian carcinoma protein. Such variants may generally be identified by modifying one of the above polypeptide
25 sequences and evaluating the reactivity of the modified polypeptide with ovarian carcinoma protein-specific antibodies or antisera as described herein. Preferred variants include those in which one or more portions, such as an N-terminal leader sequence or transmembrane domain, have been removed. Other preferred variants include variants in which a small portion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids) has been
30 removed from the N- and/or C-terminal of the mature protein.

Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity to the native polypeptide. Preferably, a variant contains conservative substitutions. A "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydropathic nature of the polypeptide to be substantially unchanged. Amino acid substitutions may generally be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values include leucine, isoleucine and valine; glycine and alanine; asparagine and glutamine; and serine, threonine, phenylalanine and tyrosine. Other groups of amino acids that may represent conservative changes include: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his. A variant may also, or alternatively, contain nonconservative changes. Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the immunogenicity, secondary structure and hydropathic nature of the polypeptide.

As noted above, polypeptides may comprise a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (e.g., poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

Polypeptides may be prepared using any of a variety of well known techniques. Recombinant polypeptides encoded by DNA sequences as described above may be readily prepared from the DNA sequences using any of a variety of expression vectors known to those of ordinary skill in the art. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells

include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line such as COS or CHO. Supernatants from suitable host/vector systems which secrete recombinant protein or polypeptide into culture media may be first concentrated using a commercially available
5 filter. Following concentration, the concentrate may be applied to a suitable purification matrix such as an affinity matrix or an ion exchange resin. Finally, one or more reverse phase HPLC steps can be employed to further purify a recombinant polypeptide.

Portions and other variants having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may also be generated by synthetic
10 means, using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is
15 commercially available from suppliers such as Applied BioSystems, Inc. (Foster City, CA), and may be operated according to the manufacturer's instructions.

Within certain specific embodiments, a polypeptide may be a fusion protein that comprises multiple polypeptides as described herein, or that comprises one polypeptide as described herein and a known tumor antigen, such as an ovarian
20 carcinoma protein or a variant of such a protein. A fusion partner may, for example, assist in providing T helper epitopes (an immunological fusion partner), preferably T helper epitopes recognized by humans, or may assist in expressing the protein (an expression enhancer) at higher yields than the native recombinant protein. Certain preferred fusion partners are both immunological and expression enhancing fusion
25 partners. Other fusion partners may be selected so as to increase the solubility of the protein or to enable the protein to be targeted to desired intracellular compartments. Still further fusion partners include affinity tags, which facilitate purification of the protein.

Fusion proteins may generally be prepared using standard techniques,
30 including chemical conjugation. Preferably, a fusion protein is expressed as a recombinant protein, allowing the production of increased levels, relative to a non-fused

protein, in an expression system. Briefly, DNA sequences encoding the polypeptide components may be assembled separately, and ligated into an appropriate expression vector. The 3' end of the DNA sequence encoding one polypeptide component is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide component so that the reading frames of the sequences are in phase. This permits translation into a single fusion protein that retains the biological activity of both component polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptide components by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may generally be from 1 to about 50 amino acids in length. Linker sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Fusion proteins are also provided that comprise a polypeptide of the present invention together with an unrelated immunogenic protein. Preferably the immunogenic protein is capable of eliciting a recall response. Examples of such proteins include tetanus, tuberculosis and hepatitis proteins (*see, for example, Stoute et al. New Engl. J. Med.*, 336:86-91, 1997).

Within preferred embodiments, an immunological fusion partner is derived from protein D, a surface protein of the gram-negative bacterium *Haemophilus influenza B* (WO 91/18926). Preferably, a protein D derivative comprises approximately the first third of the protein (*e.g.*, the first N-terminal 100-110 amino acids), and a protein D derivative may be lipidated. Within certain preferred
10 embodiments, the first 109 residues of a Lipoprotein D fusion partner is included on the N-terminus to provide the polypeptide with additional exogenous T-cell epitopes and to increase the expression level in *E. coli* (thus functioning as an expression enhancer). The lipid tail ensures optimal presentation of the antigen to antigen present cells. Other
15 fusion partners include the non-structural protein from influenzae virus, NS1 (hemagglutinin). Typically, the N-terminal 81 amino acids are used, although different fragments that include T-helper epitopes may be used.

In another embodiment, the immunological fusion partner is the protein known as LYTA, or a portion thereof (preferably a C-terminal portion). LYTA is
20 derived from *Streptococcus pneumoniae*, which synthesizes an N-acetyl-L-alanine amidase known as amidase LYTA (encoded by the *LytA* gene; *Gene* 43:265-292, 1986). LYTA is an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible for the affinity to the choline or to some choline analogues such as DEAE. This property has been
25 exploited for the development of *E. coli* C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins containing the C-LYTA fragment at the amino terminus has been described (*see Biotechnology* 10:795-798, 1992). Within a preferred embodiment, a repeat portion of LYTA may be incorporated into a fusion protein. A repeat portion is found in the C-terminal region starting at
30 residue 178. A particularly preferred repeat portion incorporates residues 188-305.

In general, polypeptides (including fusion proteins) and polynucleotides as described herein are isolated. An "isolated" polypeptide or polynucleotide is one that is removed from its original environment. For example, a naturally-occurring protein is isolated if it is separated from some or all of the coexisting materials in the natural system. Preferably, such polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. A polynucleotide is considered to be isolated if, for example, it is cloned into a vector that is not a part of the natural environment.

Binding Agents

The present invention further provides agents, such as antibodies and antigen-binding fragments thereof, that specifically bind to an ovarian carcinoma protein. As used herein, an antibody, or antigen-binding fragment thereof, is said to "specifically bind" to an ovarian carcinoma protein if it reacts at a detectable level (within, for example, an ELISA) with an ovarian carcinoma protein, and does not react detectably with unrelated proteins under similar conditions. As used herein, "binding" refers to a noncovalent association between two separate molecules such that a "complex" is formed. The ability to bind may be evaluated by, for example, determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind," in the context of the present invention, when the binding constant for complex formation exceeds about 10^3 L/mol. The binding constant may be determined using methods well known in the art.

Binding agents may be further capable of differentiating between patients with and without a cancer, such as ovarian cancer, using the representative assays provided herein. In other words, antibodies or other binding agents that bind to a ovarian carcinoma antigen will generate a signal indicating the presence of a cancer in at least about 20% of patients with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without the cancer. To determine whether a binding agent satisfies this requirement, biological

samples (e.g., blood, sera, leukophoresis, urine and/or tumor biopsies) from patients with and without a cancer (as determined using standard clinical tests) may be assayed as described herein for the presence of polypeptides that bind to the binding agent. It will be apparent that a statistically significant number of samples with and without the
5 disease should be assayed. Each binding agent should satisfy the above criteria; however, those of ordinary skill in the art will recognize that binding agents may be used in combination to improve sensitivity.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome, with or without a peptide component,
10 an RNA molecule or a polypeptide. In a preferred embodiment, a binding agent is an antibody or an antigen-binding fragment thereof. Antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. *See, e.g.,* Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, antibodies can be produced by cell culture techniques, including the generation
15 of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies. In one technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (e.g., mice, rats, rabbits, sheep or goats). In this step, the polypeptides of this invention may serve as the immunogen
20 without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically.
25 Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for an antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve
30 the preparation of immortal cell lines capable of producing antibodies having the

desired specificity (*i.e.*, reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized
5 animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks,
10 colonies of hybrids are observed. Single colonies are selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the
15 yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process
20 in, for example, an affinity chromatography step.

Within certain embodiments, the use of antigen-binding fragments of antibodies may be preferred. Such fragments include Fab fragments, which may be prepared using standard techniques. Briefly, immunoglobulins may be purified from rabbit serum by affinity chromatography on Protein A bead columns (Harlow and Lane,
25 *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988) and digested by papain to yield Fab and Fc fragments. The Fab and Fc fragments may be separated by affinity chromatography on protein A bead columns.

Monoclonal antibodies of the present invention may be coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides,
30 differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include ^{90}Y , ^{123}I , ^{125}I , ^{131}I , ^{186}Re , ^{188}Re , ^{211}At , and ^{212}Bi . Preferred drugs include

methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed antiviral protein.

- 5 A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-
10 containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

- Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker
15 group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

- It will be evident to those skilled in the art that a variety of bifunctional
20 or polyfunctional reagents, both homo- and hetero-functional (such as those described in the catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

- 25 Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction
30 of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitler), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of

derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one
5 embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for
10 attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih et al.). A carrier may
15 also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be
20 formed from chelating compounds that include those containing nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and
25 immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

Also provided herein are anti-idiotypic antibodies that mimic an
30 immunogenic portion of an ovarian carcinoma protein. Such antibodies may be raised against an antibody, or antigen-binding fragment thereof, that specifically binds to an

immunogenic portion of an ovarian carcinoma protein, using well known techniques. Anti-idiotypic antibodies that mimic an immunogenic portion of an ovarian carcinoma protein are those antibodies that bind to an antibody, or antigen-binding fragment thereof, that specifically binds to an immunogenic portion of an ovarian carcinoma protein, as described herein.

T Cells

Immunotherapeutic compositions may also, or alternatively, comprise T cells specific for an ovarian carcinoma protein. Such cells may generally be prepared *in vitro* or *ex vivo*, using standard procedures. For example, T cells may be present within (or isolated from) bone marrow, peripheral blood or a fraction of bone marrow or peripheral blood of a mammal, such as a patient, using a commercially available cell separation system, such as the CEPRATE™ system, available from CellPro Inc., Bothell WA (see also U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). Alternatively, T cells may be derived from related or unrelated humans, non-human animals, cell lines or cultures.

T cells may be stimulated with an ovarian carcinoma polypeptide, polynucleotide encoding an ovarian carcinoma polypeptide and/or an antigen presenting cell (APC) that expresses such a polypeptide. Such stimulation is performed under conditions and for a time sufficient to permit the generation of T cells that are specific for the polypeptide. Preferably, an ovarian carcinoma polypeptide or polynucleotide is present within a delivery vehicle, such as a microsphere, to facilitate the generation of specific T cells.

T cells are considered to be specific for an ovarian carcinoma polypeptide if the T cells kill target cells coated with an ovarian carcinoma polypeptide or expressing a gene encoding such a polypeptide. T cell specificity may be evaluated using any of a variety of standard techniques. For example, within a chromium release assay or proliferation assay, a stimulation index of more than two fold increase in lysis and/or proliferation, compared to negative controls, indicates T cell specificity. Such assays may be performed, for example, as described in Chen et al., *Cancer Res.* 54:1065-1070, 1994. Alternatively, detection of the proliferation of T cells may be

accomplished by a variety of known techniques. For example, T cell proliferation can be detected by measuring an increased rate of DNA synthesis (e.g., by pulse-labeling cultures of T cells with tritiated thymidine and measuring the amount of tritiated thymidine incorporated into DNA). Contact with an ovarian carcinoma polypeptide (200 ng/ml - 100 µg/ml, preferably 100 ng/ml - 25 µg/ml) for 3 - 7 days should result in at least a two fold increase in proliferation of the T cells and/or contact as described above for 2-3 hours should result in activation of the T cells, as measured using standard cytokine assays in which a two fold increase in the level of cytokine release (e.g., TNF or IFN-γ) is indicative of T cell activation (see Coligan et al., Current Protocols in Immunology, vol. 1, Wiley Interscience (Greene 1998). T cells that have been activated in response to an ovarian carcinoma polypeptide, polynucleotide or ovarian carcinoma polypeptide-expressing APC may be CD4⁺ and/or CD8⁺. Ovarian carcinoma polypeptide-specific T cells may be expanded using standard techniques. Within preferred embodiments, the T cells are derived from a patient or a related or unrelated donor and are administered to the patient following stimulation and expansion.

For therapeutic purposes, CD4⁺ or CD8⁺ T cells that proliferate in response to an ovarian carcinoma polypeptide, polynucleotide or APC can be expanded in number either *in vitro* or *in vivo*. Proliferation of such T cells *in vitro* may be accomplished in a variety of ways. For example, the T cells can be re-exposed to an ovarian carcinoma polypeptide, with or without the addition of T cell growth factors, such as interleukin-2, and/or stimulator cells that synthesize an ovarian carcinoma polypeptide. Alternatively, one or more T cells that proliferate in the presence of an ovarian carcinoma polypeptide can be expanded in number by cloning. Methods for cloning cells are well known in the art, and include limiting dilution. Following expansion, the cells may be administered back to the patient as described, for example, by Chang et al., *Crit. Rev. Oncol. Hematol.* 22:213, 1996.

Pharmaceutical Compositions and Vaccines

Within certain aspects, polypeptides, polynucleotides, binding agents and/or immune system cells as described herein may be incorporated into

pharmaceutical compositions or vaccines. Pharmaceutical compositions comprise one or more such compounds or cells and a physiologically acceptable carrier. Vaccines may comprise one or more such compounds or cells and a non-specific immune response enhancer. A non-specific immune response enhancer may be any substance
5 that enhances an immune response to an exogenous antigen. Examples of non-specific immune response enhancers include adjuvants, biodegradable microspheres (e.g., polylactic galactide) and liposomes (into which the compound is incorporated; see e.g., Fullerton, U.S. Patent No. 4,235,877). Vaccine preparation is generally described in, for example, M.F. Powell and M.J. Newman, eds., "Vaccine Design (the subunit and
10 adjuvant approach)," Plenum Press (NY, 1995). Pharmaceutical compositions and vaccines within the scope of the present invention may also contain other compounds, which may be biologically active or inactive. For example, one or more immunogenic portions of other tumor antigens may be present, either incorporated into a fusion polypeptide or as a separate compound within the composition or vaccine.

15 A pharmaceutical composition or vaccine may contain DNA encoding one or more of the polypeptides as described above, such that the polypeptide is generated *in situ*. As noted above, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Appropriate nucleic acid
20 expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter and terminating signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface. In a preferred embodiment, the DNA may be introduced using a viral expression system (e.g., vaccinia or other pox
25 virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *PNAS* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651;
30 EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *PNAS* 91:215-219, 1994; Kass-Eisler et al.,

PNAS 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in Ulmer et al., *Science* 259:1745-1749,
5 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier
10 will vary depending on the mode of administration. Compositions of the present invention may be formulated for any appropriate manner of administration, including for example, topical, oral, nasal, intravenous, intracranial, intraperitoneal, subcutaneous or intramuscular administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer.
15 For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactate polyglycolate) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for
20 example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Such compositions may also comprise buffers (e.g., neutral buffered saline or phosphate buffered saline), carbohydrates (e.g., glucose, mannose, sucrose or dextrans), mannitol, proteins, polypeptides or amino acids such as glycine, antioxidants, chelating agents such as EDTA or glutathione, adjuvants (e.g., aluminum hydroxide)
25 and/or preservatives. Alternatively, compositions of the present invention may be formulated as a lyophilizate. Compounds may also be encapsulated within liposomes using well known technology.

Any of a variety of non-specific immune response enhancers may be employed in the vaccines of this invention. For example, an adjuvant may be included.
30 Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune

responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Suitable adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI), Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ), alum, biodegradable
5 microspheres, monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF or interleukin-2, -7, or -12, may also be used as adjuvants.

Within the vaccines provided herein, the adjuvant composition is preferably designed to induce an immune response predominantly of the Th1 type. High levels of Th1-type cytokines (e.g., IFN- γ , IL-2 and IL-12) tend to favor the
10 induction of cell mediated immune responses to an administered antigen. In contrast, high levels of Th2-type cytokines (e.g., IL-4, IL-5, IL-6, IL-10 and TNF- β) tend to favor the induction of humoral immune responses. Following application of a vaccine as provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly
15 Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman, *Ann. Rev. Immunol.* 7:145-173, 1989.

Preferred adjuvants for use in eliciting a predominantly Th1-type
20 response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A (3D-MPL), together with an aluminum salt. MPL adjuvants are available from Ribi ImmunoChem Research Inc. (Hamilton, MT; see US Patent Nos. 4,436,727; 4,877,611; 4,866,034 and 4,912,094). Also preferred is AS-2 (SmithKline Beecham). CpG-containing oligonucleotides (in which the CpG
25 dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555. Another preferred adjuvant is a saponin, preferably QS21, which may be used alone or in combination with other adjuvants. For example, an enhanced system involves the combination of a monophosphoryl lipid A and saponin derivative, such as the
30 combination of QS21 and 3D-MPL as described in WO 94/00153, or a less reactogenic composition where the QS21 is quenched with cholesterol, as described in WO

96/33739. Other preferred formulations comprises an oil-in-water emulsion and tocopherol. A particularly potent adjuvant formulation involving QS21, 3D-MPL and tocopherol in an oil-in-water emulsion is described in WO 95/17210. Any vaccine provided herein may be prepared using well known methods that result in a combination
5 of antigen, immune response enhancer and a suitable carrier or excipient.

The compositions described herein may be administered as part of a sustained release formulation (*i.e.*, a formulation such as a capsule or sponge that effects a slow release of compound following administration). Such formulations may generally be prepared using well known technology and administered by, for example,
10 oral, rectal or subcutaneous implantation, or by implantation at the desired target site. Sustained-release formulations may contain a polypeptide, polynucleotide or antibody dispersed in a carrier matrix and/or contained within a reservoir surrounded by a rate controlling membrane. Carriers for use within such formulations are biocompatible, and may also be biodegradable; preferably the formulation provides a relatively constant
15 level of active component release. The amount of active compound contained within a sustained release formulation depends upon the site of implantation, the rate and expected duration of release and the nature of the condition to be treated or prevented.

Any of a variety of delivery vehicles may be employed within pharmaceutical compositions and vaccines to facilitate production of an antigen-specific
20 immune response that targets tumor cells. Delivery vehicles include antigen presenting cells (APCs), such as dendritic cells, macrophages, B cells, monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the antigen, to improve activation and/or maintenance of the T cell response, to have anti-tumor effects *per se*
25 and/or to be immunologically compatible with the receiver (*i.e.*, matched HLA haplotype). APCs may generally be isolated from any of a variety of biological fluids and organs, including tumor and peritumoral tissues, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

Certain preferred embodiments of the present invention use dendritic
30 cells or progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, *Nature* 392:245-251, 1998) and have been shown to

be effective as a physiological adjuvant for eliciting prophylactic or therapeutic antitumor immunity (*see* Timmerman and Levy, *Ann. Rev. Med.* 50:507-529, 1999). In general, dendritic cells may be identified based on their typical shape (stellate *in situ*, with marked cytoplasmic processes (dendrites) visible *in vitro*) and based on the lack of differentiation markers of B cells (CD19 and CD20), T cells (CD3), monocytes (CD14) and natural killer cells (CD56), as determined using standard assays. Dendritic cells may, of course, be engineered to express specific cell-surface receptors or ligands that are not commonly found on dendritic cells *in vivo* or *ex vivo*, and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within a vaccine (*see* Zitvogel et al., *Nature Med.* 4:594-600, 1998).

Dendritic cells and progenitors may be obtained from peripheral blood, bone marrow, tumor-infiltrating cells, peritumoral tissues-infiltrating cells, lymph nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated *ex vivo* by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNF α to cultures of monocytes harvested from peripheral blood. Alternatively, CD34 positive cells harvested from peripheral blood, umbilical cord blood or bone marrow may be differentiated into dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNF α , CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce maturation and proliferation of dendritic cells.

Dendritic cells are conveniently categorized as "immature" and "mature" cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this nomenclature should not be construed to exclude all possible intermediate stages of differentiation. Immature dendritic cells are characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fc γ receptor, mannose receptor and DEC-205 marker. The mature phenotype is typically characterized by a lower expression of these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and class II MHC, adhesion molecules (*e.g.*, CD54 and CD11) and costimulatory molecules (*e.g.*, CD40, CD80 and CD86).

APCs may generally be transfected with a polynucleotide encoding a ovarian carcinoma antigen (or portion or other variant thereof) such that the antigen, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place *ex vivo*, and a composition or vaccine comprising such transfected cells
5 may then be used for therapeutic purposes, as described herein. Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be administered to a patient, resulting in transfection that occurs *in vivo*. *In vivo* and *ex vivo* transfection of dendritic cells, for example, may generally be performed using any methods known in the art, such as those described in WO 97/24447, or the gene gun
10 approach described by Mahvi et al., *Immunology and cell Biology* 75:456-460, 1997. Antigen loading of dendritic cells may be achieved by incubating dendritic cells or progenitor cells with the polypeptide, DNA (naked or within a plasmid vector) or RNA; or with antigen-expressing recombinant bacterium or viruses (*e.g.*, vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide may be covalently
15 conjugated to an immunological partner that provides T cell help (*e.g.*, a carrier molecule). Alternatively, a dendritic cell may be pulsed with a non-conjugated immunological partner, separately or in the presence of the polypeptide.

Cancer Therapy

In further aspects of the present invention, the compositions described
20 herein may be used for immunotherapy of cancer, such as ovarian cancer. Within such methods, pharmaceutical compositions and vaccines are typically administered to a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may or may not be afflicted with cancer. Accordingly, the above pharmaceutical compositions and vaccines may be used to prevent the development of a
25 cancer or to treat a patient afflicted with a cancer. Within certain preferred embodiments, a patient is afflicted with ovarian cancer. Such cancer may be diagnosed using criteria generally accepted in the art, including the presence of a malignant tumor. Pharmaceutical compositions and vaccines may be administered either prior to or following surgical removal of primary tumors and/or treatment such as administration
30 of radiotherapy or conventional chemotherapeutic drugs.

Within certain embodiments, immunotherapy may be active immunotherapy, in which treatment relies on the *in vivo* stimulation of the endogenous host immune system to react against tumors with the administration of immune response-modifying agents (such as tumor vaccines, bacterial adjuvants and/or cytokines).

Within other embodiments, immunotherapy may be passive immunotherapy, in which treatment involves the delivery of agents with established tumor-immune reactivity (such as effector cells or antibodies) that can directly or indirectly mediate antitumor effects and does not necessarily depend on an intact host immune system. Examples of effector cells include T lymphocytes (such as CD8⁺ cytotoxic T lymphocytes and CD4⁺ T-helper tumor-infiltrating lymphocytes), killer cells (such as Natural Killer cells and lymphokine-activated killer cells), B cells and antigen-presenting cells (such as dendritic cells and macrophages) expressing a polypeptide provided herein. T cell receptors and antibody receptors specific for the polypeptides recited herein may be cloned, expressed and transferred into other vectors or effector cells for adoptive immunotherapy. The polypeptides provided herein may also be used to generate antibodies or anti-idiotypic antibodies (as described above and in U.S. Patent No. 4,918,164) for passive immunotherapy.

Effector cells may generally be obtained in sufficient quantities for adoptive immunotherapy by growth *in vitro*, as described herein. Culture conditions for expanding single antigen-specific effector cells to several billion in number with retention of antigen recognition *in vivo* are well known in the art. Such *in vitro* culture conditions typically use intermittent stimulation with antigen, often in the presence of cytokines (such as IL-2) and non-dividing feeder cells. As noted above, immunoreactive polypeptides as provided herein may be used to rapidly expand antigen-specific T cell cultures in order to generate a sufficient number of cells for immunotherapy. In particular, antigen-presenting cells, such as dendritic, macrophage or B cells, may be pulsed with immunoreactive polypeptides or transfected with one or more polynucleotides using standard techniques well known in the art. For example, antigen-presenting cells can be transfected with a polynucleotide having a promoter appropriate for increasing expression in a recombinant virus or other expression system.

Cultured effector cells for use in therapy must be able to grow and distribute widely, and to survive long term *in vivo*. Studies have shown that cultured effector cells can be induced to grow *in vivo* and to survive long term in substantial numbers by repeated stimulation with antigen supplemented with IL-2 (*see*, for example, Cheever et al.,
5 *Immunological Reviews* 157:177, 1997).

Alternatively, a vector expressing a polypeptide recited herein may be introduced into stem cells taken from a patient and clonally propagated *in vitro* for autologous transplant back into the same patient.

Routes and frequency of administration, as well as dosage, will vary
10 from individual to individual, and may be readily established using standard techniques. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g.*, intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration), orally or in the bed of a resected tumor. Preferably, between 1 and 10 doses may be administered over a 52 week period. Preferably, 6 doses are
15 administered, at intervals of 1 month, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of a compound that, when administered as described above, is capable of promoting an anti-tumor immune response, and is at least 10-50% above the basal (*i.e.*, untreated) level.. Such response can be monitored by measuring
20 the anti-tumor antibodies in a patient or by vaccine-dependent generation of cytolytic effector cells capable of killing the patient's tumor cells *in vitro*. Such vaccines should also be capable of causing an immune response that leads to an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial or longer disease-free survival) in vaccinated patients as compared to non-vaccinated patients. In general, for
25 pharmaceutical compositions and vaccines comprising one or more polypeptides, the amount of each polypeptide present in a dose ranges from about 100 µg to 5 mg per kg of host. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

In general, an appropriate dosage and treatment regimen provides the
30 active compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such a response can be monitored by establishing an improved clinical

outcome (*e.g.*, more frequent remissions, complete or partial, or longer disease-free survival) in treated patients as compared to non-treated patients. Increases in preexisting immune responses to an ovarian carcinoma antigen generally correlate with an improved clinical outcome. Such immune responses may generally be evaluated
5 using standard proliferation, cytotoxicity or cytokine assays, which may be performed using samples obtained from a patient before and after treatment.

Screens for Identifying Secreted Ovarian Carcinoma Antigens

The present invention provides methods for identifying secreted tumor antigens. Within such methods, tumors are implanted into immunodeficient animals
10 such as SCID mice and maintained for a time sufficient to permit secretion of tumor antigens into serum. In general, tumors may be implanted subcutaneously or within the gonadal fat pad of an immunodeficient animal and maintained for 1-9 months, preferably 1-4 months. Implantation may generally be performed as described in WO 97/18300. The serum containing secreted antigens is then used to prepare antisera in
15 immunocompetent mice, using standard techniques and as described herein. Briefly, 50-100 μ L of sera (pooled from three sets of immunodeficient mice, each set bearing a different SCID-derived human ovarian tumor) may be mixed 1:1 (vol:vol) with an appropriate adjuvant, such as RIBI-MPL or MPL + TDM (Sigma Chemical Co., St. Louis, MO) and injected intraperitoneally into syngeneic immunocompetent animals at
20 monthly intervals for a total of 5 months. Antisera from animals immunized in such a manner may be obtained by drawing blood after the third, fourth and fifth immunizations. The resulting antiserum is generally pre-cleared of *E. coli* and phage antigens and used (generally following dilution, such as 1:200) in a serological expression screen.

25 The library is typically an expression library containing cDNAs from one or more tumors of the type that was implanted into SCID mice. This expression library may be prepared in any suitable vector, such as λ -screen (Novagen). cDNAs that encode a polypeptide that reacts with the antiserum may be identified using standard techniques, and sequenced. Such cDNA molecules may be further characterized to

evaluate expression in tumor and normal tissue, and to evaluate antigen secretion in patients.

The methods provided herein have advantages over other methods for tumor antigen discovery. In particular, all antigens identified by such methods should
5 be secreted or released through necrosis of the tumor cells. Such antigens may be present on the surface of tumor cells for an amount of time sufficient to permit targeting and killing by the immune system, following vaccination.

Methods for Detecting Cancer

In general, a cancer may be detected in a patient based on the presence of
10 one or more ovarian carcinoma proteins and/or polynucleotides encoding such proteins in a biological sample (such as blood, sera, urine and/or tumor biopsies) obtained from the patient. In other words, such proteins may be used as markers to indicate the presence or absence of a cancer such as ovarian cancer. In addition, such proteins may be useful for the detection of other cancers. The binding agents provided herein
15 generally permit detection of the level of protein that binds to the agent in the biological sample. Polynucleotide primers and probes may be used to detect the level of mRNA encoding a tumor protein, which is also indicative of the presence or absence of a cancer. In general, an ovarian carcinoma-associated sequence should be present at a level that is at least three fold higher in tumor tissue than in normal tissue

20 There are a variety of assay formats known to those of ordinary skill in the art for using a binding agent to detect polypeptide markers in a sample. *See, e.g.,* Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, the presence or absence of a cancer in a patient may be determined by (a) contacting a biological sample obtained from a patient with a binding agent; (b)
25 detecting in the sample a level of polypeptide that binds to the binding agent; and (c) comparing the level of polypeptide with a predetermined cut-off value.

In a preferred embodiment, the assay involves the use of binding agent immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a detection
30 reagent that contains a reporter group and specifically binds to the binding

agent/polypeptide complex. Such detection reagents may comprise, for example, a binding agent that specifically binds to the polypeptide or an antibody or other agent that specifically binds to the binding agent, such as an anti-immunoglobulin, protein G, protein A or a lectin. Alternatively, a competitive assay may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding agent after incubation of the binding agent with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding agent is indicative of the reactivity of the sample with the immobilized binding agent. Suitable polypeptides for use within such assays include full length ovarian carcinoma proteins and portions thereof to which the binding agent binds, as described above.

The solid support may be any material known to those of ordinary skill in the art to which the tumor protein may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the agent and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10 μ g, and preferably about 100 ng to about 1 μ g, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports
5 having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (*see, e.g.,* Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay.
10 This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a detection reagent (preferably a second antibody capable of binding to a
15 different site on the polypeptide) containing a reporter group is added. The amount of detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically
20 blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20™ (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact
25 time (*i.e.,* incubation time) is a period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with ovarian cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve
30 equilibrium may be readily determined by assaying the level of binding that occurs over

a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second
5 antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include those groups recited above.

The detection reagent is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of
10 binding that occurs over a period of time. Unbound detection reagent is then removed and bound detection reagent is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups
15 and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

20 To determine the presence or absence of a cancer, such as ovarian cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value for the detection of a cancer is the average mean signal obtained when the immobilized antibody is incubated with
25 samples from patients without the cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for the cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985,
30 p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity)

that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for a cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the binding agent is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized binding agent as the sample passes through the membrane. A second, labeled binding agent then binds to the binding agent-polypeptide complex as a solution containing the second binding agent flows through the membrane. The detection of bound second binding agent may then be performed as described above. In the strip test format, one end of the membrane to which binding agent is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second binding agent and to the area of immobilized binding agent. Concentration of second binding agent at the area of immobilized antibody indicates the presence of a cancer. Typically, the concentration of second binding agent at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of binding agent immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferred binding agents for use in such assays are antibodies and antigen-binding fragments thereof. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 μ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the tumor proteins or binding agents of the present invention. The above descriptions are intended to be exemplary only. For example, it will be apparent to those of ordinary skill in the art that the above protocols may be readily modified to use
5 ovarian carcinoma polypeptides to detect antibodies that bind to such polypeptides in a biological sample. The detection of such ovarian carcinoma protein specific antibodies may correlate with the presence of a cancer.

A cancer may also, or alternatively, be detected based on the presence of T cells that specifically react with an ovarian carcinoma protein in a biological sample.
10 Within certain methods, a biological sample comprising $CD4^+$ and/or $CD8^+$ T cells isolated from a patient is incubated with an ovarian carcinoma protein, a polynucleotide encoding such a polypeptide and/or an APC that expresses at least an immunogenic portion of such a polypeptide, and the presence or absence of specific activation of the T cells is detected. Suitable biological samples include, but are not limited to, isolated
15 T cells. For example, T cells may be isolated from a patient by routine techniques (such as by Ficoll/Hypaque density gradient centrifugation of peripheral blood lymphocytes). T cells may be incubated *in vitro* for 2-9 days (typically 4 days) at 37°C with an ovarian carcinoma protein (*e.g.*, 5 - 25 µg/ml). It may be desirable to incubate another aliquot of a T cell sample in the absence of ovarian carcinoma protein to serve as a control. For
20 $CD4^+$ T cells, activation is preferably detected by evaluating proliferation of the T cells. For $CD8^+$ T cells, activation is preferably detected by evaluating cytolytic activity. A level of proliferation that is at least two fold greater and/or a level of cytolytic activity that is at least 20% greater than in disease-free patients indicates the presence of a cancer in the patient.

25 As noted above, a cancer may also, or alternatively, be detected based on the level of mRNA encoding an ovarian carcinoma protein in a biological sample. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify a portion of an ovarian carcinoma protein cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is
30 specific for (*i.e.*, hybridizes to) a polynucleotide encoding the ovarian carcinoma protein. The amplified cDNA is then separated and detected using techniques well

known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes that specifically hybridize to a polynucleotide encoding an ovarian carcinoma protein may be used in a hybridization assay to detect the presence of polynucleotide encoding the tumor protein in a biological sample.

5 To permit hybridization under assay conditions, oligonucleotide primers and probes should comprise an oligonucleotide sequence that has at least about 60%, preferably at least about 75% and more preferably at least about 90%, identity to a portion of a polynucleotide encoding an ovarian carcinoma protein that is at least 10 nucleotides, and preferably at least 20 nucleotides, in length. Preferably,
10 oligonucleotide primers and/or probes hybridize to a polynucleotide encoding a polypeptide described herein under moderately stringent conditions, as defined above. Oligonucleotide primers and/or probes which may be usefully employed in the diagnostic methods described herein preferably are at least 10-40 nucleotides in length. In a preferred embodiment, the oligonucleotide primers comprise at least 10 contiguous
15 nucleotides, more preferably at least 15 contiguous nucleotides, of a DNA molecule having a sequence provided herein. Techniques for both PCR based assays and hybridization assays are well known in the art (*see*, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989).

20 One preferred assay employs RT-PCR, in which PCR is applied in conjunction with reverse transcription. Typically, RNA is extracted from a biological sample such as a biopsy tissue and is reverse transcribed to produce cDNA molecules. PCR amplification using at least one specific primer generates a cDNA molecule, which may be separated and visualized using, for example, gel electrophoresis. Amplification
25 may be performed on biological samples taken from a test patient and from an individual who is not afflicted with a cancer. The amplification reaction may be performed on several dilutions of cDNA spanning two orders of magnitude. A two-fold or greater increase in expression in several dilutions of the test patient sample as compared to the same dilutions of the non-cancerous sample is typically considered
30 positive.

In another embodiment, ovarian carcinoma proteins and polynucleotides encoding such proteins may be used as markers for monitoring the progression of cancer. In this embodiment, assays as described above for the diagnosis of a cancer may be performed over time, and the change in the level of reactive polypeptide(s) evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, a cancer is progressing in those patients in whom the level of polypeptide detected by the binding agent increases over time. In contrast, the cancer is not progressing when the level of reactive polypeptide either remains constant or decreases with time.

10 Certain *in vivo* diagnostic assays may be performed directly on a tumor. One such assay involves contacting tumor cells with a binding agent. The bound binding agent may then be detected directly or indirectly via a reporter group. Such binding agents may also be used in histological applications. Alternatively, polynucleotide probes may be used within such applications.

15 As noted above, to improve sensitivity, multiple ovarian carcinoma protein markers may be assayed within a given sample. It will be apparent that binding agents specific for different proteins provided herein may be combined within a single assay. Further, multiple primers or probes may be used concurrently. The selection of tumor protein markers may be based on routine experiments to determine combinations
20 that results in optimal sensitivity. In addition, or alternatively, assays for tumor proteins provided herein may be combined with assays for other known tumor antigens.

Diagnostic Kits

The present invention further provides kits for use within any of the above diagnostic methods. Such kits typically comprise two or more components
25 necessary for performing a diagnostic assay. Components may be compounds, reagents, containers and/or equipment. For example, one container within a kit may contain a monoclonal antibody or fragment thereof that specifically binds to an ovarian carcinoma protein. Such antibodies or fragments may be provided attached to a support material, as described above. One or more additional containers may enclose elements, such as
30 reagents or buffers, to be used in the assay. Such kits may also, or alternatively, contain

a detection reagent as described above that contains a reporter group suitable for direct or indirect detection of antibody binding.

Alternatively, a kit may be designed to detect the level of mRNA encoding an ovarian carcinoma protein in a biological sample. Such kits generally
5 comprise at least one oligonucleotide probe or primer, as described above, that hybridizes to a polynucleotide encoding an ovarian carcinoma protein. Such an oligonucleotide may be used, for example, within a PCR or hybridization assay. Additional components that may be present within such kits include a second
10 polynucleotide encoding an ovarian carcinoma protein.

The following Examples are offered by way of illustration and not by way of limitation.

EXAMPLES

EXAMPLE 1

IDENTIFICATION OF REPRESENTATIVE OVARIAN CARCINOMA PROTEIN CDNAS

This Example illustrates the identification of cDNA molecules encoding
5 ovarian carcinoma proteins.

Anti-SCID mouse sera (generated against sera from SCID mice carrying
late passage ovarian carcinoma) was pre-cleared of E. coli and phage antigens and used
at a 1:200 dilution in a serological expression screen. The library screened was made
from a SCID-derived human ovarian tumor (OV9334) using a directional RH oligo(dT)
10 priming cDNA library construction kit and the λ Screen vector (Novagen). A
bacteriophage lambda screen was employed. Approximately 400,000 pfu of the
amplified OV9334 library were screened.

196 positive clones were isolated. Certain sequences that appear to be
novel are provided in Figures 1A-1S and SEQ ID NO:1 to 71. Three complete insert
15 sequences are shown in Figures 2A-2C (SEQ ID NO:72 to 74). Other clones having
known sequences are presented in Figures 15A-15EEE (SEQ ID NO:82 to 310).
Database searches identified the following sequences that were substantially identical to
the sequences presented in Figures 15A-15EEE.

These clones were further characterized using microarray technology to
20 determine mRNA expression levels in a variety of tumor and normal tissues. Such
analyses were performed using a Synteni (Palo Alto, CA) microarray, according to the
manufacturer's instructions. PCR amplification products were arrayed on slides, with
each product occupying a unique location in the array. mRNA was extracted from the
tissue sample to be tested, reverse transcribed and fluorescent-labeled cDNA probes
25 were generated. The microarrays were probed with the labeled cDNA probes and the
slides were scanned to measure fluorescence intensity. Data was analyzed using
Synteni's provided GEMtools software. The results for one clone (13695, also referred
to as O8E) are shown in Figure 3.

EXAMPLE 2

IDENTIFICATION OF OVARIAN CARCINOMA cDNAs USING MICROARRAY TECHNOLOGY

This Example illustrates the identification of ovarian carcinoma polynucleotides by PCR subtraction and microarray analysis. Microarrays of cDNAs
5 were analyzed for ovarian tumor-specific expression using a Synteni (Palo Alto, CA) microarray, according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997).

A PCR subtraction was performed using a tester comprising cDNA of
10 four ovarian tumors (three of which were metastatic tumors) and a driver of cDNA from five normal tissues (adrenal gland, lung, pancreas, spleen and brain). cDNA fragments recovered from this subtraction were subjected to DNA microarray analysis where the fragments were PCR amplified, adhered to chips and hybridized with fluorescently labeled probes derived from mRNAs of human ovarian tumors and a variety of normal
15 human tissues. In this analysis, the slides were scanned and the fluorescence intensity was measured, and the data were analyzed using Synteni's GEMtools software. In general, sequences showing at least a 5-fold increase in expression in tumor cells (relative to normal cells) were considered ovarian tumor antigens. The fluorescent results were analyzed and clones that displayed increased expression in ovarian tumors
20 were further characterized by DNA sequencing and database searches to determine the novelty of the sequences.

Using such assays, an ovarian tumor antigen was identified that is a splice fusion between the human T-cell leukemia virus type I oncoprotein TAX (*see* Jin et al., *Cell* 93:81-91, 1998) and an extracellular matrix protein called osteonectin. A
25 splice junction sequence exists at the fusion point. The sequence of this clone is presented in Figure 4 and SEQ ID NO:75. Osteonectin, unspliced and unaltered, was also identified from such assays independently.

Further clones identified by this method are referred to herein as 3f, 6b, 8e, 8h, 12c and 12h. Sequences of these clones are shown in Figures 5 to 9 and SEQ ID
30 NO:76 to 81. Microarray analyses were performed as described above, and are presented in Figures 10 to 14. A full length sequence encompassing clones 3f, 6b, 8e

and 12h was obtained by screening an ovarian tumor (SCID-derived) cDNA library. This 2996 base pair sequence (designated O772P) is presented in SEQ ID NO:311, and the encoded 914 amino acid protein sequence is shown in SEQ ID NO:312. PSORT analysis indicates a Type 1a transmembrane protein localized to the plasma membrane.

- 5 In addition to certain of the sequences described above, this screen identified the following sequences which are described in detail in Table 1:

Table 1

Sequence	Comments
OV4vG11 (SEQ ID NO:313)	human clone 1119D9 on chromosome 20p12
OV4vB11 (SEQ ID NO:314)	human UWGC:y14c094 from chromosome 6p21
OV4vD9 (SEQ ID NO:315)	human clone 1049G16 chromosome 20q12-13.2
OV4vD5 (SEQ ID NO:316)	human KIAA0014 gene
OV4vC2 (SEQ ID NO:317)	human KIAA0084 gene
OV4vF3 (SEQ ID NO:318)	human chromosome 19 cosmid R31167
OV4VC1 (SEQ ID NO:319)	novel
OV4vH3 (SEQ ID NO:320)	novel
OV4vD2 (SEQ ID NO:321)	novel
O815P (SEQ ID NO:322)	novel
OV4vC12 (SEQ ID NO:323)	novel
OV4vA4 (SEQ ID NO:324)	novel
OV4vA3 (SEQ ID NO:325)	novel
OV4v2A5 (SEQ ID NO:326)	novel
O819P (SEQ ID NO:327)	novel
O818P (SEQ ID NO:328)	novel
O817P (SEQ ID NO:329)	novel
O816P (SEQ ID NO:330)	novel
Ov4vC5 (SEQ ID NO:331)	novel
21721 (SEQ ID NO:332)	human lumican
21719 (SEQ ID NO:333)	human retinoic acid-binding protein II
21717 (SEQ ID NO:334)	human26S proteasome ATPase subunit
21654 (SEQ ID NO:335)	human copine I
21627 (SEQ ID NO:336)	human neuron specific gamma-2 enolase

Sequence	Comments
21623 (SEQ ID NO:337)	human geranylgeranyl transferase II
21621 (SEQ ID NO:338)	human cyclin-dependent protein kinase
21616 (SEQ ID NO:339)	human prepro-megakaryocyte potentiating factor
21612 (SEQ ID NO:340)	human UPH1
21558 (SEQ ID NO:341)	human RalGDS-like 2 (RGL2)
21555 (SEQ ID NO:342)	human autoantigen P542
21548 (SEQ ID NO:343)	human actin-related protein (ARP2)
21462 (SEQ ID NO:344)	human huntingtin interacting protein
21441 (SEQ ID NO:345)	human 90K product (tumor associated antigen)
21439 (SEQ ID NO:346)	human guanine nucleotide regulator protein (tim1)
21438 (SEQ ID NO:347)	human Ku autoimmune (p70/p80) antigen
21237 (SEQ ID NO:348)	human S-laminin
21436 (SEQ ID NO:349)	human ribophorin I
21435 (SEQ ID NO:350)	human cytoplasmic chaperonin hTRiC5
21425 (SEQ ID NO:351)	humanEMX2
21423 (SEQ ID NO:352)	human p87/p89 gene
21419 (SEQ ID NO:353)	human HPBR11-7
21252 (SEQ ID NO:354)	human T1-227H
21251 (SEQ ID NO:355)	human cullin I
21247 (SEQ ID NO:356)	kunitz type protease inhibitor (KOP)
21244-1 (SEQ ID NO:357)	human protein tyrosine phosphatase receptor F (PTPRF)
21718 (SEQ ID NO:358)	human LTR repeat
OV2-90 (SEQ ID NO:359)	novel
Human zinc finger (SEQ ID NO:360)	
Human polyA binding protein (SEQ ID NO:361)	
Human pleiotrophin (SEQ ID NO:362)	
Human PAC clone 278C19 (SEQ ID NO:363)	
Human LLRep3 (SEQ ID NO:364)	
Human Kunitz type protease inhib (SEQ ID NO:365)	
Human KIAA0106 gene (SEQ ID NO:366)	
Human keratin (SEQ ID NO:367)	
Human HIV-1TAR (SEQ ID NO:368)	
Human glia derived nexin (SEQ ID NO:369)	

Sequence	Comments
Human fibronectin (SEQ ID NO:370)	
Human ECMproBM40 (SEQ ID NO:371)	
Human collagen (SEQ ID NO:372)	
Human alpha enolase (SEQ ID NO:373)	
Human aldolase (SEQ ID NO:374)	
Human transf growth factor BIG H3 (SEQ ID NO:375)	
Human SPARC osteonectin (SEQ ID NO:376)	
Human SLP1 leucocyte protease (SEQ ID NO:377)	
Human mitochondrial ATP synth (SEQ ID NO:378)	
Human DNA seq clone 461P17 (SEQ ID NO:379)	
Human dbpB pro Y box (SEQ ID NO:380)	
Human 40 kDa keratin (SEQ ID NO:381)	
Human arginosuccinate synth (SEQ ID NO:382)	
Human acidic ribosomal phosphoprotein (SEQ ID NO:383)	
Human colon carcinoma laminin binding pro (SEQ ID NO:384)	

This screen further identified multiple forms of the clone O772P, referred to herein as 21013, 21003 and 21008. PSORT analysis indicates that 21003 (SEQ ID NO:386; translated as SEQ ID NO:389) and 21008 (SEQ ID NO:387; translated as SEQ ID NO:390) represent Type 1a transmembrane protein forms of

5 O772P. 21013 (SEQ ID NO:385; translated as SEQ ID NO:388) appears to be a truncated form of the protein and is predicted by PSORT analysis to be a secreted protein.

Additional sequence analysis resulted in a full length clone for O8E (2627 bp, which agrees with the message size observed by Northern analysis; SEQ ID

10 NO:391). This nucleotide sequence was obtained as follows: the original O8E sequence (OrigO8Econs) was found to overlap by 33 nucleotides with a sequence from an EST clone (IMAGE#1987589). This clone provided 1042 additional nucleotides upstream of the original O8E sequence. The link between the EST and O8E was confirmed by sequencing multiple PCR fragments generated from an ovary primary tumor library

15 using primers to the unique EST and the O8E sequence (ESTxO8EPCR). Full length status was further indicated when anchored PCR from the ovary tumor library gave

several clones (AnchoredPCR cons) that all terminated upstream of the putative start methionine, but failed to yield any additional sequence information. Figure 16 presents a diagram that illustrates the location of each partial sequence within the full length O8E sequence.

5 Two protein sequences may be translated from the full length O8E. For "a" (SEQ ID NO:393) begins with a putative start methionine. A second form "b" (SEQ ID NO:392) includes 27 additional upstream residues to the 5' end of the nucleotide sequence.

EXAMPLE 3

10 This example discloses the identification and characterization of antibody epitopes recognized by the O8E polyclonal anti-sera.

Rabbit anti-sera was raised against E. coli derived O8E recombinant protein and tested for antibody epitope recognition against 20 or 21 mer peptides that correspond to the O8E amino acid sequence. Peptides spanning amino acid regions 31
15 to 65, 76 to 110, 136 to 200 and 226 to 245 of the full length O8E protein were recognized by an acid eluted peak and/or a salt eluted peak from affinity purified anti-O8E sera. Thus, the corresponding amino acid sequences of the above peptides constitute the antibody epitopes recognized by affinity purified anti-O8E antibodies.

ELISA analysis of anti-O8E rabbit sera is shown in Figure 23, and ELISA
20 analysis of affinity purified rabbit anti-O8E polyclonal antibody is shown in Figure 24.

For epitope mapping, 20 or 21 mer peptides corresponding to the O8E protein were synthesized. For antibody affinity purification, rabbit anti-O8E sera was run over an O8E-sepharose column, then antibody was eluted with a salt buffer containing 0.5 M NaCl and 20 mM PO₄, followed by an acid elution step using 0.2 M
25 Glycine, pH 2.3. Purified antibody was neutralized by the addition of 1M Tris, pH 8 and buffer exchanged into phosphate buffered saline (PBS). For enzyme linked immunosorbant assay (ELISA) analysis, O8E peptides and O8E recombinant protein were coated onto 96 well flat bottom plates at 2 µg/ml for 2 hours at room temperature (RT). Plates were then washed 5 times with PBS + 0.1 % Tween 20 and blocked with
30 PBS + 1 % bovine serum albumin (BSA) for 1 hour. Affinity purified anti-O8E antibody, either an acid or salt eluted fraction, was then added to the wells at 1 µg/ml

and incubated at RT for 1 hr. Plates were again washed, followed by the addition of donkey anti-rabbit-Ig-horseradish peroxidase (HRP) antibody for 1 hour at RT. Plates were washed, then developed by the addition of the chromagenic substrate 3, 3', 5, 5'-tetramethylbenzidine (TMB) (described by Bos *et al.*, *J. of Immunoassay* 2:187-204 (1981); available from Sigma (St. Louis, MO)). The reaction was incubated 15 minutes at RT and then stopped by the addition of 1 N H₂SO₄. Plates were read at an optical density of 450 (OD450) in an automated plate reader. The sequences of peptides corresponding to the OE8 antibody epitopes are disclosed herein as SEQ ID NO: 394-415. Antibody epitopes recognized by the O8E polyclonal anti-sera are disclosed herein in Figure 17.

EXAMPLE 4

This example discloses IHC analysis of O8E expression in ovarian cancer tissue samples.

For immunohistochemistry studies, paraffin-embedded formalin fixed ovarian cancer tissue was sliced into 8 micron sections. Steam heat induced epitope retrieval (SHIER) in 0.1 M sodium citrate buffer (pH 6.0) was used for optimal staining conditions. Sections were incubated with 10% serum/PBS for 5 minutes. Primary antibody (anti-O8E rabbit affinity purified polyclonal antibody) was added to each section for 25 min followed by a 25 min incubation with an anti-rabbit biotinylated antibody. Endogenous peroxidase activity was blocked by three 1.5 min incubations with hydrogen peroxidase. The avidin biotin complex/horse radish peroxidase system was used along with DAB chromogen to visualize antigen expression. Slides were counterstained with hematoxylin. One (papillary serous carcinoma) of six ovarian cancer tissue sections displayed O8E immunoreactivity. Upon optimization of the staining conditions, 4/5 ovarian cancer samples stained positive using the O8E polyclonal antibody. O8E expression was localized to the plasma membrane.

Six ovarian cancer tissues were analyzed with the anti-O8E rabbit polyclonal antibody. One (papillary serous carcinoma) of six ovarian cancer tissue samples stained positive for O8E expression. O8E expression was localized to the surface membrane.

EXAMPLE 5

This example discloses O8E peptides that are predicted to bind HLA-A2 and to be immunogenic for CD8 T cell responses in humans.

Potential HLA-A2 binding peptides of O8E were predicted by using the full-length open-reading frame (ORF) from O8E and running it through "Episeek," a program used to predict MHC binding peptides. The program used is based on the algorithm published by Parker, K.C. *et al.*, *J. Immunol.* 152(1):163-175 (1994) (incorporated by reference herein in its entirety). 10-mer and 9-mer peptides predicted to bind HLA-0201 are disclosed herein as SEQ ID NO: 416-435 and SEQ ID NO: 436-455, respectively.

EXAMPLE 6

This example discloses O8E cell surface expression measured by fluorescence activated cell sorting.

For FACS analysis, cells were washed with ice cold staining buffer (PBS/1% BSA/azide). Next, the cells were incubated for 30 minutes on ice with 10 micrograms/ml of affinity purified rabbit anti-B305D polyclonal antibody. The cells were washed 3 times with staining buffer and then incubated with a 1:100 dilution of a goat anti-rabbit Ig (H+L)-FITC reagent (Southern Biotechnology) for 30 minutes on ice. Following 3 washes, the cells were resuspended in staining buffer containing prodium iodide, a vital stain that allows for identification of permeable cells, and analyzed by FACS. O8E surface expression was confirmed on SKBR3 breast cancer cells and HEK293 cells that stably overexpress the cDNA for O8E. Neither MB415 cells nor HEK293 cells stably transfected with a control irrelevant plasmid DNA showed surface expression of O8E (Figures 18 and 19).

EXAMPLE 7

This example further evaluates the expression and surface localization of O8E.

For expression and purification of antigen used for immunization, O8E expressed in an E. coli recombinant expression system was grown overnight in LB Broth with the appropriate antibiotics at 37°C in a shaking incubator. The next morning,

10 ml of the overnight culture was added to 500 ml of 2x YT plus appropriate antibiotics in a 2L-baffled Erlenmeyer flask. When the Optical Density (at 560 nanometers) of the culture reached 0.4-0.6 the cells were induced with IPTG (1 mM). 4 hours after induction with IPTG the cells were harvested by centrifugation. The cells
5 were then washed with phosphate buffered saline and centrifuged again. The supernatant was discarded and the cells were either frozen for future use or immediately processed. Twenty milliliters of lysis buffer was added to the cell pellets and vortexed. To break open the E. coli cells, this mixture was then run through the French Press at a pressure of 16,000 psi. The cells were then centrifuged again and the supernatant and
10 pellet were checked by SDS-PAGE for the partitioning of the recombinant protein. For protein that localized to the cell pellet, the pellet was resuspended in 10 mM Tris pH 8.0, 1% CHAPS and the inclusion body pellet was washed and centrifuged again. This procedure was repeated twice more. The washed inclusion body pellet was solubilized with either 8 M urea or 6 M guanidine HCl containing 10 mM Tris pH 8.0 plus 10 mM
15 imidazole. The solubilized protein was added to 5 ml of nickel-chelate resin (Qiagen) and incubated for 45 min to 1 hour at room temperature with continuous agitation. After incubation, the resin and protein mixture were poured through a disposable column and the flow through was collected. The column was then washed with 10-20 column volumes of the solubilization buffer. The antigen was then eluted from the column using
20 8M urea, 10 mM tris pH 8.0 and 300 mM imidazole and collected in 3 ml fractions. A SDS-PAGE gel was run to determine which fractions to pool for further purification. As a final purification step, a strong anion exchange resin such as Hi-Prep Q (Biorad) was equilibrated with the appropriate buffer and the pooled fractions from above were loaded onto the column. Each antigen was eluted off of the column with an increasing
25 salt gradient. Fractions were collected as the column was run and another SDS-PAGE gel was run to determine which fractions from the column to pool. The pooled fractions were dialyzed against 10 mM Tris pH 8.0. This material was then evaluated for acceptable purity as determined by SDS-PAGE or HPLC, concentration as determined by Lowry assay or Amino Acid Analysis, identity as determined by amino terminal
30 protein sequence, and endotoxin level as determined by the Limulus (LAL) assay. The

proteins were then vialled after filtration through a 0.22 micron filter and the antigens were frozen until needed for immunization.

For generation of polyclonal anti-sera, 400 micrograms of each prostate antigen was combined with 100 micrograms of muramyl dipeptide (MDP). Equal
5 volume of Incomplete Freund's Adjuvant (IFA) was added and then mixed. Every four weeks animals were boosted with 100 micrograms of antigen mixed with an equal volume of IFA. Seven days following each boost the animal was bled. Sera was generated by incubating the blood at 4°C for 12-24 hours followed by centrifugation.

For characterization of polyclonal antisera, 96 well plates were coated
10 with antigen by incubating with 50 microliters (typically 1 microgram) at 4°C for 20 hrs. 250 microliters of BSA blocking buffer was added to the wells and incubated at RT for 2 hrs. Plates were washed 6 times with PBS/0.01% tween. Anti-O8E rabbit sera or affinity purified anti-O8e antibody was diluted in PBS. Fifty microliters of diluted antibody was added to each well and incubated at RT for 30 min. Plates were washed as
15 described above before 50 microliters of goat anti-rabbit horse radish peroxidase (HRP) at a 1:10000 dilution was added and incubated at RT for 30 min. Plates were washed as described above and 100 microliters of TMB microwell Peroxidase Substrate was added to each well. Following a 15 minute incubation in the dark at room temperature the
20 colorimetric reaction was stopped with 100 microliters of 1N H₂SO₄ and read immediately at 450 nm. All polyclonal antibodies showed immunoreactivity to the O8E antigen.

For recombinant expression in mammalian HEK293 cells, full length O8E cDNA was subcloned into the mammalian expression vectors pcDNA3.1+ and pCEP4 (Invitrogen) which were modified to contain His and FLAG epitope tags,
25 respectively. These constructs were transfected into HEK293 cells (ATCC) using Fugene 6 reagent (Roche). Briefly, HEK293 cells were plated at a density of 100,000 cells/ml in DMEM (Gibco) containing 10% FBS (Hyclone) and grown overnight. The following day, 2 ul of Fugene6 was added to 100 ul of DMEM containing no FBS and incubated for 15 minutes at room temperature. The Fugene6/DMEM mixture was then
30 added to 1ug of O8E/pCEP4 or O8E/pcDNA3.1 plasmid DNA and incubated for 15 minutes at room temperature. The Fugene/DNA mix was then added to the HEK293

cells and incubated for 48-72 hrs at 37°C with 7% CO₂. Cells were rinsed with PBS then collected and pelleted by centrifugation. For Western blot analysis, whole cell lysates were generated by incubating the cells in Triton-X100 containing lysis buffer for 30 minutes on ice. Lysates were then cleared by centrifugation at 10,000rpm for 5 minutes at 4 C. Samples were diluted with SDS-PAGE loading buffer containing beta-mercaptoethanol, then boiled for 10 minutes prior to loading the SDS-PAGE gel. Protein was transferred to nitrocellulose and probed using anti-O8E rabbit polyclonal sera #2333L at a dilution of 1:750. The blot was revealed with a goat anti-rabbit Ig coupled to HRP followed by incubation in ECL substrate.

For FACS analysis, cells were washed further with ice cold staining buffer (PBS+1%BSA+Azide). Next, the cells were incubated for 30 minutes on ice with 10ug/ml of Protein A purified anti-O8E polyclonal sera. The cells were washed 3 times with staining buffer and then incubated with a 1:100 dilution of a goat anti-rabbit Ig(H+L)-FITC reagent (Southern Biotechnology) for 30 minutes on ice. Following 3 washes, the cells were resuspended in staining buffer containing Propidium Iodide (PI), a vital stain that allows for the identification of permeable cells, and analyzed by FACS.

From these experiments, the results of which are illustrated in Figures 20-21, O8E expression was detected on the surface of transfected HEK293 cells and SKBR3 cells by FACS analysis using rabbit anti-O8E sera. Expression was also detected in transfected HEK293 cell lysates by Western blot analysis (Figure 22).

EXAMPLE 8

GENERATION AND CHARACTERIZATION OF ANTI-O8E MABS.

Mouse monoclonal antibodies were raised against E. coli derived O8E proteins as follows. A/J mice were immunized intraperitoneally (IP) with Complete Freund's Adjuvant (CFA) containing 50 µg recombinant O8E, followed by a subsequent IP boost with Incomplete Freund's Adjuvant (IFA) containing 10µg recombinant O8E protein. Three days prior to removal of the spleens, the mice were immunized intravenously with approximately 50µg of soluble O8E recombinant protein. The spleen of a mouse with a positive titer to O8E was removed, and a single-cell suspension made and used for fusion to SP2/0 myeloma cells to generate B cell

hybridomas. The supernatants from the hybrid clones were tested by ELISA for specificity to recombinant O8E, and epitope mapped using peptides that spanned the entire O8E sequence. The mAbs were also tested by flow cytometry for their ability to detect O8E on the surface of cells stably transfected with O8E and on the surface of a breast tumor cell line.

For ELISA analysis, 96 well plates were coated with either recombinant O8E protein or overlapping 20-mer peptides spanning the entire O8E molecule at a concentration of either 1-2 μ g/ml or 10 μ g/ml, respectively. After coating, the plates were washed 5 times with washing buffer (PBS + 0.1% Tween-20) and blocked with PBS containing 0.5% BSA, 0.4% Tween-20. Hybrid supernatants or purified mAbs were then added and the plates incubated for 60 minutes at room temperature. The plates were washed 5 times with washing buffer and the secondary antibody, donkey-anti mouse Ig linked to horseradish peroxidase (HRP)(Jackson ImmunoResearch), was added for 60 minutes. The plates were again washed 5 times in washing buffer, followed by the addition of the peroxidase substrate. Of the hybridoma clones generated, 15 secreted mAbs that recognized the entire O8E protein. Epitope mapping revealed that of these 15 clones, 14 secreted mAbs that recognized the O8E amino acid residues 61-80 and one clone secreted a mAb that recognized amino acid residues 151-170.

For flow cytometric analysis, HEK293 cells which had been stably transfected with O8E and SKBR3 cells which express O8E mRNA, were harvested and washed in flow staining buffer (PBS+1%BSA+Azide). The cells were incubated with the supernatant from the mAb hybrids for 30 minutes on ice followed by 3 washes with staining buffer. The cells were incubated with goat-anti mouse Ig-FITC for 30 minutes on ice, followed by three washes with staining buffer before being resuspended in wash buffer containing propidium iodide. Flow cytometric analysis revealed that 15/15 mAbs were able to detect O8E protein expressed on the surface of O8E-transfected HEK293 cells. 6/6 mAbs tested on SKBR3 cells were able to recognize surface expressed O8E.

EXAMPLE 9

EXTENDED DNA AND PROTEIN SEQUENCE ANALYSIS OF SEQUENCE O772P

A full-length sequence encompassing clones 3f, 6b, 8e, and 12 was obtained by screening an ovarian tumor (SCID-derived) cDNA library described in detail in Example 2. This 2996 base pair sequence, designated O772P, is presented in SEQ ID NO: 311, and the encoded 914 amino acid protein sequence is shown in SEQ ID NO: 312. The DNA sequence O772P was searched against public databases including Genbank and showed a significant hit to Genbank Accession number AK024365 (SEQ ID NO: 457). This Genbank sequence was found to be 3557 base pairs in length and encodes a protein 1156 amino acids in length (SEQ ID NO: 459). A truncated version of this sequence, residues 25-3471, in which residue 25 corresponds to the first ATG initiation codon in the Genbank sequence, (SEQ ID NO: 456), encodes a protein that is 1148 amino acids in length (SEQ ID NO: 458). The published DNA sequence (SEQ ID NO: 457) differs from O772P in that it has a 5 base pair insertion corresponding to bases 958-962 of SEQ ID NO: 457. This insertion results in a frame shift such that SEQ ID NO: 457 encodes an additional N-terminal protein sequence relative to O772P (SEQ ID NO: 312). In addition, O772P encodes a unique N-terminal portion contained in residues 1-79 (SEQ ID NO: 460). The N-terminal portion of SEQ ID NO: 456, residues 1-313, also contains unique sequence and is listed as SEQ ID NO: 461.

EXAMPLE 10

THE GENERATION OF POLYCLONAL ANTIBODIES FOR IMMUNOHISTOCHEMISTRY
AND FLOW CYTOMETRIC ANALYSIS OF THE CELL ASSOCIATED EXPRESSION
PATTERN OF MOLECULE O772P

The O772P molecule was identified in Examples 2 and 9 of this application. To evaluate the subcellular localization and specificity of antigen expression in various tissues, polyclonal antibodies were generated against O772P. To produce these antibodies, O772P-1 (amino acids 44-772 of SEQ ID NO:312) and O772P-2 (477-914 of SEQ ID NO:312) were expressed in an E. coli recombinant expression system and grown overnight at 37°C in LB Broth. The following day, 10ml

of the overnight culture was added to 500ml of 2xYT containing the appropriate antibiotics. When the optical density of the cultures (560 nanometers) reached 0.4-0.6 the cells were induced with IPTG. Following induction, the cells were harvested, washed, lysed and run through a French Press at a pressure of 16000 psi. The cells were
5 then centrifuged and the pellet checked by SDS-PAGE for the partitioning of the recombinant protein. For proteins that localize to the cell pellet, the pellet was resuspended in 10mM Tris, pH 8.0, 1% CHAPS and the inclusion body pellet washed and centrifuged. The washed inclusion body was solubilized with either 8M urea or 6M guanidine HCL containing 10mM Tris, pH 8.0, plus 10mM imidazole. The solubilized
10 protein was then added to 5ml of nickel-chelate resin (Qiagen) and incubated for 45 minutes at room temperature.

Following the incubation, the resin and protein mixture was poured through a column and the flow through collected. The column was washed with 10-20 column volumes of buffer and the antigen eluted using 8M urea, 10mM Tris, pH 8.0,
15 and 300 mM imidazole and collected in 3ml fractions. SDS-PAGE was run to determine which fractions to pool for further purification. As a final purification step, a strong anion exchange resin was equilibrated with the appropriate buffer and the pooled fractions were loaded onto the column. Each antigen was eluted from the column with an increasing salt gradient. Fractions were collected and analyzed by a SDS-PAGE to
20 determine which fractions from the column to pool. The pooled fractions were dialyzed against 10mM Tris, pH 8.0, and the resulting protein was submitted for quality control for final release. The release criteria were: (a) purity as determined by SDS-PAGE or HPLC, (b) concentration as determined by Lowry assay or Amino Acid Analysis, (c) identity as determined by amino terminal protein, and (d) endotoxin levels as
25 determined by the Limulus (LAL) assay. The proteins were then filtered through a 0.22µM filter and frozen until needed for immunizations.

To generate polyclonal antisera, 400µg of O772P-1 or O772P-2 was combined with 100µg of muramyl dipeptide (MDP). The rabbits were immunized every 4 weeks with 100µg of antigen mixed with an equal volume of Incomplete Freund's
30 Adjuvant (IFA). Seven days following each boost, the animals were bled and sera was generated by incubating the blood at 4°C for 12-24 hours followed by centrifugation.

To characterize the antisera, 96 well plates were coated with antigen followed by blocking with BSA. Rabbit sera was diluted in PBS and added to each well. The plates were then washed, and goat anti-rabbit horseradish peroxidase (HRP). The plates were again washed and TMB microwell Peroxidase Substrate was added.

5 Following this incubation, the colormetric reaction was stopped and the plates read immediately at 450nm. All polyclonal antibodies showed immunoreactivity to the appropriate antigen.

Immunohistochemistry analysis of O772P expression was performed on paraffin-embedded formalin fixed tissue. O772P was found to be expressed in normal

10 ovary and ovarian tumor, but not in normal heart, kidney, colon, lung or liver. Additionally, immunohistochemistry and flow cytometric analysis indicates that O772P is a plasma membrane-associated molecule. O772P contains 1 plasma transmembrane domain predicted to be encoded by amino acids 859-880. The N-terminus of O772P is extracellular and is encoded by amino acids 1-859, while the C-terminus is intracellular.

15 Sequence analysis shows that there are 17 potential N-linked glycosylation sites.

EXAMPLE 11

O772P IS EXPRESSED ON THE SURFACE OF PRIMARY OVARIAN TUMOR CELLS

For recombinant expression in mammalian cells, the O772P-21008 (SEQ ID NO:387) and O772P full length cDNA (SEQ ID NO:311 encoding the protein of

20 SEQ ID NO:312) were subcloned into mammalian expression vectors pBIB or pCEP4 respectively. These constructs were transfected into HEK293 cells using Fugene 6 (Roche). The HEK cells were then plated at a density of 100,000 cells/ml in DMEM containing fetal bovine serum (FBS) and grown overnight. The following day, 2µl of Fugene 6 was added to 100µl of DMEM, which contained no FBS, and incubated for 15

25 minutes at room temperature. The Fugene 6/DMEM mixture was then added to 1µg of O772P/pBIB or O772P/pCEP4 plasmid DNA and incubated for an additional 15 minutes at room temperature. The Fugene 6/DNA mix was then added to the HEK293 cells and incubated for 48-72 hours at 37°C with 7% CO₂. The cells were rinsed and pelleted by centrifugation.

For Western Blot analysis, whole cell lysates were generated by incubating the cells in lysis buffer followed by clarification by centrifugation. The samples were diluted and run on SDS-PAGE. The gel was then transferred to nitrocellulose and probed using purified anti-O772P-2 rabbit polyclonal antibody. The blot was revealed with a goat anti-rabbit Ig coupled to HRP followed by incubation in ECL substrate. Western Blot analysis revealed that O772P-21008 could be detected in HEK293 cells that had been transfected with O772P.

To determine the cell expression profile of O772P in cells, primary ovarian tumor cells were grown in SCID mice. The cells were retrieved from the mice and analyzed by flow cytometry. Briefly, cells washed in cold staining buffer containing PBS, 1% BSA, and Na Azide. The cells were incubated for 30 minutes with 10µg/ml of purified anti-O772P-1 and O772P-2 polyclonal sera. Following this incubation, the cells were washed three times in staining buffer and incubated with goat anti-rabbit Ig (H+L) conjugated to FITC (Southern Biotechnology). The cells were washed and resuspended in staining buffer containing Propidium Iodide (PI), a vital stain that identifies non-viable cells. The cells were then analyzed using Fluorescence Activated Cell Sorting (FACS). FACS analysis revealed that O772P was present on the cells surface. Surface expression of O772P on tumor cells allows for immune targeting by therapeutic antibodies.

20

EXAMPLE 12

FUNCTIONAL CHARACTERIZATION OF ANTI-O8E MONOCLONAL ANTIBODIES

Mouse monoclonal antibodies (mAb) raised against E. coli derived O8E, as described in Example 8, were tested for their ability to promote O8E antigen internalization. Internalization of the antibody was determined using an in vitro cytotoxicity assay. Briefly, HEK293 and O8E/HEK transfected cells were plated into 96 well plates containing DME plus 10% heat-inactivated FBS in the presence of 50ng/well of purified anti-O8E or control antibodies. The isotype of the anti-O8E mAbs are as follows: 11A6-IgG1/kappa, 15C6-IgG2b/kappa, 18A8-IgG2b/kappa, and 14F1-IgG2a/kappa. W6/32 is a pan anti-human MHC class I mouse monoclonal antibody that serves as a positive control, and two irrelevant mAbs, Ir-Pharm and Ir-

30

Crxa were included as negative controls. Following incubation with the O8E specific antibodies or the relevant controls antibodies, the mAb-zap, a goat anti-mouse Ig-saporin conjugated secondary antibody (Advanced Targeting Systems) was added at a concentration of 100ng/ml to half of the wells, and the plates were incubated for 48 to 5 72 hours at 37°C in a 7% CO₂ incubator. This assay takes advantage of the toxic nature of saporin, a ribozyme inactivating protein, which when internalized has a cytotoxic effect. Following incubation with the mAb-zap, internalization was quantitated by the addition of MTS reagent, followed by reading the OD490 of the plate on a microplate ELISA reader. Figure 25 depicts the results from these assays. The top panel represents 10 HEK cells that have not been transfected with O8E and therefore O8E antibody should not bind and be internalized. Levels of proliferation were the same in all samples whether they were incubated with or without the mAb-zap, with the exception of the positive control Ab, W6/32. The lower panel represents cells that have been transfected with O8E and therefore should bind O8E specific antibodies. Antibodies from the 15 hybridomas 11H6, 14F1, and 15C6, which recognize the amino acids 61-80 of O8E were able to promote internalization of the O8E surface protein as measured by decreased levels of proliferation due to the toxic nature of the mAb-zap (See Figure 25). The antibody generated by the hybridoma 18A8, which recognizes amino acids 151-170 of O8E, was unable to promote internalization as determined by normal levels of 20 proliferation either in the absence or presence of the mAb-zap.

EXAMPLE 13

CHARACTERIZATION OF THE OVARIAN TUMOR ANTIGEN, O772P

The cDNA and protein sequences for multiple forms of the ovarian tumor antigen O772P have been described in the above (e.g., Examples 2 and 9). A 25 Genbank search indicated that O772P has a high degree of similarity with FLJ14303 (Accession # AK024365; SEQ ID NO:457 and 463). Protein sequences corresponding to O772P and FLJ14303 are disclosed in SEQ ID NO:478 and 479, respectively. FLJ14303 was identical to the majority of O772P, with much of the 3'-end showing 100% homology. However, the 5'-end of FLJ14303 was found to extend further 5' than 30 O772P. In addition, FLJ14303 contained a 5 bp insert (SEQ ID NO:457) resulting in a

frame shift of the amino-terminus protein sequence such that FLJ14303 utilizes a different starting methionine than O772P and therefore encodes a different protein. This insertion was present in the genomic sequence and seen in all EST clones that showed identity to this region, suggesting that FLJ14303 (SEQ ID NO:457) represents a splice variant of O772P, with an ORF that contains an extended and different amino-terminus. The additional 5'-nucleotide sequence included repeat sequences that were identified during the genomic mapping of O772P. The 5'-end of O772P and the corresponding region of FLJ14303 showed between 90-100% homology. Taken together, this suggests that O772P and FLJ14303 are different splice variants of the same gene, with different unique repeat sequences being spliced into the 5'-end of the gene.

The identification of an additional ten or more repeat sequences within the same region of chromosome 19, indicates that there may be many forms of O772P, each with a different 5'-end, due to differential splicing of different repeat sequences. Northern blot analysis of O772P demonstrated multiple O772P-hybridizing transcripts of different sizes, some in excess 10kb.

Upon further analysis, 13 additional O772P-related sequences were identified, the cDNA and amino acid sequences of which are described in Table 2.

Table 2

SEQ ID NO:	Description	Transmembrane Domains
464	LS #1043400.1 (cDNA)	nd
465	LS #1043400.10 (cDNA)	0
466	LS #1043400.11 (cDNA)	2
467	LS #1043400.12 (cDNA)	2
468	LS #1043400.2 (cDNA)	nd
469	LS #1043400.3 (cDNA)	
470	LS #1043400.5 (cDNA)	nd
471	LS #1043400.8 (cDNA)	1
472	LS #1043400.9 (cDNA)	0

473	LS #1043400.6 (cDNA)	nd
474	LS #1043400.7 (cDNA)	nd
475	LS #1043400.4 (cDNA)	nd
476	LS #1397610.1 (cDNA)	0
477	1043400.10 Novel 5' (cDNA)	-
480	LS #1043400.9 (amino acid)	-
481	LS #1043400.8B (amino acid) Contains a transmembrane domain	-
482	LS #1043400.8A (amino acid)	-
483	LS #1043400.12 (amino acid) Contains a transmembrane domain	-
484	LS #1043400.11B (amino acid) Contains a transmembrane domain	-
485	LS #1043400.11A (amino acid)	-
486	LS #1043400.10 (amino acid)	-
487	LS #1043400.1 (amino acid)	-

nd=not determined

Initially it appeared that these sequences represented overlapping and/or discrete sequences of O772P splice forms that were capable of encoding polypeptides unique to the specific splice forms of O772P. However, nucleotide alignment of these sequences failed to identify any identical regions within the repeat elements. This indicates that the sequences may represent different specific regions of a single O772P gene, one that contains 16 or more repeat domains, all of which form a single linear transcript. The 5'-end of sequence LS #1043400.10 (Table 2; SEQ ID NO:465) is unique to both O772P and FLJ14303 and contains no repeat elements, indicating that this sequence may represent the 5'-end of O772P.

Previously, transmembrane prediction analysis had indicated that O772P contained between 1 and 3 transmembrane spanning domains. This was verified by the

use of immunohistochemistry and flow cytometry, which demonstrated the existence of a plasma membrane-associated molecule representing O772P. However, immunohistochemistry also indicated the presence of secreted form(s) of O772P, possibly resulting from an alternative splice form of O772P or from a post-translational cleavage event. Analysis of several of the sequences presented in Table 2 showed that sequences 1043400B.12, 1043400.8B, and 1043400.11B all contained transmembrane regions, while 1043400.8A, 1043400.10, 1043400.1, 1043400.11A, and 1043400.9 were all lacking transmembrane sequences, suggesting that these proteins may be secreted.

10 Analysis indicates a part of O772P is expressed and/or retained on the plasma membrane, making O772P an attractive target for directing specific immunotherapies, e.g., therapeutic antibodies, against this protein. The predicted extracellular domain of O772P is disclosed in SEQ ID NO:489 and secretion of O772P is likely to occur as a result of a cleavage event within the sequence:

15 SLVEQVFLDKTLNASFHWLGSTYQLVDIHVTEMESSVYQP.

Proteolytic cleavage is most likely to occur at the Lysine (K) at position 10 of SEQ ID NO:489. The extracellular, transmembrane, and cytoplasmic regions of O772P are all disclosed in SEQ ID NO:488:

Extracellular:

20 SLVEQVFLDKTLNASFHWLGSTYQLVDIHVTEMESSVYQPTSSSS
TQHFYLNFTITNLPYSQDKAQPGTTNYQRNKRNIEDALNQLFRNSSIKSYFSDCQ
VSTFRSVPNRHHTGVDSL CNFSPLARRVDRVAIYEEFLRMTRNGTQLQNFTLDR
SSVLVDGYFPNRNEPLTGNSDLPF

Transmembrane:

25 WAVILIGLAGLLGLITCLICGVLVTT

Cytoplasmic:

RRRKKEGEYNVQQQCPGYYSYSHLDLEDLQ

EXAMPLE 14

IMMUNOHISTOCHEMISTRY (IHC) ANALYSIS OF O8E EXPRESSION IN OVARIAN CANCER
AND NORMAL TISSUES

In order to determine which tissues express the ovarian cancer antigen O8E, IHC analysis was performed on a diverse range of tissue sections using both polyclonal and monoclonal antibodies specific for O8E. The generation of O8E specific polyclonal antibodies is described in detail in Example 8. The monoclonal antibodies used for staining were 11A6 and 14F1, both of which are specific for amino acids 61-80 of O8E and 18A8, which recognizes amino acids 151-170 of O8E (see Example 12 for details on generation).

To perform staining, tissue samples were fixed in formalin solution for 12-24 hours and embedded in paraffin before being sliced into 8 micron sections. Steam heat induced epitope retrieval (SHEIR) in 0.1M sodium citrate buffer (pH 6.0) was used for optimal staining conditions. Sections were incubated with 10% serum/PBS for 5 minutes. Primary antibody was then added to each section for 25 minutes followed by 25 minutes of incubation with either anti-rabbit or anti-mouse biotinylated antibody. Endogenous peroxidase activity was blocked by three 1.5 minute incubations with hydrogen peroxidase. The avidin biotin complex/horse radish peroxidase (ABC/HRP) system was used along with DAB chromogen to visualize the antigen expression. Slides were counterstained with hematoxylin to visualize the cell nuclei.

Results using rabbit affinity purified polyclonal antibody to O8E (a.a. 29-283; for details on the generation of this Ab, see Example 3) are presented in Table 3. Results using the three monoclonal antibodies are presented in Table 4.

25

Table 3Immunohistochemistry analysis of O8E using polyclonal antibodies

Tissue	O8E Expression
Ovarian Cancer	Positive
Breast Cancer	Positive

Normal Ovary	Positive
Normal Breast	Positive
Blood Vessel	Positive
Kidney	Negative
Lung	Negative
Colon	Negative
Liver	Negative
Heart	Negative

Table 4

Immunohistochemistry analysis of O8E using monoclonal antibodies

Normal Tissue	11A6		18A8		14F1	
	Endothelial	Epithelial	Endothelial	Epithelial	Endothelial	Epithelial
	1					
Skin	2	2	0	0	1	1
Skin	1	1	0	0	1	1
Breast	0	1	n/a	n/a	1	1
Colon	0	0	0	0	0	0
Jejunum	0	0	0	0	0	0
Colon	0	0	0	0	0	0
Colon	0	0	0	0	0	0
Ovary	0	0	0	0	1	0
Colon	0	0	0	0	0	1
Liver	0	0	0	0	1	2
Skin	0	0	0	0	1	0
Duodenum and Pancreas	0	0	0	0	0	0
Appendix	0	0	0	0	0	0
Ileum	0	0	0	0	0	0

0=no staining, 1=light staining, 2=moderate staining, n/a=not available

EXAMPLE 15

EPI TOPE MAPPING OF O772P POLYCLONAL ANTIBODIES

To perform epitope mapping of O772P, peptides were generated, the sequences of which were derived from the sequence of O772P. These peptides were 15mers that overlapped by 5 amino acids and were generated via chemical synthesis on membrane supports. The peptides were covalently bound to Whatman 50 cellulose support by their C-terminus with the N-terminus unbound. In order to determine epitope specificity, the membranes were wet with 100% ethanol for 1 minute, and then blocked for 16 hours in TBS/Tween/Triton buffer (50mM Tris, 137 mM NaCl, 2.7 mM KCl, 0.5% BSA, 0.05% Tween 20, 0.05% Triton X-100, pH 7.5). The peptides were then probed with 2 O772P specific antibodies, O772P-1 (amino acids 44-772 of SEQ ID NO:312) and O772P-2 (477-914 of SEQ ID NO:312; see Example 10 for details of antibody generation), as well as irrelevant rabbit antibodies for controls. The antibodies were diluted to 1µg/ml and incubated with the membranes for 2 hours at room temperature. The membranes were then washed for 30 minutes in TBS/Tween/Triton buffer, prior to being incubated with a 1:10,000 dilution of HRP-conjugated anti-rabbit secondary antibody for 2 hours. The membranes were again washed for 30 minutes in TBS/Tween/Triton and anti-peptide reactivity was visualized using ECL. Specific epitope binding specificity for each of the O772P-polyclonal antibodies is described in Table 5.

Table 5

SEQ ID NO:	Peptide #	Anti-O772P1	Anti-O772P2	Peptide Sequence
490	2	***	-	TCGMRRTCSTLAPGS
491	6	*	*/-	CRLTLRPEKDGTAT
492	7	*	-	DGTATGVDAICTHHP
493	8	-	-	CTHHPDPKSPRLDRE
494	9	***	***	RLDREQLYWELSQLT
495	11	*/-	-	LGPYALDNDSLFVNG
496	13	****	-	SVSTSTPGTPTYVL
497	22	-	-	LRPEKDGEATGVDAI
498	24	**	*/-	DPTGPGLDREQLYLE
499	27	*/-	-	LDRDSLYVNGFTHRS
500	40	*/-	-	GPYSLDKDSLYLNGY
501	41	-	-	YLNGYNEPGPDEPPT
502	47	***	***	ATFNSTEGVLQHLLR

503	50	-	***	QLISLRPEKDGAATG
504	51	-	**	GAATGVDTTCTYHPD
505	52	-	*/-	TYHPDPVGPGLDIQQ
506	53	-	*	LDIQQLYWELSQLTH
507	58	-	*	HIVNWNLSNPDPTSS
508	59	-	*	DPTSSEYITLLRDIQ
509	60	-	*	LRDIQDKVTTLYKGS
510	61	-	***	LYKGSQQLHDTFRFCL
511	71	-	**	DKAQPGTTNYQRNKR

*= relative reactive level, -; no binding, ****, maximal binding

EXAMPLE 16

IDENTIFICATION OF A NOVEL N-TERMINAL REPEAT STRUCTURE ASSOCIATED WITH O772P

5 Various O772P cDNA and protein forms have been identified and characterized as detailed above (e.g., Examples 1, 2, 9, and 14). Importantly, O772P RNA and protein have been demonstrated to be over-expressed in ovarian cancer tissue relative to normal tissues and thus represents an attractive target for ovarian cancer diagnostic and therapeutic applications.

10 Using bioinformatic analysis of open reading frames (ORFs) from genomic nucleotide sequence identified previously as having homology with O772P, multiple nucleotide repeat sequences were identified in the 5' region of the gene encoding the O772P protein. A number of these repeat sequences were confirmed by RT-PCR using primers specific for the individual repeats. Fragments which contained
15 multiple repeats were amplified from cDNA, thus confirming the presence of specific repeats and allowing an order of these repeats to be established.

 Unexpectedly, when various sets of O772P sequences derived from different database and laboratory sources were analyzed, at least 20 different repeat structures, each having substantial levels of identity with each other (see Table 6), were
20 identified in the 5' region of the O772P gene and the corresponding N-terminal region of the O772P protein. Each repeat comprises a contiguous open reading frame encoding a polypeptide unit that is capable of being spliced to one or more other repeats such that concatomers of the repeats are formed in differing numbers and orders. Interestingly, other molecules have been described in the scientific literature that have repeating
25 structural domains analogous to those described herein for O772P. For example, the

mucin family of proteins, which are the major glycoprotein component of the mucous which coats the surfaces of cells lining the respiratory, digestive and urogenital tracts, have been shown to be composed of tandemly repeated sequences that vary in number, length and amino acid sequence from one mucin to another (Perez-Vilar and Hill, *J. Biol. Chem.* 274(45):31751-31754, 1999).

The various identified repeat structures set forth herein are expected to give rise to multiple forms of O772P, most likely by alternative splicing. The cDNA sequences of the identified repeats are set forth in SEQ ID NOs:513-540, 542-546, and 548-567. The encoded amino acid sequences of the repeats are set forth in SEQ ID NOs:574-593. In many instances these amino acid sequences represent consensus sequences that were derived from the alignment of more than one experimentally derived sequence.

Each of these splice forms is capable of encoding a unique O772P protein with multiple repeat domains attached to a constant carboxy terminal protein portion of O772P that contains a trans membrane region. The cDNA sequence of the O772P constant region is set forth in SEQ ID NO:568 and the encoded amino acid sequence is set forth in SEQ ID NO:594.

All of the available O772P sequences that were obtained were broken down into their identifiable repeats and these sequences were compared using the Clustal method with weighted residue weight table (MegAlign software within DNASTAR sequence analysis package) to identify the relationship between the repeat sequences. Using this information, the ordering data provided by the RT-PCR, and sequence alignments (automatic and manual) using SeqMan (DNASTAR), one illustrative consensus full length O772P contig was identified comprising 20 distinct repeat units. The cDNA for this O772P cDNA contig is set forth in SEQ ID NO:569 and the encoded amino acid sequence is set forth in SEQ ID NO:595. This form of the O772P protein includes the following consensus repeat structures in the following order:

SEQ ID NO:572- SEQ ID NO:574- SEQ ID NO:575-SEQ ID NO:576-
SEQ ID NO:577- SEQ ID NO:578- SEQ ID NO:579- SEQ ID NO:580- SEQ ID
NO:581- SEQ ID NO:582- SEQ ID NO:583- SEQ ID NO:584- SEQ ID NO:585- SEQ

ID NO:586- SEQ ID NO:587- SEQ ID NO:588- SEQ ID NO:589- SEQ ID NO:590-
SEQ ID NO:591- SEQ ID NO:592- SEQ ID NO:593.

SEQ ID NO:595, therefore, represents one illustrative full-length
consensus sequence for the O772P protein. As discussed above, however, based on
5 current knowledge of this protein and based upon scientific literature describing
proteins containing analogous repeating structures, many other forms of O772P are
expected to exist with either more or less repeats. In addition, many forms of O772P
are expected to have differing arrangements, e.g., different orders, of these N-terminal
repeat structures. The existence of multiple forms of O772P having differing numbers
10 of repeats is supported by Northern analysis of O772P. In this study, Northern
hybridization of a O772P-specific probe resulted in a smear of multiple O772P-
hybridizing transcripts, some in excess 10kb.

Thus, the variable repeat region of the O772 protein can be illustratively
represented by the structure $X_n - Y$, wherein X comprises a repeat structure having at
15 least 50% identity with the consensus repeat sequence set forth in SEQ ID NO:596; n is
the number of repeats present in the protein and is expected to typically be a integer
from 1 to about 35; Y comprise the O772P constant region sequence set forth in SEQ
ID NO:594 or sequences having at least 80% identity with SEQ ID NO:594. Each X
present in the X_n repeat region of the O772 molecule is different.

20 To determine the consensus sequences of each of the 20 repeat regions,
sequences that were experimentally determined for a discrete repeat region were aligned
and a consensus sequence determined. In addition to determining the consensus
sequences for individual repeat regions, a consensus repeat sequence was also
determined. This sequence was obtained by aligning the 20 individual consensus
25 sequences. Variability of the repeats was determined by aligning the consensus amino
acid sequences from each of the individual repeat regions with the over all repeat
consensus sequence. Identity data is presented in Table 6.

Table 6
Percent identities of Repeat Sequences with Reference to the Consensus Repeat
Sequence

Repeat Number (amino acid)	SEQ ID NO:	Percent Identity to Consensus Repeat Sequence
2	574	88
3	575	84
4	576	88
5	577	89
6	578	93
7	579	90
8	580	91
9	581	88
10	582	85
11	583	86
12	584	87
13	585	87
14	586	89
15	587	89
16	588	89
17	589	83
18	590	84
19	591	83
20	592	57
21	593	68

5 From the foregoing it will be appreciated that, although specific embodiments of the invention have been described herein for purposes of illustration,

various modifications may be made without deviating from the spirit and scope of the invention. Accordingly, the invention is not limited except as by the appended claims.

CLAIMS

What is Claimed:

1. An O772P polypeptide having the structure:

X_n -Y

wherein X comprises a sequence having at least 50% identity with the consensus O772P repeat sequence set forth in SEQ ID NO: 596;

Y comprises a sequence having at least 80% identity with the O772P constant region sequence set forth in SEQ ID NO: 594;

n is an integer from 1 to 35;

wherein each X present in said polypeptide is different.

2. The polypeptide of claim 1, wherein X comprises a sequence selected from the group consisting of any one of SEQ ID NOs: 574-593.

3. The polypeptide of claim 1, wherein Y comprises the sequence set forth in SEQ ID NO: 594.

4. The polypeptide of claim 1, wherein n is an integer from 15 to 25.

5. The polypeptide of claim 1, wherein n is 20.

6. The polypeptide of claim 1, wherein said polypeptide comprises SEQ ID NO: 595.

7. The polypeptide of claim 1, wherein said polypeptide is overexpressed in ovarian cancer cells compared with normal tissues.

8. An O772P polypeptide having the structure:

X_n -Y

wherein X comprises an O772P repeat sequence selected from the group consisting of any one of SEQ ID NOs: 574-593;

Y comprises a sequence having at least 90% identity with the O772P constant region sequence set forth in SEQ ID NO: 594;

n is an integer from 15 to 25;

wherein each X present in said polypeptide is different.

9. The polypeptide of claim 8, wherein n is 20.

10. The polypeptide of claim 8, wherein said polypeptide comprises SEQ ID NO: 595.

11. The polypeptide of claim 8, wherein said polypeptide is overexpressed in ovarian cancer cells compared with normal tissues.

12. An O772P polypeptide having the structure:

X_n -Y

wherein n is 20 and X comprises the following O772P repeat sequences:

SEQ ID NO: 574 - SEQ ID NO: 575 - SEQ ID NO: 576 - SEQ ID NO: 577 - SEQ ID NO: 578 - SEQ ID NO: 579 - SEQ ID NO: 580 - SEQ ID NO: 581 - SEQ ID NO: 582 - SEQ ID NO: 583 - SEQ ID NO: 584 - SEQ ID NO: 585 - SEQ ID NO: 586 - SEQ ID NO: 587 - SEQ ID NO: 588 - SEQ ID NO: 589 - SEQ ID NO: 590 - SEQ ID NO: 591 - SEQ ID NO: 592 - SEQ ID NO: 593; and

Y comprises the sequence set forth in SEQ ID NO: 594.

13. The polypeptide of claim 12, wherein said polypeptide comprises SEQ ID NO: 595.

14. The polypeptide of claim 12, wherein said polypeptide is overexpressed in ovarian cancer cells compared with normal tissues.

15. An O772P polynucleotide having the structure:

X_n-Y

wherein X comprises an O772P repeat sequence selected from the group consisting of any one of SEQ ID NOs: 512-540, 542-546 and 548-567;

Y comprises a sequence having at least 95% identity with the O772P constant region sequence set forth in SEQ ID NO: 568;

n is an integer from 1 to 35;

wherein each X present in said polypeptide is different.

16. The polynucleotide of claim 15, wherein said polynucleotide comprises SEQ ID NO: 569.

17. The polynucleotide of claim 15, wherein n is from 15 to 25.

18. The polynucleotide of claim 15, wherein n is 20.

19. The polynucleotide of claim 15, wherein said polynucleotide is overexpressed in ovarian cancer cells compared with normal tissues.

20. An isolated polynucleotide comprising a sequence selected from the group consisting of:

- (a) sequences provided in SEQ ID NOs: 464-477 and 512-569;
- (b) complements of the sequences provided in SEQ ID NOs: 464-477 and 512-569;
- (c) sequences consisting of at least 20 contiguous residues of a sequence provided in SEQ ID NOs: 464-477 and 512-569;
- (d) sequences that hybridize to a sequence provided in SEQ ID NOs: 464-477 and 512-569, under highly stringent conditions;
- (e) sequences having at least 75% identity to a sequence of SEQ ID NOs: 464-477 and 512-569;

(f) sequences having at least 90% identity to a sequence of SEQ ID NOs: 464-477 and 512-569; and

(g) degenerate variants of a sequence provided in SEQ ID NOs: 464-477 and 512-569.

21. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:

(a) sequences encoded by a polynucleotide of claim 20; and

(b) sequences having at least 80% identity to a sequence encoded by a polynucleotide of claim 20; and

(c) sequences having at least 90% identity to a sequence encoded by a polynucleotide of claim 20.

22. An expression vector comprising a polynucleotide of claim 20 operably linked to an expression control sequence.

23. A host cell transformed or transfected with an expression vector according to claim 22.

24. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a polypeptide of claim 21.

25. A method for detecting the presence of a cancer in a patient, comprising the steps of:

(a) obtaining a biological sample from the patient;

(b) contacting the biological sample with a binding agent that binds to a polypeptide of claim 21;

(c) detecting in the sample an amount of polypeptide that binds to the binding agent; and

(d) comparing the amount of polypeptide to a predetermined cut-off value and therefrom determining the presence of a cancer in the patient.

26. A fusion protein comprising at least one polypeptide according to claim 21.

27. A method for stimulating and/or expanding T cells specific for a tumor protein, comprising contacting T cells with at least one component selected from the group consisting of:

- (a) polypeptides according to claim 21;
- (b) polynucleotides according to claim 20; and
- (c) antigen-presenting cells that express a polynucleotide according to claim 20,

under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells.

28. An isolated T cell population, comprising T cells prepared according to the method of claim 27.

29. A composition comprising a first component selected from the group consisting of physiologically acceptable carriers and immunostimulants, and a second component selected from the group consisting of:

- (a) polypeptides according to claim 21;
- (b) polynucleotides according to claim 20;
- (c) antibodies according to claim 24;
- (d) fusion proteins according to claim 26;
- (e) T cell populations according to claim 28; and
- (f) antigen presenting cells that express a polypeptide according to claim 21.

30. A method for stimulating an immune response in a patient, comprising administering to the patient a composition of claim 29.

31. A method for the treatment of a ovarian cancer in a patient, comprising administering to the patient a composition of claim 29.

32. A method for determining the presence of a cancer in a patient, comprising the steps of:

- (a) obtaining a biological sample from the patient;
- (b) contacting the biological sample with an oligonucleotide that hybridizes to a polynucleotide sequence according to claim 21 under moderately stringent conditions;
- (c) detecting in the sample an amount of said polynucleotide that hybridizes to the oligonucleotide; and
- (d) comparing the amount of said polynucleotide that hybridizes to the oligonucleotide to a predetermined cut-off value, and therefrom determining the presence of the cancer in the patient.

33. An O772 polypeptide comprising at least an antibody epitope sequence set forth in any one of SEQ ID NOs: 490-511.

34. An O8E polypeptide comprising at least an antibody epitope sequence set forth in any one of SEQ ID NOs: 394-415.

35. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a polypeptide of claim 1.

11729.1 contg

11729-45.21.21.cons1

11729-45.21.21.cons2

11731.1contig

Fig. 1A

2/101

11731.2contig

AGCCAGATGGCTGAGAGCTGCAAGAAGAAGTCAGGATCATGATGGCTCAGTTTCCACAGCGATGAATGGAGGG
CCAAATATGTGGGCTATTACATCTGAAGAACGTACTAAGCATGATAAACAGTTTGATAACCTCAAACCTTCAGG
AGGTTACATAACAGGTGATCAAGCCCGTACTTTTTCTACAGTCAGGTCTGCCGGCCCCGGTTTTAGCTGAAA
TATGGGCTTATCAGATCTGAACAAGGATGGGAAGATGGACCAGCAAGAGTTCTCTATAGCTATGAAACTCATC
AAGTTAAAGTTGCAGGGCCAACAGCTGCCTGTAGTCTCTCCCTCTATCATGAAACAACCCCTATGTTCTCTCC
ACTAATCTCTGCTCGTTTTGGGATGGGAAGCATGCCAATCTGTCCATTATCAGCCATTGCCTCCAGTTGCAC
CTATAGCAACACCCTTGTCTTCTGCTACTTCAGGGACCAGTATTCTCCCTAATGATGCCTGCTCCCCTAGTG
CCTTCTGTAGTA

11734.1contig

AATAGATTTAATGCAGAGTGTCAACTTCAATTGATTGATAGTGGCTGCCTAGAGTGCTGTGTTGAGTAGGTTTC
TGAGGATGCAACCCTGGCTTGAAGAGAAAGACTGGCAGGATTAACAATATCTAAAATCTCACTTGTAGGAGAAAC
CACAGGCACCAGAGCTGCCACTGGTGCTGGCACCAGCTCCACCAAGGCCAGCGAAGAGCCCAAATGTGAGAGTG
GCGGTCAAGCTGGCACCAGCACTGAAGCCACCAGTGGTGCTGGCACTGGCACTGGCACTGTTATTGGTACTGGT
ACTGGCACCAGTGCTGGCACTGCCACTCTTTGGGCTTTGGCTTTAGCTTCTGCTCCGCTGGATCCGGGCTT
TGGCCAGGGTCCGATATCAGCTTCGTCCAGTTGCAGGGCCCGGCAGCATTCTCCAGCCGAGCCCAATGCC
ATTCGAGCTCTAATCTCGGCCCTAGCCTTGGCTTCAGCTGCAGCCTCAGCTGCAGCCTTCAAATCCGCTTCCAT
CGCCTCTCGGTAC

11734.2contig

GCCAAGAAAGCCCGAAAGGTGAAGCATCTGGATGGGGAAGAGGATGGCAGCAGTGATCAGAGTCAGGCTTCTGG
AACCACAGGTGGCCGAAGGTCTCAAAGGCCCTAATGGCCTCAATGGCCCGCAGGGCTTCAAGGGGTCCCATAG
CCTTTTGGGCCCGCAGGGCATCAAGGACTCGGTTGGCTGCTTGGGCCCGAGAGCCTTGCTCTCCCTGAGATCA
CCTAAAGCCCGTAGGGCAAGGCTCGCCGTAGAGCTGCCAAGCTCCAGTCATCCAAGAGCCTGAAGCACCACC
ACCTCGGGATGTGGCCCTTTTGAAGGGAGGGCAAATGATTTGGTGAAGTACCTTTTGGCTAAAGACCAGACGA
AGATTCCCATCAAGCGCTCGGACATGCTGAAGGACATCATCAAAGAATACACTGATGTGTACCCCGAAATCATT
GAACGAGCAGGCTATTCTTGGAGAAGGTATTGGGATTCAATTGAAGGAAATTGATAAGAATGACCACTTGTA
CATTCTTCTCAGC

11736.1contg

GAGGTCTCACTATGTTGCCAGGCTGTTCTTGAACCTCTGGGATCAAGCAATCCACCCATGTTGGTCTCAAAA
GTGCTGGGATCATAGGCGTGAGCCACCTACCCAGCCACCAATTTTCAATCAGGAAGACTTTTCTTCTTCAA
GAAGTGAAGGGTTTCCAGAGTATAGCTACACTATTGCTTGCTGAGGGTGACTACAAAATTGCTTGCTAAAAGG
TTAGGATGGGTAAAGAATTAGATTTTCTGAATGCAAAAATAAAATGTGAACCTAATGAACCTTATAGTAATACATA
TTCATAAAATAATTATTCACATATTTCTGATTTATCACAGAAATAATGTATGAAATGCTTTGAGTTTCTTGGA
GTAACTCCATTACTCATCCCAAGAAACCATATTATAAGTATCACTGATAATAAGAACACAGGACCTTGTCTAT
AAATCTGGATAAGAGAAAATAGTCTCTGGGTGTTGXTCTTAATTGATAAAATTTACTTGCCATCTTTAGTT
CAGAATCACAAA

Fig. 1B

3/101

11736.2contig

AAGCGGAAATGAGAAAGGAGGGAAAATCATGTGGTATTGAGCGGAAACTGCTGGATGACAGGGCTCAGTCCTG
TTGGAGAACTCTGGGTGGTGTGTAGAACAGGGCCACTCACAGTGGGGTGACAGACCAGCACGGCTCTGTGAC
CTGTTTGTACAGGTCCATGATGAGGTAACAATACTAGTATAAGGGTTGGTTTAGAACTCTTACAGCAA
TTTGACAAAGTAATCTTCTGTGCAGTGAATCTAAGAAAAAATTGGGGCTGTATTTGTATGTTCTTTTTTTCA
TTTCATGTTCTGAGTTACCTATTTTTATTGCATTTTACAAAAGCATCCTTCCATGAAGGACCGGAAGTTAAAAA
CAAAGCAGGTCTTTATCACAGCACTGTCTAGAACACAGTTCAGAGTTATCCACCAAGGAGCCAGGGAGCTG
GGCTAAACCAAAGAATTTTGCTTTTGGTTAATCATCAGGTACTTGAGTTGGAATTGTTTAAATCCCATCATTAC
CAGGCTGGAXGTG

11739-1&2

CCGCGGCTCCTGTCCAGACCCTGACCCTCCCTCCCAAGGCTCAACCGTCCCCAACAACCGCCAGCCTTGTA
GATGTGCGCTGCGAGAGCCTGTGCTTAAGTAAGAATCAGGCCTTATTGGAGACATTCAAGCAAAGGTTGGACAA
CTACTTTTCCAGAACAGAAAGGAAACTCATGCATCAGAAAAGGTGACTAATAAAGGTACCAGAAGAATATGGCT
GCACAAATACCAGAACTGATCAGATAAAACAGTTTAAGGAATTTCTGGGGACCTACAATAAACTTACAGAGAC
CTGCTTTTTGGACTGTGTTAGAGACTTCACAACAAGAGAAGTAAACCTGAAGAGACCACCTGTTTCAAGCATT
GCTTACAGAAATATTTAAAAATGACACAAGAATATCCATGAGATTTTCAAGGAATATCATATTCAGCAGAATGAA
GCCCTGGCAGCCAAAGCAGGACTCCTTGCCCAACCACGATAGAGAAGTCTGATGGATGAACTTTTGATGAAAG
ATTGCCAACAGCTGCTTTATTGGAAATGAGGACTCATCTGATAGAATCCCTGAAAGCAGTAGCCACCATGTTT
AACCATCTGTCATGACTGTTTGGCAATGGAACCGCTGGAGAAACAAAATTGCTATTTACCAGGAATAATCAC
AATAGAAGGTCTTATTGTTTCAAGTAAATAAAGATGCAACATTTGTTGAGGCCTTATGATTCAGCAGCTTGGT
CACTTGATTAGAAAAATAACCATGTTTCTTCAATTGTGACTGTTAATTTTAAAGCAACTTATGTGTTTCGATC
ATGTATGAGATAGAAAAATTTTATTACTCAAAGTAAAATAAATGGA

11740.1.contig

GAAAAAAATATAAACACACTTTTGGGAAAACGGTGGCCCTAAAAGAGGAAAAGAATTTACCAATATAAATC
CAATTTTATGAAACTGACAATTTAATCCAAGAATCACTTTTGTAAATGAAGCTAGCAAGTGATGATATGATAA
AATAACGTGGAGGAAATAAAAACACAAGACTTGGCATAAGATATATCCACTTTTGATATTAACTTGTGAAGC
ATATTCTTCGACAAATTTGTAAAGCGTTCCTGATCTTGCTTGTCTCCATTTCAAATAAGGAGGCATATCACAT
CCCAAGAGTAACAGAAAAAGAAAAAGACATTTTGCATTTTGAGATGAACCAAGACACAAAACAAAACGAAC
AAAGTGTCTATGCTAATTCTAGCCTCTGAAATAAACCTTGAACATCTCTACAAGGCACCGTGATTTTGTAAAT
TCTAACCTGAAGAAATGTGATGACTTTTGTGGACATGAAAATCAGATGAGAAAAGTGTGGTCTTCCAAAGCCT
GAACTCCCTGAAAACCTTTGCA

Fig. 1C

4/101

11766.1.contig

CTGGGATCATTCTCTTGATGTCATAAAAGACTCTTCTTCTCCTCTTCATCCTCTTCTTCATCCTCTTCTGTGTA
CAGTGTGCTGCCGGGTACAACGGCTATCTTTGTCTTTATCCTGAGATGAAGATGATGCTTCTGTTTCTCCTACCAT
AACTGAAGAAATTTGCTGGAAGTCGTTTGACTGGCTGTTTCTCTGACTTCACCTTCTTTGTCAAACCTGAGTC
TTTTTACCTCATGCCCTCAGCTTCCACAGCATCTTCATCTGGATGTTTATTTTCAAAGGGCTCACTGAGGAA
ACTTCTGATTCAGAGGTCGAAGAGTCACTGTGATTTTCTCCTCATTTTGCTGCAAATTTGCCTCTTTGCTGTC
TGTGCTCTCAGGCAACCCATTTGTTGTCTGAGGGGCTGACAAAGAAACCTTTGGTCGATTAAGTGGCCTGGGTG
TCCAGGCCCATTTATATTAGACCTCTCAGTATAGCTTGGTGAATTTCCAGGAAACATAACACCATTCAATCGA
TTTAAACTATTGGAATTGGTTTT

11766.2.contig

GAGGGTTGGTGGTAGCGGCTTGGGGAGGTGCTCGCTCTGTGGTCTTGCTCTCTCGCACGCTTCCCCGGCTCC
CTTCGTTTCCCCCCCCGGTGCCTGCGTGCCGGAGTGTGTGCGAGGGAGGGGGAGGGCGTCGGGGGGTGGGG
GGAGGCGTTCCGGTCCCAAGAGACCCGCGGAGGGAGGCGGAGGCTGTGAGGGACTCCGGAAGCCATGGACGT
CGAGAGGCTCCAGGAGGCGCTGAAAGATTTTGAGAAGAGGGGGAAAAAGGAAGTTTGCTGTCTGGATCAGT
TTCTTTGTCTGTAGCCAAGACTGGAGAAACAATGATTCAGTGGTCCCAATTTAAGGCTATTTATTTTCAA
CTGGAGAAAGTGATGGATGATTTCAGAACTTCAGCTCCTGAGCCAAGAGGTCTCCCAACCTAATGTGCA

11773.2.contig

AAGCAGGCGGCTCCCGCTCGCAGGGCCGTGCCACCTGCCCGCCCGCCGCTCGCTCGCTCGCCCGCCGCGCC
GCGCTGCCGACCGCCAGCATGCTGCCGAGAGTGGGTGCCCGCGCTGCCGXTGCCG

11775-1&2

ATCTCTTGATGCCAAATATTTAATATAAATCTTTGAAACAAGTTCAGATGAAATAAAATCAAAGTTTGCAA
AACGTGAAGATTAACCTAATTGTCAAATATTCCTCATTGCCCAAATCAGTATTTTTTTATTTCTATGCAAAA
GTATGCCTTCAAACCTGCTTAAATGATATATGATATGATACACAAACCAGTTTTCAAATAGTAAAGCCAGTCATC
TTGCAATTGTAAGAAATAGGTAAAAGATTATAAGACACCTTACACACACACACACACACACAGTGTGCAGG
CCAATGACAAAAACAATTTGGCCTCTCCTAAAATAAGAACATGAAGACCCTTAATTGCTGCCAGGAGGGAACA
CTGTGTACCCCTCCCTACAATCCAGGTAGTTTCTTTAATCCAATAGCAAATCTGGGCATATTTGAGAGGAGT
GATTCTGACAGCCACGTTGAAATCCTGTGGGGAACCATTATGTCCACCCACTGGTGCCCTGAAAAATGCCAA
TAATTTTTGCTCCCACTTCTGCTGCTGCTCTTCCACATCCTCACATAGACCCAGACCCGCTGGCCCTGGC
TGGGCATCGATTGCTGGTAGAGCAAGTCATAGGTCTCGTCTTTGACGTCACAGAAGCGATACACCAAATTGCC
TGGTGGTCAATTGTCATAACCAGAGA

Fig. 1D

5/101

11777.1&2.cons

CAGACGGGGTTTCACTATGTTGGCTAGGCTGGTCTTGAACCTCTGACTTCAGGTGATCTGCCTGCCTTGGCCTC
CCAAAGTGCTGGGATTACAGGCATAAGCCACTGCGCCCGGCTGATCTGATGGTTTCATAAGGCTTTTCCCCCTT
TTGCTCAGCACTTCTCCTTCTGCGCCATGTGAAGAAGGACATGTTTGCTTCCCCTTCCACCACGATTGTAAG
TTGTTTCTGAGGCCTCCCCGGCCATGCTGAACGTGAGTCAATTAACCTCTTCTTTATAAATTATCCAGT
TTTGGGTATGCTTTATTAGTAGAATGAGAACAGACTAATACAACCTTAAAGGAGACTGACGGAGAGGATTCT
TCCTGGATCCCAGCACTTCTCTGAATGCTACTGACATTCTTCTTGAGGACTTTAACTGGGAGATAGAAAACA
GATTCATGGCTCAGCAGCCTGAGAGCAGGGAGGGAGCCAAGCTATAGATGACATGGGCAGCCTCCCCTGAGGC
CAGGTGTGGCCGAACCTGGGCAGTGCTGCCACCCACCCACAGGGCCAAGTCCTGTCTTGGAGAGCCAAGCC
TCAATCACTGCTAGCCTCAAGTGTCCCAAGCCACAGTGGCTAGGGGGACTCAGGGAACAGTTCCAGTCTGCC
CTACTTCTTTACCTTTACCCCTCATACCTCCAAAGTAGACCATGTTTCATGAGGTCCAAAGG

11779.2.contig

AAGCGAGGAAGCCACTGCGGCTCCTGGCTGAAAAGCGGCGCCAGGCTCGGGAACAGAGGGAACGCGAAGAACAG
GAGCGGAAGCTGCAGGCTGAAAGGGACAAGCGAATGCGAGAGGAGCAGCTGGCCCGGGAGGCTGAAGCCCGGGC
TGAACGTGAGGCGAGGCGGAGAGCGGGAGGAGCAGGAGGCTCGAGAGAAGGCGCAGGCTGAGCAGGAGGAGC
AGGAGCGACTGCAGAAGCAGAAAGAGGAAGCCGAAGCCCGGTCCCGGGAAGAAGCTGAGCGCCAGCGCCAGGAG
CGGGAAGCACTTTTCAAGGAGGAACAGGAGAGACAAGAGCGAAGAAAGCGGCTGGAGGAGATAATGAAGAG
GACTCGGAAATCAGAAGCCGCCGAAACCAAGAAGCAGGATGCAAAGGAGACCGCAGCTAACAAATCCGGCCAG
ACCCTTGTGAAAGCTGTAGAGACTCGGCCCTCTGGGCTTCCAGAAAGGATTCTATTGCAGAAAGGAAGGAGCTX
GGCCCCCAXGGA

11781 & 37.cons

CTCTGTGAAAACTGATGAGGAATGAATTTACCATTACCCATGTTCTCATCCCCAAGCAAAGTGCTGGGTCTGA
TTACTGCAACACAGAGAACGAAGAAGAACTTTTCTCATACAGGATCAGCAGGGCTCATCAGCTGGGCTGGA
TTCATACTACCCACACAGACCGGTTTCTCTCCAGTGTGACCTACACACTCACTGCTTTACCAGATGATG
TTGCCAGAGTCAGTAGCCATTGTTTGCTCCCCAAGTTCCAGGAACTGGATTCTTTAACTAACTGACCATGG
ACTAGAGGAGATTTCTTCTGTCGCCAGAAAGGATTTATCCACACAGCAAGGATCCACCTCTGTTCTGTAGCT
GCAGCCACGTGACTGTTGTGGACAGAGCAGTGACCATCACAGACCTTCGATGAGCGTTTGAGTCCAACACCTTC
CAAGAACAACAAAACCATATCAGTGTACTGTAGCCCTTAATTTAAGCTTTCTAGAAAGCTTTGGAAGTTTTTG
TAGATAGTAGAAAGGGGGCATCACXTGAGAAAGAGCTGATTTTGTATTTAGGTTTGAAGAAATAACTGAA
CATATTTTTTAGGCAAGTCAGAAAGAGAACATGGTCACCCAAAAGCAACTGTAACCTAGAAATTAAGTACTCA
GAAATTAAGTAGCTCAGAAATTAAGAAAGAATGGTATAATGAACCCCATATACCTTCTCTGGAATTCACCA
ATTGTTAACATTTTTTCTCTCAGCTATCCTTCTAATTTCTCTAATTTCAATTTGTTTATATTTACCTCTG
GGCTCAATAAGGGCATCTGTGCAGAAATTTGGAAGCCATTTAGAAAATCTTTTGGATTTTCTGTGGTTTATGG
CAATATGAATGGAGCTTATTACTGGGGTGAGGGACAGCTTACTCCATTTGACCAGATTGTTTGGCTAACACATC
CCGAAGAATGATTTTGTGAGGAATTATGTTATTTAATAAATATTTTCAGGATATTTTCTCTACAATAAAGTA
ACAAT

Fig. 1E

6/101

11781-76-87-37

CTCTGTGGAAACTGATGAGGAATGAATTTACCATTACCCATGTTCTCATCCCCAAGCAAAGTGCTGGGTCTGA
T TACTGCAACACAGAGAACGAAGAAGAACTTTTCTCATACAGGATCAGCAGGGCCTCATCACTGGGCTGGA
TTCATACTCACCCACACAGACCGGTTTCTCTCCAGTGTGCGACCTACACACTCACTGCTCTTACCAGATGATG
TTGCCAGAGTCAGTAGCCATTGTTTGCTCCCCAAGTTCAGGAACTGGATTCTTTAACTAACTGACCATGG
ACTAGAGGAGATTTCTTCTGTGCGCCAGAAAGGATTTTCATCCACACAGCAAGGATCCACCTCTGTTCTGTAGCT
GCAGCCACGTGACTGTTGTGGACAGAGCAGTGACCATCACAGACCTTCGATGAGCGTTTGAGTCCAACACCTTC
CAAGAACAACAAAACCATATCAGTGTACTGTAGCCCCCTTAATTTAAGCTTTCTAGAAAGCTTTGGAAGTTTTTG
TAGATAGTAGAAAGGGGGGCATCACCTGAGAAAGAGCTGATTTTGTATTTAGGTTTGAAAAGAAATAACTGAA
CATATTTTTTAGGCAAGTCAGAAAGAGAACATGGTCACCCAAAAGCAACTGTAACCTAGAAATTAAGTTACTCA
GAAATTAAGTAGCTCAGAAATTAAGAAAGAATGGTATAATGAACCCCATATACCCTTCCTTCTGGATTACCA
ATTGTTAACAATTTTTCTCTCAGCTATCCTTCTAATTTCTCTCTAATTTCAATTTGTTTATATTTACCTCTG
GGCTCAATAAGGGCATCTGTGCAGAAATTTGGAAGCCATTTAGAAAATCTTTTGGATTTTCTGTGGTTTATGG
CAATATGAATGGAGCTTATTACTGGGGTGAGGGACAGCTTACTCCATTTGACCAGATTGTTTGGCTAACACATC
CCGAAGAATGATTTTGTGAGGAATTATTGTTATTTAATAAATATTTAGGATATTTTCTCTACAATAAAGTA
ACAATTA

11784-1 & 2

GGACGACAAGGCCATGGCGATATCGGATCCGAATTCAGCCTTTGGAATTAATAAACCTGGAACAGGGAAGGT
GAAAGTTGGAGTGAGATGTCTTCCATATCTATACCTTTGTGCACAGTTGAATGGGAAGTGTGTTGGGTTAGGGC
ATCTTAGAGTTGATTGATGGAAAAAGCAGACAGGAAGTGGTGGGAGGTCAAGTGGGGAAGTTGGTGAATGTGGA
ATAACTTACCTTTGTGCTCCACTTAAACCAGATGTGTTGCAGCTTTCTGACATGCAAGGATCTACTTTAATTC
CACACTCTCATTAAATAAATTGAATAAAAGGGAATGTTTGGCACCTGATATAATCTGCCAGGCTATGTGACAGT
AGGAAGGAATGGTTTCCCTAACAAGCCCAATGCACTGGTCTGACTTTATAAATTATTTAATAAAATGAACTAT
TATC

11785.2.contig

GGCAGTGACATTCACCATCATGGGAACCACTTCCCTTTTCTTCAGGATTCTCTGTAGTGGAAGAGAGCACCCA
GTGTTGGGCTGAAAACATCTGAAAGTAGGGAGAAGAACCTAAAATAATCAGTATCTCAGAGGGCTCTAAGGTGC
CAAGAAGTCTCACTGGACATTTAAGTGCCAACAAAGGCATACTTTCGGAATCGCCAAGTCAAACTTTCTAACT
TCTGTCTCTCTCAGAGACAAGTGAGACTCAAGAGTCTACTGCTTTAGTGGCAACTACAGAAAAGTGGTGTACC
CAGAAAAACAGGAGCAATTAGAAATGGTTCCAATATTTCAAAGCTCCGCAACAGGATGTGCTTTCCTTTGCCC
ATTTAGGGTTTCTTCTTTTCTTTCTTTTATTAACCACT

Fig. 1F

7/101

11718-1&2 cons

TGCGCTGAAAACAACGGCCTCCTTTACTGTAAAAATGCAGCCACAGGTGCTTAGCCGTGGGCATCTCAACCACC
AGCCTCTGTGGGGGGCAGGTGGGCGTCCCTGTGGGCTCTGGGCCCACGTCCAGCCTCTGTCTCTGCCTTCCG
TTCTTCGACAGTGTTCCGGCATCCCTGGTCACCTTGGTACTTGGCGTGGGCTCCTGTGCTGCTCCAGCAGCTC
CTCCAGGXGGTCGGCCCGCTTCACCGCAGCCTCATGTTGTGTCCGGAGGCTGCTCACGGCCTCCTCCTTCTCG
CGAGGGCTGTCTTACCCTCCGGXGCACCTCCTCCAGTCCAGTGTGGCGGGCCTGCAGCGTGGCCAGCTCG
GCCTTGGCCTGCCGCGTCTCCTCCTCARAGGCTGCCAGCCGGTCTCGAACTCCTGGCGGATCACCTGGGCCAG
GTTGCTGCGCTCGCTAGAAAGCTGCTCGTTCACCGCTGCGCATCCTCCAGCGCCGCTCCTTCTGCCGCACAA
GGCCCTGCAGACGCAGATTCTCGCCCTCGGCcTCCCCAAGCTGGCCCTTCAGTCCGAGCACCGCTCCTGAAGC
TTCCGCTCCGACTGCTCCAGCTCGGAGAGCTCGGCCTCGTACTTGTCCCGTAAGCGCTTGATGCGGCTCTCGGC
AGCCTTCTCACTCTCCTCCTTGGCCAGCGCCATGTGGGCTCCAGCCGGTGAATGACCAGCTCAATCTCCTTGT
CCCGGCCCTTCCGGATTTCTTCCCTCAGCTCCTGTTCCCGGTTAGCAGCCACGCCTCCTCCTTCTGGTGCGG
CCGGCCTCCACGCCTGCCTCTCCAGTCCAGTGTGCTTCAGGGTATTAGCTCCATCTGGCGGGCCTGCAG
CGTGGCCA

13690.4

CAACTTATTACTTGAAATTATAATATAGCCTGTCCGTTTGCTGTTTCCAGGCTGTGATATATTTTCTAGTGGT
TTGACTTTAAAAATAAATAAGGTTTAATTTTCTCCCC

13693.1

TGCAAGTCACGGGAGTTTATTTATTTAATTTTTTTTCCCCAGATGGAGACTCTGTGCCCCAGGCTGGAGTGCAAT
GGTGTGATCTTGGCTCACTGCAACCTCCACCTCCTGGGTTCAAGCGATTCTCCTGCCACAGCCTCCCGAGTAGC
TGGGATTACAGGTGCCCGCCACCACCCAGCTAATTTTTATATTTTAGTAAAGACAGGGTTTCCCCATGTTG
GCCAGGCTGGTCTTGAACCTCTGACCTCAGGTGATCCACCTGCCTCGGCCTCCCAAAGTGTGGGATTACAGGC
GTGAGCTACCCGTGCCTGGCCAGCCACTGGAGTTTAAAGGACAGTCATGTTGGCTCCAGCCTAAGGCGGCATTT
TCCCCATCAGAAAGCCCGCGGCTCCTGTACCTCAAAATAGGGCACCTGTAAAGTCAGTCAGTGAAGTCTCTGC
TCTAACTGGCCACCCGGGGCCATTGGCNTCTGACACAGCCTTGCCAGGANGCCTGCATCTGCAAAAGAAAAGTT
CACTTCTTTCCG

13694.1

CAGAGAATCTKAGAAAGATGTCGCGTTTTCTTTTAAATGAATGAGAGAAGCCCATTTGTATCCCTGAATCATTGA
GAAAAGCGGGGTGGCGACAGCGGCGACCTAGGGATCGATCTGGAGGGACTTGGGGAGCGTGCGAGACCTCT
AGCTCGAGCGCGAGGGACCTCCCGCCGGGATGCCTGGGAGCAGATGGACCCTACTGGAAGTCAGTTGGATTCA
GATTTCTCTCAGCAAGATACTCCTTGCCTGATAATTGAAGATTCTCAGCCTGAAAGCCAGGTTCTAGAGGATGA
TTCTGGTTCTCACTTCAGTATGCTATCTCGACACCTTCTAATCTCCAGACGCACAAAGAAAAATCCTGTGTTGG
ATGTTNGTCCAATCCTTGAACAAACAGCTGGAGAAGAACGAGGAGACCGGTAATAGTGGGTTCAATGAACATT
TGAAAGAAAACCAGGTTGCAGACCCTG

Fig. 1G

8/101

13694.2

GACTGTCCTGAACAAGGGACCTCTGACCAGAGAGCTGCAGGAGATGCAGAGTGGTGGCAGGAGTGGGAAGCCAAA
GAACACCCACCTTCCTCCCTTGAAGGAGTAGAGCAACCATCAGAAGATACTGTTTTATTGCTCTGGTCAAACAA
GTCTTCCTGAGTTGACAAAACCTCAGGCTCTGGTGACTTCTGAATCTGCAGTCCACTTTCATAAGTTCTTG
CAGACAACTGTTCTTTGCTTCCATAGCAGCAACAGATGCTTTGGGGCTAAAAGGCATGTCCTCTGACCTTGCA
GGTGGTGGATTTTGCTCTTTACAACATGTACATCCTTACTGGGCTGTGCTGTCACAGGGATGTCCTTGCTGGA
CTGTTCTGCTATGGGGATATCTTCGTTGGACTGTTCTTCATGCTTAATTGCAGTATTAGCATCCACATCAGAÇA
GCCTGGTATAACCAGAGTTGGTGGTACTGATTGTAGCTGCTCTTGTCCACTTCATATGGCACAAGTATTTTC
CTCAACATCCTGGCTCTGGGAAG

13695.1

GAAATGTATATTTAATCATTCTCTGAACGATCAGAACTCTRAAATCAGTTTTCTATAACARCATGTAATACAG
TCACCGTGGCTCCAAGGTCCAGGAAGGCAGTGGTTAACACATGAAGAGTGTGGGAAGGGGGCTGGAAACAAAGT
ATTCTTTTCCTTCAAAGCTTCATTCTCAAGGCCTCAATTCAAGCAGTCATTGTCCTTGCTTCAAAGTCTGT
GTGTGCTTCATGGAAGGTATATGTTTGTTCCTTAATTTGAATTGTGGCCAGGAAGGGTCTGGAGATCTAAATT
CAGAGTAAGAAAACCTGAGCTAGAACTCAGGCATTTCTCTTACAGAACTTGGCTTGAGGGTGAATGAANGGA
AAGAACTTAGAAGCTCAACAAGCTGAAGATAATCCCATCAGGCATTTCCCATAGGCCTTGCAACTCTGTTTAC
TGAGAGATGTTATCCTG

13695.2

AGTCTGGAGTGAGCAAACAAGAGCAAGAAACAARRAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAA
ATCTATCTTCAAAGACATATTAGAAGTTGGGAAAATAATTCATGTGAAGTAGACAAGTGTGTTAAGAGTGATAA
GTAAATGCACGTGGAGACAAGTGCATCCCGATCTCAGGGACCTCCCCCTGCCTGTACCTGGGGAGTGAGA
GGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTAGTTATATGTGCTGTAATGTTGCTCTGAGGAAGCCCC
TGGAAAGTCTATCCCAACATATCCACATCTTATATCCACAAATTAAGCTGTAGTATGTACCTAAGACGCTGC
TAATTGACTGCCACTTCGCAACTCAGGGGCGGCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTTATGATG
CTTCCCAAGGTGCCTTGGCTTCTCTTCCCAACTGACAAATGCCCAAGTTGAGAAAAATGATCATAATTTTAGCA
TAAACCGAGCAATCGGCGACCCC

13697.1

TAGCTGTCTTCCTCACTCTTATGGCAATGACCCCATATCTTAATGGATTAAGATAATGAAAGTGATTTCTTAC
ACTCTGTATCTATCACCAGAAGCTGAGGTGATAGCCCGTTGTCAATTGTCATCCATATTCTGGGACTCAGGCGG
GAACTTTCTGGAATATTGCCAGGGAGCATGGCAGAGGGGCACAGTGCATTCTGGGGGAATGCACATTGGCTCAG
CCTGGGTAATGAGTGATATACATTACCTCTGTTCACTCACTGTTGCCAGCACCAGTCAAGGCCCAACAAA
TACCAGAGCCCAAGAAATGTAGTCTGTTGATATGTTTTGCTGTGTCCCAACCCAAATCTCATCTTGAATTGT
AAGTCCCATAATTCCCATGTGTTGTGGGAGGGACCTGGTG

Fig. 1H

9/101

13697.2

ATCATGAGGATGTTACCAAAGGGATGGTACTAAACCATTTGTATTGCTCTGTTTTCACTGCTTTGAAGATAC
TACCTGAGACTGGGTAATTTATAACAAAAGAGATTTAATTGACTCACAGTTCTGCATGGCTGAAGAGGCCTCA
GGAACTTACAGTCATGGTGAAGGCAAAGGAGGAGCAAGGCATGTCTTACATGTCAGTAGGAGAGAGAGCGAG
AGCAGGAGAACCTGCCACTTATAAACCATTCAGATCTCATAACTCCCTATCATGAGAAAAACATGGAGGAAACC
ACCCTCATGATCCAATCACCTCCCGCCAGGTCCCTCCCTCGACACGTGGGGATTATAATTGAGGATTAGAGGGA
CACAGAGACAAACCATATCATCATTATGAGAAATCCACCCTCATAGTCCAATCAGCTCTACCAGGCCCCACC
TCCAACACTGGGGATTGCAATTCAACATGAGATTTGGATGGGGACACAGATTCAAACCATATCATAC

13699.1&2

CATGGCCTTTCTCCTTAGAGGCCAGAGGTGCTGCCCTGGCTGGGAGTGAAGCTCCAGGCACTACCAGCTTTCTT
GATTTTCCCGTTTGGTCCATGTGAAGAGCTACCACGAGCCCCAGCCTCACAGTGCTCAAGGGCAGCTTGG
TCCTCTTGCTGTCAGAGGCAGGCTGGTGTGACCTGGGAACTTGACCCGGGAACAACAGGTGGCCAGAGTGA
GTGTGGCCTGGCCCCCTCAACCTAGTGTCCGTCTCCTCTCTCCTGGAGCCAGTCTTGAGTTTAAAGGCATTAAG
TGTTAGATACAAGCTCCTTGCTGGCTGGAAAAACACCCTCTGCTGATAAAGCTCAGGGGGCACTGAGGAAGCAG
AGGCCCTTGGGGTGCCCTCTGAAGAGAGCGTCAGGCCATCAGCTCTGTCCCTCTGGTGCTCCACGTCTGT
TCCTCACCTCCATCTCTGGGAGCAGCTGCACCTGACTGGCCACGCGGGGCAGTGGAGGCACAGGCTCAGGGT
GGCCGGGCTACCTGGCACCTATGGCTTACAAAGTAGAGTTGGCCAGTTTCTTCCACCTGAGGGGAGCACTC
TGACTCCTAACAGTCTTCTTGCCCTGCCATCATCTGGGGTGGCTGGCTGTCAAGAAAGGCCGGGCATGCTTTC
TAAACACAGCCACAGGAGGCTTGTAAGGCATCTTCCAGGTGGGGAAACAGTCTTAGATAAGTAAGGTGACTTGC
CTAAGGCCTCCAGCACCTTGATCTTGAGTCTCACAGCAGACTGCATGTSAAACACTGGAACCGAAACATG
CCTCAGTATAAAA

13703.3

CCAGAACCTCCTTCTCTTTGGAGAATGGGGAGGCCTCTTGAGACACAGAGGGTTTCACCTTGGATGACCTCTA
GAGAAATTGCCAAGAAGCCACCTTCTGGTCCCAACCTGCAGACCCACAGCAGTCAGTTGGTCAGGCCCTGC
TGTAAGAGGTCACTTGGCTCCATTGCCTGCTTCCAACCAATGGGCAGGAGAGAAGGCCTTTATTTCTGCCCCAC
CCATTCTCCTGTACCAGCACCTCCGTTTTAGTCAGYGTGTCCAGCAACGGTACCGTTTACACAGTCA

13705.1

TGCATGTAGTTTTATTTATGTGTTTTSGTCTGGAACCAAGTGTCCAGCAGCATGACTGAACATCACTCACT
TCCCCTACTTGATCTACAAGGCCAACGCCGAGAGCCAGACCAGGATTCAAACACACTGCACGAGAATATTGT
GGATCCGCTGTGAGGTAAGTGTCCGTCACTGACCCARACGCTGTTACGTGGCACATGACTGTACAGTGCCACGT
AACAGCACTGTACTTTTCTCCATGAACAGTTACCTGCCATGTATCTACATGATTGAGAACATTTTGAACAGTT
AATTCTGACACTTGAATAATCCCATCAAAACCGTAAATCACTTTGATGTTTGTAAACGACAACATAGCATCAC
TTTACGACAGAATCATCTGGAAAAACAGAAACGAATACATACATCTTAAAAATGCTGGGGTGGGCCAGGCA
CAGCTTCACGCCTGTAATCCAGCACTTTGGGAGGCTTAAGCGGGTG

Fig. 11

10/101

13705.2

TGGGGCGGAAAGAAGCCAAGGCCAAGGAGCTGGTGCGGCAGCTGCAGCTGGAGGCCGAGGAGCAGAGGAAGCAG
AAGAAGCGGCAGAGTGTGTGCGGGCTGCACAGATACCTTCACTTGCTGGATGGAAATGAAATTACCCGTGTCT
TGTGGATGCAGACGGTGATGTGATTTCCCTTCCCACCAATAACCAACAGTGAGAAGACAAAGGTTAAGAAAACGA
CTTCTGATTTGTTTTTGGAAAGTAACAAGTGCCACCAGTCTGCAGATTTGCAAGGATGTCATGGATGCCCTCATT
CTGAAATGGCAAGAAATGAAAAAGTACACTTTAGAAAATAAGAGGAAGGATCACTCTCAGATACTGAAGCCG
ATGCAGTCTCTGGACAACCTCCAGATCCCACAACGAATCCAGTGCTGGAAAGGACGGGCCCTTCCTTCTGGTG
GTGGAACANGTCCCGTGGTGGATCTTGAANGAACCTGAANGTGGTGTACCCCGTCCAAGGCCGACCTTGGC
CAC

13707.4

TCCCGCGCTCGCAGGGCNCGTGCCACCTGCCYGTCCGCCCGCTCGCTCGCTCGCCCGCCGCGCCGCTGCCGA
CCGYCAGCATGCTGCCGAGAGTGGGCTGCCCCGCGCTGCCGCTGCCGCGCCGCGCTGCTGCCGCTGCTGCCG
CTGCTGCTGCTGC

13708.1&2

GGCGGGTAGGCATGGAAGTGAAGAAGCAAGAAGCTTTCAGACTACGTGGGGAAGAATGAAAAAACCAAAATT
ATCGCCAAGATTAGCAAGGGGACAGGGAGCTCCAGCCCGAGAGCCTATTATTAGCAGTGAGGAGCAGAAGCA
GCTGATGCTGTACTATCACAGAAGACAAGAGGAGCTCAAGAGATTGGAAGAAATGATGATGATGCCTATTTAA
ACTCACCATGGGCGGATAACACTGCTTTGAAAAGACATTTTCATGGAGTGAAAGACATAAAGTGGAGACCAAGA
TGAAGTTCACCAGCTGATGACACTTCCAAAGAGATTAGCTCACCT

13709.1

TCTGAAGGTTAAATGTTTCATCTAAATAGGGATAATGRTAAACACCTATAGCATAGAGTTGTTTGAGATTAAAT
GAGATAATACATGTAAATTATGTGCCTGGCATAACAGCAAGATTGTTGTTGTTGTTGATGATGATGATGATGAT
GATAATATTTTTCTATCCCAGTGCACTGCTTGAACCTATTAGATAATCAATACATGTTTCTTGAAGTGAAG
ATCAATTTCCCATGTTGTCTGACTGATGAAGCCCTACATTTCTTCTAGAGGAGATGACATTTGAGCAAGATC
TTAAAGAAATCAGATGCCTTCACCTGACCACTGCTTGGTGATCCCATGGCACTTTGTACATCTCTCCATTAGC
TCTCATCTCACCAGCCCATCATTATTGTATGTGCTGCCTTCTGAAGCTTGCAGCTGGCTACCATCMGGTAGAAT
AAAAATCATCCTTTCATAAAATAGTGACCTCCTTTTTTATTTGCATTTCCCAAAGCCAAGCACCGTGGGANGG
TAG

Fig. 1J

11/101

13709.2

TATGAAGAAGGGAAAAGAAGATAATTTGTGAAGAAATGGGTCCAGTTACTAGTCTTTGAAAAGGGTCAGTCTG
TAGCTCTTCTTAATGAGAATAGGCAGCTTTCAGTTGCTCAGGGTCAGATTCCTTAGTGGTGTATCTAATCACA
GGAAACATCTGTGGTCCCTCCAGTCTCTTCTGGGGGACTTGGGCCACTTCTCATTTCAATTAATAGAGGA
AATAGAACTCAAAGTACAATTTACTGTTGTTAACAATGCCACAAAGACATGGTTGGGAGCTATTTCTTGATTT
GTGTAAAATGCTGTTTTGTGTGCTCATAATGGTCCAAAAATTGGGTGCTGGCCAAAGAGAGATACTGTTACA
GAAGCCAGCAAGAAGACCTCTGTTCAATCACACCCCGGGGATATCAGGAATTGACTCCAGTGTGTGCAAATCC
AGTTTGGCCTATCTTCT

13712.1&2

TGAGGGACTGATTGGTTTGCTCTCTGCTATTCAATTCCTCAAGCCCACTTGTTCTGTCAGCGTCTCTCTCTCA
TTCCCTTTAGTTGTACCTCTCTTTCATCTGAGACCTTTCCTTCTTGATGTGCGCTTTTCTTCTTCTTGCTTTT
TCTGATGTTCTGCTCAGCATGTTCTGGGTGCTTCTCATCTGCATCATTCCTTTCAGATGCTGTAGCTTCTTCT
CCTCTTTCTGCTCCTTTTCTTTTCTTTTTTGGGGGGCTTGCTCTCTGACTGCAGTTGAGGGGCCCCAGGG
TCCTGGCCTTTGAGACGAGCCAGGAAGGCCTGCTCCTGGGCCTTAGGCGAGCAAGCTTGGCCTTCATTGTGAT
CCCAAGACGGGCAGCCTTGTGTGCTGTTGCCCCCTCACAGGCTTGAGCAGCATCTCATCAGTCAGAATCTTTG
GGGACTTGGACCCCTGGTGTGCTCATCACTGCAGTCTCCAAGTCTTTGTTGGCTTCTCTCCACCTGAAGTC
AATGTAGCCATCTTCAAACTTCTGATACAGCAAGTTGGGCTTGGGATGATTATAACGGGTGGTCTCCTTAGA
AAGGCTCCTTATCTGTACTCCATCCTGCCAGTTTCCACTACCAAGTTGGCCGAGTCTTGTTGAAGAGCTCAT
TCCACCAGTGGTTTGTGAACCTCTTGGCAGGGTCATGTCTACCCCATGAGTGTCTTGCTTCAGYGTACCCCTG
AGAGCCTGAGTGATACCATCTCCTTCG

13714.1&2

GACAACATGAAATAAATCCTAGAGGACAAAATTAACTCAATAGAGTGTAGTCTAGTTAAAAACTCGAAAAATG
AGCAAGTCTGGTGGGAGTGGAGGAAGGGCTATACTATAAATCCAAGTGGGCCTCCTGATCTTAACAAGCCATGC
TCATTATACACATCTCTGAACCTGGACATACCACCTTACGCAGGAAACAGGGCTTGGAACTTCTAAGGGAAAT
AACATGCACCACCCACATCTAACCTACCTGCCGGGTAGGTACCATCCCTGCTTCGCTGAAATCAGTGCTC

13716.1&2

TTGGAATTAATAAACCTGGAACAGGGAAGGTGAAAGTTGGAGTGAGATGTCTTCCATATCTATACCTTTGTGC
ACAGTTGAATGGGAACGTTTGGGTTTAGGGCATCTTAGAGTTGATTGATGGAAAAAGCAGACAGGAACCTGGTG
GGAGGTCAAGTGGGAAGTTGGTGAATGTGGAATAACTTACCTTTGTGCTCCACTTAAACCAGATGTGTTGCAG
CTTTCCTGACATGCAAGGATCTACTTTAATTCACACTCTCATTAATAAATTGAATAAAAGGGAATGTTTTGGC
ACCTGATATAATCTGCCAGGCTATGTGACAGTAGGAAGGAATGGTTCCCTAACAAGCCCAATGCACTGGTCT
GACTTTATAAATTATTTAATAAAATGAATATTATC

Fig. 1K

12/101

13718.2

AAACTGGACCTGCAACAGGGACATGAATTTACTGCARGGTCTGAGCAAGCTCAGCCCCTCTACCTCAGGGCCCC
ACAGCCATGACTACCTCCCCAGGAGCGGGAGGGTGAAGGGGGCCTGTCTCTGCAAGTGGAGCCAGAGTGGAGG
AATGAGCTCTGAAGACACAGCACCCAGCCTTCTCGACCAGCCAAGCCTTAAGTGCCTGCCTGACCCTGAACCA
GAACCCAGCTGAAGTGGCCCTCCAAGGGACAGGAAGGCTGGGGGAGGGAGTTTACAACCCAAGCCATTCCACCC
CCTCCCCTGCTGGGGAGAATGACACATCAAGCTGCTAACAATTGGGGGAAGGGGAAGGAAGAAAACCTCTGAAAA
CAAAATCTTGT

13722.3

CATGCGTTTCACCACTGTTGGCCAGGCTGGTCTCGAACTCCTGGCCTCAAGCAATCCACCCGCCTCAGCCTCCA
AAAGTGCTGGGATTACAGATGTGAGCCATGGCACCATGCCAAAAGGCTATATTCCTGGCTCTGTGTTTCCGAGA
CTGCTTTTAAATCCCAACTTCTCTACATTTAGATTAATAAATATTTTATTCATGGTCAATCTGGAACATAATTAC
TGCATCTTAAGTTTTCACTGATGTATATAGAAGGCTAAAGGCACAATTTTTATCAAATCTAGTAGAGTAACCAA
ACATAAAATCATTAACTTTCAACTTAATAACTAATTGACATTCTCAAAGAGCTGTTTTCAATCCTGATA
GGTTCTTTATTTTTCAAATATATTTGCCATGGGATGCTAATTTGCAATAAGGCGCATAATGAGAATACCCCA
AACTGGA

13722.4

GTTGGACCCCCAGGGACTGGAAAGACACTTCTTGCCCGAGCTGTGGCGGGAGAAGCTGATGTTCTTTTTATTA
TGCTTCTGGATCCGAATTTGATGAGATGTTTGTGGGTGTGGGAGCCAGCCGTATCAGAAATCTTTTTAGGGAAG
CAAAGGCGAATGCTCCTTGTTTATATTTATTTGATGAATTAGATTCTGTTGGTGGGAAGAGAATTGAATCTCCA
ATGCATCCATATTCAAGGCAGACCATAAATCAACTTCTTGCTGAAATGGATGGTTTTAAACCAATGAAGGAGT
TATCATAATAGGAGCCACAACTTCCCAGAGGCATTAGATAATGCCTTAATACCGTCTGGTCGTTTTGACATG
CAAGTTACAGTTCCAAGGCCAGATGTAAGGTGCAACAGAAATTTTGAATGGTATCTCAATAAAATAAAGTT
TGATCAATCCCGTTGATCCAGAAATTATAGCCTCGAGGTACTGGTGGCTTTTCCGGAAGCAGAGTTGGGAGAAT
CTT

13724-13698-13748

GCCTACAACATCCAGAAAGAGTCTACCCTGCACCTGGTGTSCGTCTCAGAGGTGGGATGCAGATCTTCGTGAA
GACCCTGACTGGTAAGACCATCACTCTCGAAGTGGAGCCGAGTGACACCATYGAGAACGTCAAAGCAAAGATCC
ARGACAAGGAAGGCRTYCCTCCTGACCAGCAGAGGTTGATCTTTGCCGGAAGCAGCTGGAAGATGGDCGCACC
CTGTCTGACTACAACATCCAGAAAGAGTCYACCTGCACCTGGTGTCCGTCTCAGAGGTGGGATGCARATCTT
CGTGAAGACCCTGACTGGTAAGACCATCACCTCGAGGTGGAGCCAGTGACACCATCGAGAATGTCAAGGCAA
AGATCCAAGATAAGGAAGGCATCCCTCCTGATCAGCAGAGGTTGATCTTTGCTGGGAAACAGCTGGAAGATGGA
CGCACCTGTCTGACTACAACATCCAGAAAGAGTCCACTCTGCACTTGGTCTGCGCTTGAGGGGGGTGTCTA
AGTTTCCCCTTTAAGGTTTCMAAAATTCATTGCACTTTCCTTTCAATAAAGTTGTTGCATTCCC

Fig. 1L

13/101

13730.1

GAACTGGGCCCTGAGCCCAAGTCATGCCTTGTGTCCGCATCTGCCGTGTCACCTCTGT KCCTGCCCTCAGCCC
TCCCTCCTGGTCTTCTGAGCCAGCACCATCTCCAAATAGCCTATTCTTCCTGCAAATCACACACATGCCGG
CCACACATACCTGCTGCCCTGGAGATGGGGAAGTAGGAGAGATGAATAGAGGCCCATACATTGTACAGAAGGAG
GGGCAGGTGCAGATAAAAGCAGCAGACCCAGCGGCAGCTGAGGTGCATGGAGCACGGTTGGGGCCGGCATTGGG
CTGAGCACCTGATGGGCCTCATCTCGTGAATCCTCGAGGCAGCGCCACAGCAGAGGAGTTAAGTGGCACCTGGG
CCGAGCAGAGCAGGAGACTGAGGGTCAGAGTGGAGGCTAAGCTGCCCTGGAATCCTCAATCTTGCCTGCCCC
TAGTATGAAGCCCCCTTCTGCCCTACAATTCTGA

13732.1

ATGGATCTTACTTTGCCACCCAGGTTGGAGTGCAGTGTGCAATCTTGGCTCACTGCAGCCTTAACCTCCCAGG
CTCAAGCTATCCTCCTGCCAAAGCCTTCCACATAGCTGGGACTACAGGTACACNGCCACCACACCCAGCTAAAA
TTTTTGTATTTTTGTAGAGACGGGATCTCGCCACGTTGCCAGGCTGGTCCCATCTGACCTCAAGCAGATCT
GCCACCTCAGCCCCCAACGTGCTAGGATTACAGGCGTGAGCCACCGCACCCAGCCTTTGTTTTGCTTTTAA
GGAATCACCAGTTCCCTCCGTGTCTCAGCAGCAGCTGTGAGAAATGCTTTGCATCTGTGACCTTTATGAAGG
GAACTTCCATGCTGAATGAGGGTAGGATTACATGCTCCTGTTTCCCGGGGTCAAGAAAGCCTCAGACTCCAGC
ATGATAAGCAGGGTGAG

13732.2

ATAGGGGCTTTAAGGAGGGAATTCAGGTTCAATGAGGTGTAAGGCCAGGGCTTTATCCAGTAAGACTGGGGT
CCTTAGATGAGAAAGAGACACCCGAGGTCTTCTCTGCCGTGTGAGGATGCATCAAGAAGGCGGCCGTCTGC
AAGCGAAGGAGAGGCCGCACCAGAAACCGACACCTTCATCTTGGACTTGCAGCCTCTAGAACTGAGAAAAAAC
TGTCTGTTGGTTAAGCCACCCAGTTTGTAGTATTCTCTTATGGCTTCCTAAGCAGACTAACAAACAAACACCCA
AAATTAACCTGATGGCTTCGCTGTCTTCTGTAAAAATTGCTATGAGAGAACTTTCACTCACTGTTTGCAGTTT
CTCCCTCAGTCCCTGGTTCTTCTCTCACATAATCCCAATTTCAATTTATAGTTTCATGGCCAGGCAGAGTCA
TTCATCACGGCATCTCCTGAGCTAAACCAGCACCTGCTCTGCTCACTTCTTGACTGGCTGCTCATCATCAGCCC
TCTTGAGAGATTTCAATTCCTCCCGTGCCAGGTACTTCACGCACCAAGCTCA

Fig. 1M

14/101

13735.1

GGATAATGAAGTTGTTTTATTTAGCTTGGACAAAAAGGCATATTCCTCTATTTTCTTATACAACAAATATCCCC
AAAATAAGCAAGCATATATATCTTGAATGTGTAATAATCCAGTGATAAACAAGAGCAGTACTTTAAAGAAAA
AAAAATATGTATTTCTGTCAAGTTAAAATGAGAATCAAAACCATTTACTCTGCTAACTCATTATTTTTTGCTTT
CTTTTTGGTTAAGAGAGGCAATGCAATACACTGAAAAAGGTTTTATCTTATCTGGCATTGGAATTAGACATAT
TCAAACCCAGCCCCATTTCCAACTTTAAGACCACAAACAAGTAATTTACTTTTCTGAACATTGGTTTTTTC
TGGAAATGGGAATTATAAAATAGACTTTGCAGACTCTTATGAGATTAAATAAGATAATGTATGAAATTCCTTC
TTCTTTTTTACTTCTTTTTCTTTTTGAGATGGAGTCTACCCCGTCACCCAGGCTGGAGTACAGTG

13735.2

CCACTGCACTCCAGCCTGGGTGACGGAGTGAGACTCTGTCTCAAAAAACAAACAAACAAACAAAAAACT
GAAAGGAAATAGAGTTCCTCTTTCCTCATATATGAATATATTATTTCAACAGATTGTTGATCACCTACCATAT
GCTTGGTATTGTTCTAATTGCTGGGGATACAGCAAGAGGTTCTGCAGAACTTCATGGAGCATGAAAGTAAATAA
ACAAAGTTAATTTCAAGGCCAGGCATGGTTGCTCACACCTTTAGTCCCAGCACTTTGGGAGGCTGAGGCAGGTG
GATCACTTGGGCCAGGAGTTCAAGGCTGCAGTGAGCCAAGATTGTGCCACTACTCTCCAGGCTGGGCAACAGA
GCAAGACCCTGTCTCAGGGGGAACAAAAAGTTAATTTAGATTGTTAAGTGTGTAAGGAAGTAAATAGGT
TGATATTCAAGAGAGCACCTGAAGGCCAGGCGTGGTGGCTCACGCCTGTGGTCTAACGCTTTGGGAAGCCCGAG
CGGGCGGATCACAAGGTCAGGAGAATTTTGGCCAGGCATGGTG

13736.1

AGAATCCATTTATTGGGTTTTAACTAGTTACACAACCTGAAATCAGTTTGGCACTACTTTATACAGGGATTACG
CCTGTGTATGCCGACACTTAAATACTGTACCAGGACCACTGCTGTGCTTAGGTCTGTATTCACTCATTACGCAT
GTAGATACTAAAAATATACTGTAGTGTTCTTTAAGGAAGACTGTACAGGGTGTGTTGCAAGATGACATTCACC
AATTTGTGAATTATTTCAACCCAGAAGATACCTTTCACTCTATAAACTTGTATAGGCAACATGTGGTGTTAG
CATTGAGAGATGCACACAAAAATGTTACATAAAAGTTTCAGACATTCTAATGATAAGTGAACGTAAAAA
AACCCACATCTCAATTTTGTAAACAAGATAAAGAAAATAATTTAAAAACAAAAAATGGCATTCACTGGGTA
CAAAGCC

13737.1&2

CAAATATTTAATATAAATCTTTGAAACAAGTTCAGAKGAAATAAAATCAAAGTTTGCAAAAACGTGAAGATTA
ACTTAATTGTCAAATATTCCTCATTGCCCAAATCAGTATTTTTTTATTTCTATGCAAAAGTATGCCTTCAAA
CTGCTTAAATGATATATGATATGATACACAAACAGTTTTCAAATAGTAAAGCCAGTCATCTTGCAATTGTAAG
AAATAGGTAAAAGATTATAAGACACCTTACACACACACACACACACACACACAGTGTGCACcGCCAATGAC
AAAAACAATTTGGCCTCTCCTAAAATAAGAACATGAAGACCCTTAATTGCTGCCAGGAGGGAACACTGTGTCA
CCCCTCCCTACAATCCAGGTAGTTTCTTTAATCCAATAGCAAATCTGGGCATATTTGAGAGGAGTGATTCTGA
CAGCCACSGTTGAAATCCTGTGGGGAACCATTCATGTCCACCCACTGGTGCCCTGAAAAATGCCAATAATTTT
TCGCTCCCACTTCTGCTGCTGTCTCTTCCACATCCTCACATAGACCCAGACCCGCTGGCCCTGGCTGGGCAT
CGCATTGCTGGTAGAGCAAGTCATAGGTCTCGTCTTTGACGTCACAGAAGCGATACACCAAATTCCTGGTCCG
TCATTGTCATAACCAAG

Fig. 1N

15/101

13738.1

TTTGACTTTAGTAGGGGTCTGAACTATTTATTTTACTTTGCCMGTAATATTTARACCYTATATATCTTTCATTA
TGCCATCTTATCTTCTAATGBCAAGGGAACAGWTGCTAAMCTGGCTTCTGCATTWATCACATTAATAATGGCTT
TCTTGGAATACTTCTTGATATGAATAAAGGATCTTTTAVAGCCATCATTTAAAGCMGNTTCTCTCCAACACG
AGTCTGCTASGGGGGGKAGCTGTGAACTCTGGCTGAAGGCTTCCCATACACACTGCAATGACMTGGTTTCT
GACCAGBTGAGTTA

13738.2

AGAGAAGCCCCATAAATGCAATCAGTGTGGGAAGGCCTTCAGTCAGAGCTCAAGCCTTTTCTCCATCATCGGG
TTCATACTGGAGAGAAACCCTATGTATGTAATGAATGCGGCAGAGCCTTTGGTTTTAACTCTCATCTTACTGAA
CACGTAAGGATTACACAGGAGAGAAAACCCTATGTTTGTAAATGAGTGCGGCAAAGCCTTTCGTGCGAGTTCCAC
TCTTGTTGAGCATCGAAGAGTTCACACTGGGGAGAAGCCCTACCAGTGCGTTGAATGTGGGAAAGCTTTCAGCC
AGAGCTCCAGCTCACCTACATCAGCCGAGTTCACACTGGAGAGAAGCCCTATGACTGTGGTGACTGTGGGAA
GGCCTTCAGCCGAGGTCAACCCTCATTGAGCATCAGAAAGTTCACAGCGGAGAGACTCGTAAGTGCAGAAAAC
ATGGTCCAGCCTTTGTTGATGGCTCCAGCCTCACAGCAGATGGACAGATTCCCACTGGAGAGAAGCACGGCAGA
ACCTTTAACCATGGTGCAAATCTCATTCTGCGCTGGACAGTTC

13739.1&2

GAGACAGGGTCTCACTTTGTCAACCAGGCTGGAATGCAGTGGTGCGATCTTACGTAGCTCACTGCAGCCCTGAC
CTCCTGGACTCAAACAATTCTCCTGCCTCAGCCCTGCAAGTAGCTGGGACTGTGGGTGCATGCCACCATGCCTG
GCTAACTTTTGTAGTTTTTGTAAAGATGGGGTTTTGCCATGTTGCACATGCTGGTCTTGAAGTCTCTGAGCTCAA
ACGATCTGCCACCTCGGCCCTCCAGAATGTTGGGATTACAGGGGTAAACCACCACGCCCTGGCCCCATTAGGGT
ATTCTTAGCATCCACTTGCTCACTGAGATTAATCATAAGAGATGATAAGCACTGGAAGAAAAAATTTTACTA
GGCTTTGGATATTTTTTCTTTTTTTCAGCTTTATACAGAGGATTGGATCTTTAGTTTTCTTTAACTGATAATA
AAACATTGAAAGGAAATAAGTTTACCTGAGATTACAGAGATAACCGGCATCACTCCCTTGCTCAATTCAGTC
TTTACCACATCAATTATTTTTCAGAGGTGCAGGATAAAGGCCTTTAGTCTGCTTTTCGCACTTTTCTTCCACTTT
TTTGTAAACCTGTTGCCTGACAAATGGAATTGACAGCGTATGCCATGACTATTCCATTTGTGAGGCATACGCTG
TCAATTTTTCCACCAATCCCTTGCTCTCTTTGGAGAGATCTTCTTATCAGCTAGTCTTTGGCAAAAGTAATT
GCAACTTCTTCTAGGTATTCTATTGTCCGTTCCACTGGTGGAAACCCTGGGACCAGGACTAAAACCTCCAG

13741.1

ATCTCATATATATATTTCTTCTGACTTTATTTGCTTGCTTCTGNACGCATTTAAATATCACAGAGACCAAA
ATAGAGCGGCTTTCTGGTGGAACGCATGGCAGTCACAGGACAAAATACAAAAGTGGGGGCTCTGCTTCTCAT
ACATCATACAATTTTCAAGTATTTTTTATGTACAAAGAGCTACTCTATCTGAAAAAATTTAAAAATAAAT
GAGACAAGATAGTTTATGCATCTAGGAAGAAAGAATGGGAAGAAAGAACGGGGCAGTTGGGTACAGATTCTGT
TCCCCTGTTCCAGGGACCACTACCTTCTGCACTGAGTTCCCCACAGCCTCACCCATCATGTACAGGGCA
AGTGCCAGGGTAGGTGGGACCACTGGAGACAGGAACCAGCAACATACTTTGGCCTGGAAGATAAGGAGAAAAGT
CTCAGAAACACACTGGTGGGAAGCAATCCACNGGCCGTGCCCCANGAGCTTCCACCTGCTGCTGGCTCCCTG
GGTGGCTTTGGGAACAGCTTGGGCAGGCCCTTTGGGTGGGNCCAAGTGGGCTTTGGGCCCGTGTGGAAG

Fig. 10

16/101

13742.1

AAACATTGAGATGGAATGATAGGGTTTCCAGAATCAGGTCCATATTTTAACTAAATGAAAATTATGATTTATA
GCCTTCTCAAATACCTGCCATACTTGATATCTCAACCAGAGCTAATTTTACCTCTTTACAAATTAATAAGCAA
GTAACCTGGATCCACAATTTATAATACCTGTCAATTTTTCTGTATTAAACCTCTATCATAGTTTAAGCCTATTA
GGGTACTTAATCCTTACAAATAAACAGGTTTAAAATCACCTCAATAGGCAACTGCCCTTCTGGTTTTCTTCTTT
GACTAAACAATCTGAATGCTTAAGATTTTCCACTTTGGGTGCTAGCAGTACACAGTGTTACACTCTGTATTCCA
GACTTCTTAAATTATAGAAAAAGGAATGTACACTTTTTGTATTCTTTCTGAGCAGGGCCGGGAGGCAACATCAT
CTACCATGGTAGGGACTTGATGCATGGACTACTTTA

14351.1

ACTCTGTGCGCCAGGCTGGAGCCCBTGGMCGGATCTCGACTCCCTGCAAGCTMCGCCTCACAGGWTGATGCCA
TTCTCCTGCCTCAGCATCTGGAGTAGCTGGGACTACAGGCGCCAGCCACCATGCCAGCTAATTTTT

14351.2

ACCTTAAAGACATAGGAGAATTTATACTGGGAGAGAAAGCTTACAAATGTAAGGTTTCTGACAAGACTTGGGAG
TGATTCACACCTGGAACAACATACTGGACTTCACACTGGABAGAAACCTTACAAGTGTAATGAGTGTGGCAAAG
CCTTTGGCAAGCAGTCAACACTTATTCACCATCAGGCAATTCA

14354.2

AGTCAGGATCATGATGGCTCAGTTTCCACAGCGATGAATGGAGGGCCAAATATGTGGGCTATTACATCTGAAG
AACGTAATAAGCATGATAAACAGTTTGATAACCTCAAACCTTCAGGAGGTACATAACAGGTGATCAAGCCCGT
ACTTTTTTCTACAGTCAGGTCTGCCGGCCCCGGTTTTAGCTGAAATATGGGCCTTATCAGATCTGAACAAGGA
TGGAAGATGGACCAGCAAGAGTTCTCTATAGCTATGAACTCATCAAGTTAAAGTTGCAGGGCCAACAGCTGC
CTGTAGTCCTCCCTCCTATCATGAAACAACCCCTATGTTCTCTCCACTAATCTCTGCTCGTTTTGGGATGGGA
AGCATGCCAATCTGTCCATTATCAGCCATTGCCTCCAGTTGCACCTATAGCAACACCCTTGCTCTTCTGCTAC
TTCAGGGACCAGTATTCCTCCCTAATGATGCCTGCT

14354.1

CTTTCGATTTCTTCAATTTGTCACGTTTGATTTTATGAAGTTGTTCAAGGGCTAACTGCTGTGTATTATAGCT
TTCTCTGAGTTCCTCAGCTGATTGTTAAATGAATCCATTTCTGAGAGCTTAGATGCAGTTTCTTTTTCAAGAG
CATCTAATTGTTCTTTAAGTCTTTGGCATAATTCTTCTTTTCTGATGACTTTCTATGAAGTAACTGATCCCT
GAATCAGGTGTGTTACTGAGCTGCATGTTTTAATTCCTTTCTGATGACTTTCTATGAAGTAACTGATCCCT
AAGCTTATTTTGATATTCCTTAAGCTCTTGGTGAAGTTGTCGATTTCCATAATTTCCAGGTCACACTGGTTAT
CCCAAACCTCT

Fig. 1P

17/101

16431.1.2

GTGGAGGTGAAACGGAGGCAAGAAAGGGGGCTACCTCAGGAGCGAGGGACAAAGGGGGCGTGAGGCACCTAGGC
CGCGGCACCCCGGCGACAGGAAGCCGTCCTGAACCGGGCTACCGGGTAGGGGAAGGGCCCGCTAGTCTCGCA
GGGCCCCAGAGCTGGAGTCGGCTCCACAGCCCCGGGCGTCGGCTTCTCACTTCTTGACCTCCCCGGCGCCCG
GGCCTGAGGACTGGCTCGGCGGAGGGAGAAGAGGAAACAGACTTGAGCAGCTCCCCGTTGTCTCGCAACTCCAC
TGCCGAGGAACCTCATTTTCTTCCCTCGCTCCTTACCCCCACCTCATGTAGAAAGGTGCTGAAGCGTCCGGA
GGGAAGAAGAACCTGGGCTACCGTCTGGCCTTCCMCCCCCTTCCGGGGCGCTTTGGTGGGCGTGAGTTGG
GGTTGGGGGGGTGGGTGGGGGTTCTTTTTGGAGTGCTGGGGAACTTTTTCCCTTCTCAGGTGAGGGGAAAG
GGAATGCCCAATTCAGAGAGACATGGGGGCAAGAAGGACGGGAGTGAGGAGCTTCTGGAACTTTGCAGCCGTC
ATCGGGAGGCGGCAGCTCTAACAGCAGAGAGCGTCACCGCTTGGTATCGAAGCACAAGCGGCATAAGTCCAAAC
ACTCCAAAGACATGGGGTTGGTGACCCCGAAGCAGCATCCCTGGGCACAGTTATCAAACCTTTGGTGGAGTAT
GATGATATCAGCTCTGATTCCGACACCTTCTCCGATGACATGGCCTTCAAACCTAGACCGAAGGGAGAACGACGA
ACGTCGTGGATCAGATCGGAGCGACCGCTGCACAAACATCGTCACCACCAGCACAGGCGTTCCCGGGACTTAC
TAAAGCTAAACAGACCG

16432-1

GACATGTTTGCCTGCAGGGGACCAGAGACAATGGGATTAGCCAGTGCTCACTGTTCTTTATGCTTCCAGAGAGG
ATGGGGACAGCTCTCAGGTGAGAATCCAGGCTGAGAAGGCCATGCTGGTTGGGGGCCCCCGGAAGCACGGTCCG
GATCCTCCCTGGCATCAGCGTAGACCGCTGCTCAGGCTTGGGGTACCAAACCTATGCTCTGTACTGTTTTGGC
CCCATGCGGTGAGAGGAAAACCTAGAAAAAGATTGGTCGTGCTAAGGAATCAGCTGCCCCCTCATCTCCGCAT
CCAATGCTGGTGACAACATATCCCTCTCCAGGACACAGACTCGGTGACTCCACACTGGGCTGAGTGGCCTCT
GGAGGCTCGTGGCCTAAGGCAGGGCTCCGTAAGGCTGATCGGCTGAACTGGGTGGGGTGAGGGTTTCTGACCTT
TCGCTTCCCATCCCATACCGCTGTCAATGAGCTCACACTGTGGTCA

16432-2

GATGGCATGGTCGTTGCTAATGTGCCTGCTGGGATGGAGCACTTCTCCTGTGAGCCCAGGGGACCCGCTGTC
CCTGGAGCTTGGGGCAAGGAGGGAAGAGTGATACCAGGAAGGTGGGGCTGCAGCCAGGGGCCAGAGTCAGTTCA
GGGAGTGGTCCTCGGCCCTCAAAGCTCCTCCGGGACTGCTCAGGAGTGATGGTGCCCTGGAGTTTGGCCCAAC
TTCCCTGGCCACCCTGGAAGGTGCCTGGCTGCTCCAGGCCTCTAGGCTGGGCTGATGGGTTTCTCCAGGACACA
AGTATCATTAAAGCCACCCTCTCCTCAGCTTGTCAGGCCGCACATGTGGGACAGGCTGTGCTCACAAACCCCTC
GCCTGCCCTGCCCTCCATCAGGAGGAGCCAGTGGAACCTTCGGAAGCTCCAGCATCTCAGCAGCCCTCAAAA
GTCGTCCTGGGGCAAGCTCTGGTTCTCCTGACTGGAGGTGATCTGGGCTTGGCCTGCTCTCTCGC

17184.3

TAAAAAGTGTAACAAAGGTTTATTTAGACTTTCTTCATGCCCCAGATCCAGGATGTCTATGTAAACCGTTAT
CTTACAAAGAAAGCACAATATTTGGTATAAATAAGTCAGTGACTTGCTTAACTGAAATAGCGTCCATCAAAA
GTGGGTTTAAGGTAAGTAACCTGACGATATTGGCGGGGATCCTGCAGTTTGGACTGCTTGCCGGGTTTGTCCA
GGGTTCCGGGTCTGTTCTTGGCACTCATGGGGACAGGCATCCTGCTCGTCTGTGGGGCCCCGCTGGAGCCCTTA
CGTGAAGCTGAAGGTATCGACCTAGGGGGCTCTAGGGCAGTGGGACCTTCATCCGGAACATAACAAGGTGCGG
GAGAGGCCTCTTGGGCTATGTGGG

Fig. 1Q

18/101

17184.4

CAAGCGTTCCTTTATGGATGTAAATTCAAACAGTCATGCTGAGCCATCCCGGGCTGACAGTCACGTTWAAGACA
CTAGGTCGGGCGCCACAGTGCCACCCAAGGAGAAGAAGAATTTGGAATTTTCCATGAAGATGTACGGAAATCT
GATGTTGAATATGAAAATGGCCCCAAATGGAATTCAAAAGGTTACCACAGGGGCTGTAAGACCTAGTGACCC
TCCTAAGTGGGAAAGAGGAATGGAGAATAGTATTTCTGATGCATCAAGAACATCAGAATATAAACTGAGATCA
TAATGAAGGAAAATTCCATATCCAATATGAGTTTACTCAGAGACAGTAGAACTATTCCCAGG

17185.1

TAGGAATAACAAATGTTTATTTCAGAAATGGATAAGTAATACATAATCACCTTCATCTCTTAATGCCCTTCCT
CTCCTTCTGCACAGGAGACACAGATGGGTAAACATAGAGGCATGGGAAGTGGAGGAGGACACAGGACTAGCCAC
CACCTTCTCTTCCCGGTCTCCAAGATGACTGCTTATAGAGTGGAGGAGGCAACAGGTCCCTCAATGTACCA
GATGGTCACCTATAGCACAGCTCCAGATGGCCACGTGGTTGCAGCTGGACTCAATGAACTCTGTGACAACCA
GAAGATACCTGCTTTGGGATGAGAGGGAGGATAAAGCCATGCAGGGAGGATATTTACCATCCCTACCCTAAGCA
CAGTGCAAGCAGTGAGCCCCGGCTCCAGTACCTGAAAAACCAAGGCCTACTGNCTTTTGGATGCTCTCTTGG
GCCAG

17188.2

AAGCCTCCTGCCCTGGAAATCTGGAGCCCCCTTGAGCTGAGCTGGACGGGGCAGGGAGGGGCTGAGAGGCAAGA
CCGTCTCCCTCCTGCTGCAGCTGCTTCCCAGCAGCCACTGCTGGGCACAGCAGAAACGCCAGCAGAGAAAATG
GGAGCCGAGAGTCCTTAGCCCTGGAGCTGAGGCTGCCTCTGGGCTGACCCGCTGGCTGTACGTGGCCAGAATG
GGGTTGGCATCTGGCATCCATTTGAGGCCAGGGTGGAGGAAAGGGAGGCCAACAGAGGAAAACCTATTCTGCT
GTGACAACACAGCCCTTGTCACGCAGCCTAAGTGCAGGGAGCGTGATGAAGTCAGGCAGCCAGTCGGGGAGG
ACGAGGTAACCTCAGCAGCAATGTCACCTTGAGCCTATGCGCTCAATGGCCCGAGGGGCGAGCAACCCCCGCA
CACGTCAGCCAACAGCAGTGCCTCTGCAGGCACCAAGAGAGCGATGATGGACTTGAGCGCCGTGTTT

17190.1

GTTTGGCAGAAGACATGTTTAATAACATTTTCATATTTAAAAAATACAGCAACAATTCTCTATCTGTCCACCAT
CTTGCCCTTGCCCTTCTGGGGCTGAGGCAGACAAAGGAAAGGTAATGAGGTTAGGGCCCCCAGGCGGGCTAAGT
GCTATTGGCCTGCTCCTGCTCAAAGAGAGCCATAGCCAGCTGGGCACGGCCCCCTAGCCCCCTCCAGGTTGCTGA
GGCGGCAGCGGTGGTAGAGTTCTTCACTGAGCCGTGGGCTGCAGTCTCGCAGGGAGAACTTCTGCACCAGCCCT
GGCTCTACGGCCCGAAAGAGGTGGAGCCCTGAGAACCGGAGGAAAACATCCATCACCTCCAGCCCTCCAGGGC
TTCTCTCTTCTTCTGGCCTGCCAGTTCACCTGCCAGCCGGGCTCGGGCCGCCAGGTAGTCAGCGTTGTAGAAGC
AGCCCTCCGCAGAAGCCTGCCGGTCAAATCTCCCGCTATAGGAGCCCCCGGGAGGGGTAGCACC

Fig. 1R

19/101

17190.2

CAAGTTGAACGTCAGGCTTGGCAGAGGTGGAGTGTAGATGAAAACAAAGGTGTGATTATGAAGAGGATGTGAGT
CCTTTGGGTGTAGGAGAGAAAGGCTGTTGAGCTTCTATTTCAAGATACTTTTACCTGTGCAAAAAGCACATTTT
CCACCTCCTTCTCATGGCATTGTGTAAAGGTGAGTATGATTCTATTCCATCTGCATTTTAGAGGTGAAGAATA
ACGTACAAGGGATTAGTATTAGCAAGGGACCCCTCACTAAGTGTGATGGAGTTAGGACAGAGCTCAGCTGT
TTGAATCTCAGAGCCCAGGCAGCTGGAGCTGGGTAGGATCCTGGAGCTGGCACTAATGTGAGGTGCATTCCCTC
CAACCCAGGCTCAGATCCGGAACCTGACCGTGCTGACCCCCGAAGGGGAGGCAGGGCTGAGCTGGCCCGTTGGG
CTCCCTGCTCCTTTCACACCACACTCTCGCTTTGAGGTGCTGGGCTGGGACTACTTCACAGAGCAGC

17191.2&89.2

TGGCCTGGGCAGGATTGGGAGAGAGGTAGCTACCCGGATGCAGTCCTTTGGGATGAAGACTATAGGGTATGACC
CCATCATTTCCCAGAGGTCTCGGCCTCCTTTGGTGTTACGACAGCTGCCCTGGAGGAGATCTGGCCTCTCTGT
GATTTCACTACTGTGCACACTCCTCTCCTGCCCTCCACGACAGGCTTGCTGAATGACAACACCTTTGCCAGTG
CAAGAAGGGGGTGCGTGTGGTGAACGTGCGCCGTGGAGGGATCGTGGACGAAGGCGCCCTGCTCCGGGCCCTGC
AGTCTGGCCAGTGTGCCGGGGCTGCACTGGACGTGTTTACGGAAGAGCCGCCACGGGACCGGGCCTTGGTGGAC
CATGAGAATGTCATCAGCTGTCCCACTGGGTGCCAGCACCAAGGAGGCTCAGAGCCGCTGTGGGGAGGAAAT
TGCTGTTCAAGTTCGTGGACATGGTGAAGGGGAAATCTCTACGGGGGTTGTGAATGCCAGGCCCTT

Fig. 1S

20/101

AGCCAGATGGCTGAGAGCTGCAAGAAGAAGTCAGGATCATGATGGCTCAGTTTCCACAGCGATGAATGGAGGG
CCAAATATGTGGGCTATTACATCTGAAGAACGTAAGCATGATAAACAGTTTGATAACCTCAAACCTTCAGG
AGGTTACATAACAGGTGATCAAGCCCGTACTTTTTCTACAGTCAGGTCGCCGGCCCGGTTTTAGCTGAAA
TATGGGCCCTTATCAGATCTGAACAAGGATGGGAAGATGGACCAGCAAGAGTTCTCTATAGCTATGAAACTCATC
AAGTTAAAGTTGCAGGGCCAACAGCTGCCTGTAGTCCTCCCTCCTATCATGAAACAACCCCTATGTTCTCTCC
ACTAATCTCTGCTCGTTTTGGGATGGGAAGCATGCCAATCTGTCCATTATCAGCCATTGCCTCCAGTTGCAC
CTATAGCAACACCCTTGTCTTCTGCTACTTCAGGGACCAGTATTCCTCCCTAATGATGCCTGCTCCCTAGTG
CCTTCTGTTAGTACATCCTCATTACCAATGGAAGTGCAGTCTCATTAGCCTTTATCCATTCTTATTCTTC
TTCAACATTGCCTCATGCATCATCTTACAGCCTGATGATGGGAGGATTTGGTGGTGCTAGTATCCAGAAGGCC
AGTCTCTGATTGATTTAGGATCTAGTAGCTCAACTTCCTCAACTGCTTCCCTCTCAGGGAACCTCACCTAAGACA
GGGACCTCAGAGTGGGCAGTTCTCAGCCTTCAAGATTAAGTATCGGCAAAATTTAATAGTCTAGACAAAGG
CATGAGCGGATACCTCTCAGGTTTTCAAGCTAGAAATGCCCTTCTTCAGTCAAATCTCTCTCAAACCTCAGCTAG
CTACTATTTGGACTCTGGCTGACATCGATGGTGACGGACAGTTGAAAGCTGAAGAATTTATTCTGGCGATGCAC
CTCACTGACATGGCCAAAGCTGGACAGCCACTACCACTGACGTTGCCTCCCGAGCTTGTCCTCCATCTTTCAG
AGGGGGAAAGCAAGTTGATTCTGTTAATGGAAGTCTGCCCTCATATCAGAAAAACACAAGAAGAAGAGCCTCAGA
AGAACTGCCAGTTACTTTTGAGGACAAACGGAAGCCAACTATGAACGAGGAAACATGGAGCTGGAGAAGCGA
CGCCAAGTGTTGATGGAGCAGCAGCAGAGGGAGGCTGAACGCAAGGCCAGAAAGAGAAGGAAGAGTGGGAGCG
GAAACAGAGAGAACTGCAAGAGCAAGAATGGAAGAAGCAGCTGGAGTTGGAGAAACGCTTGGAGAAACAGAGAG
AGCTGGAGAGACAGCGGGAGGAAGAGAGGAGAAAGGAGATAGAAAGACGAGAGGCAGCAAAACAGGAGCTTGAG
AGACAACGCCGTTTAGAATGGGAAAGACTCCGTGGCAGGAGCTGCTCAGTCAGAAGACCAGGGAACAAGAAGA
CATTGTCAGGCTGAGCTCCAGAAAGAAAAGTCTCCACCTGGAAGTGAAGCAGTGAATGGAAAACATCAGCAGA
TCTCAGGCAGACTACAAGATGTCAAATCAGAAAGCAAAACAAAAAGACTGAGCTAGAAGTTTTGGATAAACAG
TGTGACCTGGAAATTATGGAAATCAAACAACCTTCAACAAGAGCTTAAGGAATATCAAAATAAGCTTATCTATCT
GGTCCCTGAGAAGCAGCTATTAACGAAAGAATTAACCAATGCAGCTCAGTAACACACCTGATTAGGGATCA
GTTTACTTCATAAAAAGTCATCAGAAAAGGAAGAATTATGCCAAAGACTTAAAGAACAATTAGATGCTCTTGAA
AAAGAACTGCATCTAAGCTCTCAGAAATGGATTCAATTAACAATCAGCTGAAGGAACTCAGAGAAAGCTATAA
TACACAGCAGTTAGCCCTTGAACAACCTCATAAAATCAAACGTGACAAATTGAAGGAAATCGAAAGAAAAAGAT
TAGAGCAAAAAAAAAAAAAA

Fig. 2A

21/101

ATGGCAGTGACATTCACCATCATGGGAACCACTTCCCTTTTCTTCAGGATTCTCTGTAGTGGAAGAGAGCACC
CAGTGTTGGGCTGAAAACATCTGAAAGTAGGGAGAAGAACCTAAAATAATCAGTATCTCAGAGGGCTCTAAGGT
GCCAAGAAGTCTCACTGGACATTTAAGTGCCAACAAAGGCATACTTTCGGAATCGCCAAGTCAAACTTTCTAA
CTTCTGTCTCTCTCAGAGACAAGTGAGACTCAAGAGTCTACTGCTTTAGTGGCAACTACAGAAAAGTGGTGTTA
CCCAGAAAAACAGGAGCAATTAGAAATGGTTCCAATATTTCAAAGCTCCGCAAACAGGATGTGCTTTCCTTTC
CCATTTAGGGTTTCTTCTTTTCTTCTTTCTTTATTAACCACTA

Fig. 2B

22/101

ATATCTAGAAGTCTGGAGTGAGCAAACAAGAGCAAGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGA
ACAAGATAAATCTATCTTCAAAGACATATTAGAAGTTGGGAAAATAATTATGTGAAGTACAGCAAGTGTGTTAA
GAGTGATAAGTAAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTCACCTGG
GGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTAGTTATATGTGCTGTAATGTTGCTCTGA
GGAAGCCCCTGGAAGTCTATCCCAACATATCCACATCTTATATCCACAAATTAAGCTGTAGTATGTACCCTA
AGACGCTGCTAATTGACTGCCACTTCGCAACTCAGGGGCGGCTGCATTTTAGTAATGGGTCAAATGATTCACCTT
TTTATGATGCTTCCAAAGGTGCCTTGGCTTCTCTTCCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATA
ATTTTAGCATAAACAGAGCAGTCGGCGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTTAAACAAACAA
ATGCGGGTTTATTTCTCAGATGATGTTTCATCCGTGAATGGTCCAGGGAAGGACCTTTCACCTTGACTATATGGC
ATTATGTCATCACAAGCTCTGAGGCTTCTCCTTTCCATCCTGCGTGGACAGCTAAGACCTCAGTTTTCAATAGC
ATCTAGAGCAGTGGGACTCAGCTGGGGTGATTTGCCCCCATCTCCGGGGGAATGTCTGAAGACAATTTTGTT
ACCTCAATGAGGGAGTGGAGGAGGATACAGTGCTACTACCAACTAGTGGATAAAGGCCAGGGATGCTGCTCAAC
CTCCTACCATGTACAGGACGTCTCCCCATTACAACCTACCAATCCGAAGTGCAACTGTGTGAGGACTAAGAAA
CCCTGGTTTTGAGTAGAAAAGGGCCTGGAAGAGGGGAGCCAACAAATCTGTCTGCTTCTCACATTAGTCATT
GGCAAATAAGCATTCTGTCTCTTTGGCTGCTGCCTCAGCACAGAGAGCCAGAACTCTATCGGGCACCAGGATAA
CATCTCTCAGTGAACAGAGTTGACAAGGCCTATGGGAAATGCCTGATGGGATTATCTTCAGCTTGTTGAGCTTC
TAAGTTTCTTTCCCTTCATTCTACCCTGCAAGCCAAGTTCTGTAAGAGAAATGCCTGAGTTCTAGCTCAGGTTT
TCTTACTCTGAATTTAGATCTCCAGACCCTTCTGGCCACAATTCAAATTAAGGCAACAAACATATACCTTCCA
TGAAGCACACAGACTTTTGAAAGCAAGGACAATGACTGCTTGAATTGAGGCCTTGAGGAATGAAGCTTTGAA
GGAAGAATACTTTGTTTCCAGCCCCCTTCCACACTCTTCATGTGTTAACCAGTGCCTTCTGGACCTTGGA
GCCACGGTGACTGTATTACATGTTGTTATAGAAAAGTATTTAGAGTTCTGATCGTTCAAGAGAATGATTTAA
TATACATTTCTTA

Fig. 2C

23/101

Element Display									
Off Exp	Picture 1	Exp	Picture 2	Picture 3	Picture 4	Picture 5	Picture 6	Picture 7	Picture 8
+1.7	384A Ovary T (mets)	10	372A Dendritic cells	422A0308 (420)	421G0198 (C-1)	2303	13.1	50	1430
-1.3	385A Ovary T		S7 Ovary N	422A0528 (420)	421G0198 (C-1)	355	2.7	54	352
+1.8	281A Ovary T	10	S10 Skeletal muscle N	422A0528 (420)	421G0198 (C-1)	1298	6.9	61	707
+3.1	284A Ovary T	10	S2 Pancreas N	422A0528 (420)	421G0198 (C-1)	830	44.1	62	1180
-1.2	386A Ovary T	10	S40 PEMC (activated)	422A0528 (420)	421G0198 (C-1)	518	3.8	50	819
+1.7	285A Ovary T	10	C75 Heart N	422A0528 (420)	421G0198 (C-1)	2305	14.3	53	489
-1.4	S25 Ovary T		C74 Bone Marrow N	422A0528 (420)	421G0198 (C-1)	531	3.5	53	743
	383A Ovary T (mets)	10	C11 Colon N	422A0528 (420)	421G0198 (C-1)	1843	10.1	38	671
-1.8	S22 Ovary T		C10 Kidney N	422A0528 (420)	421G0198 (C-1)	453	3.9	58	657
+3.2	388A OT 1-P (SCID)	10	388A OT 1-P (SCID)	422A0528 (420)	421G0198 (C-1)	1882	12.1	57	584
+1.5	282A Ovary T	10	384A Large Intestine N	422A0528 (420)	421G0198 (C-1)	1486	7.5	55	955
-1.1	S115 Ovary T (mets)		C110 Small Intestine N	422A0528 (420)	421G0198 (C-1)	509	3.4	51	573
+1.1	288A Ovary T		C112 Lung N	422A0528 (420)	421G0198 (C-1)	700	4.5	54	651
-2.1	201A Ovary T		S6 Stomach N	422A0528 (420)	421G0198 (C-1)	525	4.8	48	1335
+7.8	S23 Ovary T	10	S66 Spinal Cord N	422A0528 (420)	421G0198 (C-1)	3695	22.1	50	502
+1.8	205A Ovary T	10	270A Liver N	422A0528 (420)	421G0198 (C-1)	2251	14.1	48	1259
-1.8	323A Ovary T (SCID)		42 Skin N	422A0528 (420)	421G0198 (C-1)	352	3.4	72	1079
+5.5	385A Ovary T	10	S31 Fetal tissue	422A0528 (420)	421G0198 (C-1)	9128	35.1	50	1449
-3.5	283A Ovary T		S73 Breast N	422A0528 (420)	421G0198 (C-1)	439	3.2	61	1531
-3.3	382A Ovary T		C719 Brain N	422A0528 (420)	421G0198 (C-1)	387	3.2	50	1218
+4.8	286A Ovary T	10	S27 Ovary N	422A0528 (420)	421G0198 (C-1)	4242	22.1	58	853

Fig. 3

24/101

TCGAGCGGCCGCCCGGGCAGGTCCTTCAGACTTGGACTGTGTCACTGCCAGGCTTCCAGGGCTCCAATTGC
AGACGGCCTGTTGTGGGACAGTCTCTGTAATCGCGAAAGCAACCATGGAAGACCTGGGGGAAAACACCATGGTT
TTATCCACCCTGAGATCTTTGAACAACCTTCATCTCTCAGCGTGCGGAGGGAGGCTCTGGACTGGATATTTCTAC
CTCGGCCGCGACCACGCT

Fig. 4

25/101

TAGCGYGGTCGCGGCCGAGGYCTGCTTYTCTGTCCAGCCCAGGGCCTGTGGGGTCAGGGCGGTGGGTGCAGATG
GCATCCACTCCGGTGGCTTCCCCATCTTTCTCTGGCCTGAGCAAGGTCAGCCTGCAGCCAGAGTACAGAGGGCC
AACTGTTGTTCTTGAACAAGGGCCTTAGCAGGCCCTGAAGGCCCTCTCTGTAGTGTGAACCTCCTGGAGC
CAGGCCACATGTTCTCCTCATACCGCAGGYTAGYGATGGTGAAGTTGAGGGTAAAATAGTATTMANGRAGATGG
CTGGCARACCTGCCCCGGGCGGCCGCTCSAAATCC

Fig. 5

26/101

AGCGTGGTCGCGGCCGAGGTGTCCTTCAGGGTCTGCTTATGCCCTTGTTCAAGAACACCAGTGTGAGCTCTCTG
TACTCTGGTTGCAGACTGACCTTGCTCAGGCCTGAGAAGGATGGGGCAGCCACCAGAGTGGATGCTGTCTGCAC
CCATCGTCCTGACCCCAAAGCCCTGGACTGGACAGAGAGCGGCTGTACTGGAAGCTGAGCCAGCTGACCCACG
GCATCACTGAGCTGGGCCCCTACACCCTGGACAGGGACAGTCTCTATGTCAATGGTTTCACCCATCGGAGCTCT
GTACCCACCACCAGCACCGGGTGGTCAGCGAGGAGCCATTCAACCTGCCCGGGCGGCCGCTCGA

Fig. 6

27/101

TTGGGGNTTTGMAGCGGCCGCCGGGCAGGTACCGGGGTGGTCAGCGAGGAGCCATTCACTGAACTTCACCA
TCAACAACCTGCGGTATGAGGAGAACATGCAGCACCTGGCTCCAGGAAGTTCAACACCACGGAGAGGGTCCTT
CAGGGCCTGCTCAGGTCCCTGTTCAAGAGCACCAGTGTGGCCCTCTGTACTCTGGCTGCAGACTGACTTTGCT
CAGACTTGAGAAACATGGGGCAGCCACTGGAGTGGACGCCATCTGCACCCTCCGCCCTTGATCCCACTGGTCCTG
GACTGGACAGAGAGCGGCTATACTGGGAGCTGAGCCAGTCCTCTGGCGGNGACNCCNCTT

Fig. 7A

AGCGTGGTCGCGGCCGAGGTCCAGTCGCAGCATGCTCTTTCTCCTGCCCACTGGCACAGTGAGGAAGATCTCTG
CTGTCAGTGAGAAGGCTGTCATCCACTGAGATGGCAGTCAAAAGTGCAATTAATACACCTAACGTATCGAACAT
CATAGCTTGGCCAGGTTATCTCATATGTGCTCAGAACACTTACAATAGGCTGCAGACCTGCCCGGGCGGCCGC
TCGA

Fig. 7B

28/101

TGTGGTGTGAACTTCCTGGAGNCAGGGTGACCCATGTCCTCCCCATACTGCAGGTTGGTGATGGTGAAGTTGA
GGGTGAATGGTACCAGGAGAGGGCCAGCAGCCATAATTGTSGRGCKGSMGMSSGAGGMWGGWGTYYCWGAGGTT
CYRARRTCCACTGTGGAGGTCCCAGGAGTGCTGGTGGTGGGCACAGAGSTCYGATGGGTGAAACCATTGACATA
GAGACTGTTCTGTCCAGGGTGTAGGGGCCAGCTCTTYRATGYCATTGGYCAGTTKGCTYAGCTCCCAGTACA
GCCRCTCTCKGYYGWCCAGSGCTTTTGGGGTCAAGATGATGGATGCAGATGGCATCCACTCCAGTGGCTGCT
CCATCCTTCTCGGACCTGAGAGAGGTCAGTCTGCAGCCAGAGTACAGAGGGCCAACACTGGTGTCTTTGAATA

Fig. 8

29/101

TCGAGCGGCCGCCCGGGCAGGTCAGGAAGCACATTGGTCTTAGAGCCACTGCCTCCTGGATTCCACCTGTGCTG
CGGACATCTCCAGGGAGTGCAGAAGGGAAGCAGGTCAAAGTCTCAGATCAGTCAGACTGGCTGTTCTCAGTTC
TCACCTGAGCAAGGTCAGTCTGCAGCCAGAGTACAGAGGGCCAACACTGGTGTCTTGAACAAGGGCTTGAGCA
GACCCTGCAGAACCTCTCCGTGGTGTGAACCTCCTGGAAACCAGGGTGTTCATGTTTTTCCTCATAATGC
AAGGTTGGTGATGG

Fig. 9

30/101

Gene Name	Ref. Probe 1 ESD Name	Probe 2 Name	Probe 1 Value	Probe 2 Value	Probe 1 S/N	Probe 2 S/N	Probe 1 A ₀	Probe 2 A ₀
42100188 (D3)	+1.0 205A Ovary T	270A Liver N	8620	1240	57.7	65	22	65
42100188 (D3)	+5.9 325 Ovary T	556 Spinal Cord N	5894	1082	37.3	89	39	89
42100188 (D3)	+5.7 385A Ovary T	S91 Fetal tissue	12151	2121	34.3	73	28	73
42100188 (D3)	+5.1 426A Ovary T (met)	415A Aorta N	7487	1480	53.0	73	9.7	73
42100188 (D3)	+3.5 263A Ovary T	S73 Breast N	7302	2116	39.2	84	4.5	84
42100188 (D3)	+3.3 383A Ovary T	11 Colon N	3714	1113	20.4	83	2.6	83
42100188 (D3)	+3.0 394 Ovary T (SCIT)	12 Skin N	2435	814	12.1	75	2.1	75
42100188 (D3)	+2.6 384A Ovary T (met)	272A Dendritic cell	4578	1734	25.0	69	2.3	69
42100188 (D3)	+2.2 244A Ovary T	S2 Pancreas N	7904	3596	38.5	81	5.6	81
42100188 (D3)	+2.0 386A Ovary T	S40 PBMC	2191	1081	14.0	90	2.9	90
42100188 (D3)	+2.0 515 Ovary T (met)	CT10 Small intestine	1978	971	10.4	80	2.7	80
42100188 (D3)	+2.0 265A Ovary T	CT3 Heart N	1911	984	13.2	83	2.8	83
42100188 (D3)	+2.0 353A Ovary T	S7 Ovary N	1666	807	9.8	100	3.0	100
42100188 (D3)	+1.9 428A Ovary T (met)	243A Esophagus N	1827	1480	13.4	97	9.8	97
42100188 (D3)	+1.5 261A Ovary T	S10 Skeletal muscle	5914	1653	30.4	86	6.0	86
42100188 (D3)	+1.5 266A Ovary T	S23 Ovary N	2039	1274	11.9	50	2.0	50
42100188 (D3)	+1.6 821 Ovary T	CT9 Kidney N	1736	1072	11.0	92	4.0	92
42100188 (D3)	+1.4 9485 OT I-P (SCIT)	9485 OT 5-P (SCIT)	4204	1074	23.0	93	7.7	93
42100188 (D3)	+1.4 262A Ovary T	334A Large Intestine	3002	2101	16.6	89	4.0	89
42100188 (D3)	+1.3 525 Ovary T	CT4 Bone Marrow	1693	1297	9.6	90	3.1	90
42100188 (D3)	+1.2 429A Ovary T (met)	364A Ovary N	2521	2084	22.0	85	23.9	85
42100188 (D3)	+1.2 392A Ovary T	CT19 Brain N	2072	1663	10.9	88	2.3	88
42100188 (D3)	+1.2 388A Ovary T	CT12 Lung N	1840	1473	10.7	87	3.8	87
42100188 (D3)	+1.1 201A Ovary T	S9 Stomach N	1329	1204	9.1	90	3.5	90

Fig. 10

31/101

Gene Name	Exp. Name	Probe 1	P1	P2	Probe 2	Gene ID	Probe1 Value	Probe2 Value	Probe1 S/B	Probe1 A%	Probe2 S/B	Probe2 A%
421B0181 (C3)	+18.8 385A Ovary T	+	+	+	S91 Fetal tissue	422X0607	26711	1424	103.3	54	2.0	54
421B0181 (C3)	+11.5 523 Ovary T	+	+	+	S56 Spinal Cord N	422X0628	13559	1179	65.3	68	3.9	68
421B0181 (C3)	+11.1 426A Ovary T (meas)	+	+	+	415A Aorta N	422X0611	14125	1273	67.3	61	5.6	61
421B0181 (C3)	+10.8 205A Ovary T	+	+	+	270A Liver N	422Q0606	16121	1488	93.3	43	2.3	43
421B0181 (C3)	+5.1 263A Ovary T	+	+	+	S73 Breast N	422H0623	11326	2235	58.2	68	4.4	68
421B0181 (C3)	+4.6 389A Ovary T (meas)	+	+	+	272A Dendritic cells	422A0608	6583	1424	24.5	40	2.1	40
421B0181 (C3)	+4.4 264A Ovary T	+	+	+	S25 Pancreas N	422N0629	9855	2245	40.9	64	3.5	64
421B0181 (C3)	+4.4 429A Ovary T (meas)	+	+	+	364A Ovary N	422D0614	2803	638	22.6	60	7.4	60
421B0181 (C3)	+4.2 251A Ovary T	+	+	+	S10 Scleral muscle	422C0621	8271	1949	39.5	68	3.6	68
421B0181 (C3)	+3.8 8115 Ovary T (meas)	+	+	+	CT10 Small intestine	422C0604	2281	607	11.6	60	2.1	60
421B0181 (C3)	+2.5 265A Ovary T	+	+	+	CT5 Heart N	422O0624	3192	1293	19.2	68	4.0	68
421B0181 (C3)	-2.3 822 Ovary T	+	+	+	CT9 Kidney N	422N0627	565	1276	3.8	70	3.9	70
421B0181 (C3)	+2.2 266A Ovary T	+	+	+	S27 Ovary N	422X0603	2774	1260	14.3	46	2.7	46
421B0181 (C3)	+2.1 934 Ovary T (SCID)	+	+	+	12 Skin N	422R0601	1774	837	8.4	56	2.1	56
421B0181 (C3)	+1.9 9483 OT 1-P (SCID)	+	+	+	9483 OT 1-P (SCID)	422X0602	6967	3726	41.5	70	9.2	70
421B0181 (C3)	+1.6 282A Ovary T	+	+	+	CT19 Brain N	422Q0610	2313	1471	6.2	50	1.9	50
421B0181 (C3)	+1.5 288A Ovary T	+	+	+	CT12 Lung N	422Y0625	1657	1054	9.7	69	2.9	69
421B0181 (C3)	+1.4 262A Ovary T	+	+	+	CT4 Bone Marrow N	422H0619	348	1243	4.5	65	2.7	65
421B0181 (C3)	+1.2 386A Ovary T	+	+	+	334A Large Intestine	422A0622	3171	2214	16.8	69	3.8	69
421B0181 (C3)	-1.2 335A Ovary T	+	+	+	S40 P8MC (antiretro)	422J0605	630	544	4.2	53	1.9	53
421B0181 (C3)	-1.0 201A Ovary T	+	+	+	S7 Ovary N	422D0626	592	730	3.7	75	2.6	75
421B0181 (C3)	-1.0 428A Ovary T (meas)	+	+	+	S6 Stomach N	422W0620	1197	1237	7.8	65	3.5	65
421B0181 (C3)	-1.0 428A Ovary T (meas)	+	+	+	263A Esophagus N	422A0612	783	797	4.5	95	2.4	95
421B0181 (C3)	-1.0 428A Ovary T (meas)	+	+	+	I1 Colon N	422B0609	3470	862	8.9	24	1.7	24

Fig. 11

32/101

[illegible]

Fig. 12

33/101

Gene Name	Rel. Probe 1 Exp. Name	P1	P2 Name	Probe 2 ID	Probe 1 Value	Probe 2 Value	Probe 1 S/B	Probe 2 S/B	Probe 1 A%	Probe 2 A%
421V0189 (D1)	+33.2 426A Ovary T (men)	421V0189 (D1)	415A Aorta N	422X0611	8072	243	55.2	2.4	67	57
421V0189 (D1)	+19.7 523 Ovary T	421V0189 (D1)	556 Spinal Cord N	422G0628	7367	537	42.6	2.5	69	69
421V0189 (D1)	+12.6 428A Ovary T (men)	421V0189 (D1)	368A Ovary N	422H0614	2850	227	21.7	3.5	64	64
421V0189 (D1)	+8.0 385A Ovary T	421V0189 (D1)	S91 Fetal tissue	422X0607	11791	1469	54.0	2.2	58	58
421V0189 (D1)	+7.3 263A Ovary T	421V0189 (D1)	573 Breast N	422H0623	6949	952	37.8	2.6	69	69
421V0189 (D1)	+5.8 515 Ovary T	421V0189 (D1)	C74 Bone Marrow	422H0619	208	1210	2.1	2.9	44	44
421V0189 (D1)	+5.0 205A Ovary T	421V0189 (D1)	270A Liver N	422Q0605	8676	1737	52.3	2.6	57	57
421V0189 (D1)	+4.5 383A Ovary T (men)	421V0189 (D1)	II Colon N	422B0609	3149	707	17.4	2.0	57	57
421V0189 (D1)	+4.4 261A Ovary T	421V0189 (D1)	S10 Skeletal muscle	42230621	6332	1443	29.1	2.9	77	77
421V0189 (D1)	+4.2 264A Ovary T	421V0189 (D1)	S2 Pancreas N	422N0629	7612	1809	38.1	3.3	79	79
421V0189 (D1)	+3.9 382A Ovary T	421V0189 (D1)	CT19 Brain N	422Q0610	468	1508	3.4	2.3	60	60
421V0189 (D1)	+2.9 934A Ovary T (SCII)	421V0189 (D1)	12 Skin N	422R0681	2300	860	12.3	2.1	51	51
421V0189 (D1)	+2.5 5115 Ovary T (met)	421V0189 (D1)	CT10 Small Intestine	422C0604	1424	569	6.7	2.1	61	61
421V0189 (D1)	+2.4 265A Ovary T	421V0189 (D1)	CT5 Heart N	422Q0624	1742	723	11.8	2.8	70	70
421V0189 (D1)	+2.3 984A Ovary T (met)	421V0189 (D1)	272A Dendritic cell	42240608	3083	1342	17.0	2.0	62	62
421V0189 (D1)	+1.9 266A Ovary T	421V0189 (D1)	S27 Ovary N	42250603	1370	732	8.0	2.0	47	47
421V0189 (D1)	+1.7 262A Ovary T	421V0189 (D1)	S40 PBMC (activated)	42210605	307	580	2.6	2.0	41	41
421V0189 (D1)	+1.3 355A Ovary T	421V0189 (D1)	334A Large Intestine	422A0622	2097	1282	11.2	2.7	86	86
421V0189 (D1)	+1.1 268A Ovary T	421V0189 (D1)	S7 Ovary N	42230626	373	470	2.9	2.0	47	47
421V0189 (D1)	+1.1 201A Ovary T	421V0189 (D1)	CT12 Lung N	422V0625	969	1094	5.6	2.9	72	72
421V0189 (D1)	+1.1 408A Ovary T (met)	421V0189 (D1)	S6 Stomach N	422W0620	750	672	5.6	2.4	82	82
421V0189 (D1)	+1.0 9485 Ovary T (met)	421V0189 (D1)	243A Esophagus	422A0612	498	446	4.2	2.1	73	73
421V0189 (D1)	+1.0 9485 Ovary T (met)	421V0189 (D1)	9485 OT 5-P (SCID)	422Y0602	3117	3174	16.7	8.2	91	91
421V0189 (D1)	+1.0 9485 Ovary T (met)	421V0189 (D1)	CT9 Kidney N	42290627	224	409	2.3	2.3	48	48

Fig. 13

34/101

Gene	Ref. Probe 1	Probe 2	GRM	Probe1 Value	Probe2 Value	Probe1 S/B	Probe2 S/B	Probe1 A%	Probe2 A%
421H0187 (B11)	+202 426A Ovary T (met)	415A Adip N	422X0611	5441	270	363	2.3	50	50
421H0187 (B11)	+100 523 Ovary T	536 Spinal Cord N	422C0628	5318	533	27.1	2.3	56	56
421H0187 (B11)	+83 429A Ovary T (met)	344A Ovary N	422U0614	1252	150	10.1	2.5	58	58
421H0187 (B11)	+57 385A Ovary T	591 Fetal tissue	422X0607	9507	1668	33.8	2.1	45	45
421H0187 (B11)	+44 205A Ovary T	270A Liver N	422Q0606	5456	1255	31.1	2.0	50	50
421H0187 (B11)	+42 265A Ovary T	CT15 Heart N	422O0624	1834	438	11.9	2.0	48	48
421H0187 (B11)	+41 382A Ovary T	CT19 Brain N	422Q0610	309	1259	2.6	2.0	48	48
421H0187 (B11)	+34 261A Ovary T	S10 Skeletal muscle	42230621	3733	1036	17.7	2.3	55	55
421H0187 (B11)	+34 263A Ovary T	S73 Breast N	422H0623	4163	1239	23.0	3.0	62	62
421H0187 (B11)	+25 5115 Ovary T (met)	CT10 Small intestine	422C0604	1365	627	8.8	2.1	47	47
421H0187 (B11)	+21 264A Ovary T	82 Pancreas N	422N0629	3435	1630	14.9	3.0	60	60
421H0187 (B11)	+21 384A Ovary T (met)	271A Dendritic cell	42240608	2657	1370	13.4	1.9	44	44
421H0187 (B11)	+21 329 Ovary T	CT9 Kidney N	42290627	291	605	2.4	2.5	51	51
421H0187 (B11)	+17 386A Ovary T	840 PBMC (activated)	42210605	410	687	3.2	2.0	47	47
421H0187 (B11)	+16 334 Ovary T (SCID)	T2 Skin N	422R0601	1622	984	7.9	2.2	44	44
421H0187 (B11)	+15 262A Ovary T	334A Large Intestine	422A0622	1892	1245	10.1	2.6	50	50
421H0187 (B11)	+15 288A Ovary T	CT12 Lung N	422V0625	604	508	4.1	2.6	62	62
421H0187 (B11)	+14 428A Ovary T (met)	243A Esophagus	42240612	236	323	2.7	1.9	78	78
421H0187 (B11)	+13 335A Ovary T	S7 Ovary N	42220626	382	501	2.9	2.0	58	58
421H0187 (B11)	+12 201A Ovary T	S6 Spleen N	422W0620	538	677	4.2	2.3	58	58
421H0187 (B11)	+10 9485 OT 1-P (SCID)	9485 OT 5-P (SCID)	422Y0602	2582	2493	15.1	6.3	57	57
421H0187 (B11)	385A Ovary T (met)	11 Colon N	422H0609	2251	562	12.5	1.7	38	38
421H0187 (B11)	265A Ovary T	S27 Ovary N	42250603	1739	565	9.7	2.2	36	36
421H0187 (B11)	S25 Ovary T	CT4 Bone Marrow	422H0619	283	845	2.2	2.2	44	44

Fig. 14

35/101

11721-1

ACGGTTTCAATGGCACTTTTATTGTTTACTTAATGGATCATCAATTTTGTCTCACTACCTACAAATGGAATTT
CATCTTGTTTCCATGCTGAGTAGTGAAAACAGTGACAAAGCTAATCATAATAACCTACATCAAAAGAGAAGTAA
CTAACTGCTCACTTTCTTTTAAACAGGCAAAATATAAATATATGCACTCTAXAATGCACAATGGTTTAGTCA
CTAAAAAATTCAAATGGGATCTTGAAGAATGTATGCAATCCAGGGTGCAGTGAAGATGAGCTGAGATGCTGTG
CAACTGTTTAAGGGTTCCTGGCACTGCATCTCTTGGCCACTAGCTGAATCTTGACATGGAAGGTTTATAGCTAAT
GCCAAGTGGAGATGCAGAAAATGCTAAGTTGACTTAGGGGCTGTGCACAGGAACTAAAAGGCAGGAAAGTACTA
AATATTGCTGAGAGCATCCACCCAGGAAGGACTTTACCTTCCAGGAGCTCCAACTGGCACCACCCCAAGTGC
TCACATGGCTGACTTTATCCTCCGTGTTCCATTTGGCACAGCAAGTGGCAGTG

11721-2

AAGGCTGGTGGGTTTTTGATCCTGCTGGAGAACCTCCGCTTTCATGTGGAGGAAGAAGGGAAGGGAAAAGATGC
TTCTGGGAACAAGGTTAAAGCCGAGCCAGCCAAAATAGAAGCTTTCGAGCTTCACTTTCGAAGCTAGGGGATG
TCTATGTCAATGATGCTTTTGGCACTGCTCACAGAGCCACAGCTCCATGGTAGGAGTCAATCTGCCACAGAAG
GCTGGTGGGTTTTTGATGAAGAAGGAGCTGAAGTACTTTGCAAAGGCCCTTGAGAGCCAGAGCGACCTTCTCT
GGCCATCCTGGGCGGAGCTAAAGTTGCAGACAAGATCCAGCTCATCAATAATATGCTGGACAAAGTCAATGAGA
TGATTATTGGTGGTGAATGGCTTTTACCTTCTTAAGGTGCTCAACAACATGGAGATTGGCACTTCTCTGTTT
GATGAAGAGGGAGCCAAGATTGTCAAAGACCTAATGTCAAAGCTGAGAAGAATGGTGTGAAGATTACCTTGCC
TGTTGACTTTGTCACTGCTGACAAGTTTGATGA

11724-1

TTTGTTCCTTACATTTTTCTAAAGAGTTACTTAAATCAGTCAACTGGTCTTTGAGACTCTTAAGTTCTGATTCC
AACTTAGCTAATTCATTCTGAGAACTGTGGTATAGGTGGCGTGTCTTCTAGCTGGGACAAAAGTTCTTTGTT
TTCCCCCTGTAGAGTATCACAGACCTTCTGCTGAAGCTGGACCTCTGTCTGGGCTTGGACTCCCAAATCTGCT
TGTCATGTTCAAGCCTGGAATGTTAATCTTTAATCTTCCATATGGATGGACATCTGTCTAAGTTGATCCTTT
AGAACTGCAATTATCTTCTTTGAGTCTAATTTCTTCTTCTTTGCTTTGAATCGCATCACTAAACTTCTCTC
CCATTTCTTAGCTTCATCTATCACCTGTACGATCATCTGGAGGGAAGACATGCTCTTAGTAAAGGCTGCAA
GCTGGGTACAGTACTGTCCAAGTTTTCTGAAGTTGCTGAAGTCTCTTGTCTTTCTTGTTCAAAGTAACCTGA
ATCTCTCAAATTGTCTCTTCCAAGTGGACTTTTTCTCTGCGCAAAGCATCCAG

11724-2

TCATTGCCTGTGATGGCATCTGGAATGTGATGAGCAGCCAGGAAGTTGTAGATTTTATTCAATCAAAGGATTCA
GCATGTGGTGAAGCTGTGAGGCAAGAGAAACAAGAACTGTATGGCAAGTTAAGAAGCACAGAGGCAACAAGA
AGGAGACAGAAAAGCAGTTGCAGGAAGCTGAGCAAGAAATGGAGGAAATGAAAGAAAAGATGAGAAAGTTTGCT
AAATCTAAACAGCAGAAAATCCTAGAGCTGGAAGAAGAGAATGACCGGCTTAGGGCAGAGGTGCACCCTGCAGG
AGATACAGCTAAAGAGTGTATGGAACACTTCTTTCTTCCAATGCCAGCATGAAGGAAGAACTTGAAAGGGTCA
AAATGGAGTATGAAACCTTTCTAAGAAGTTTCAGTCTTTAATGTCTGAGAAAGACTCTCTAAGTGAAGAGGTT
CAAGATTTAAAGCATCAGATAGAAGGTAATGTATCTAAACAAGCTAACCTAGAGGCCACCGAGAAACATGATAA
CCAAACGAATGTCACTGAAGAGGGAACACAGTCTATACCAGGT

Fig. 15A

36/101

11725-32-1.2

AAGCCAATAATCACCATTTATTACTTAATATATGCCAACCACTGTACTTGGCAGTTCACAAATTCTCACCCTTA
CAACAACCCCATGAGGTATTTATCCCATTTCTATAGATAGGGAAACCACAGCTCAAGTAAGTTAGGAACTGAG
CCAAGTATACACAGAATACGAAGTGGCAAACTAGAAAGGAAAGACTGACACTGCTATCTGCTGGCCTCCAGTGT
CCTGGCTCTTTTACACGGGtTCAATGTCTCCAGCGCTGCTGCTGCTGCTGCATTACCATGCCCTCATTGTTTT
TCTTCTCTGGTGTTCAACTGCATCCTTCAAAGAATCTAACTCATTCCAGAGACCCTTATTTCTTTCTCTCTT
TCTGAAATTACTTTTAATAATTCTTCATGAGGGGGAAAAGAAGATGCCTGTTGGTAGTTTTGTTGTTAAGCTG
CTCAATTTGGGACTTAACAATTTGTTTTCATCTTGACATCCTGTAACAGCTGTGTTTTGCTAGAAAGATCAC
TCTCCCTCTCTTTTAGCATGGCTTCTAACCTCTTCAATTCATTTTCTTTTCTTTCAACACAATCTCAAGTTCT
TCAAAGTGTGATGCAGAAGAGGCCTCTTCAAGTTATGTTGTGCTACTTCTGAACATGTGCTTTTAAAGATTC
ATTTCTTCTTGAAGATCCTGTAACCACTTCCCTGTATTGGCTAGGTCTTTCTTTCTTCCAAAACAGCCT
TCATGGTATTCATCTGTTCTCTTTTCTTTTAATAAGTTCAAGAGCTTCAGAAC

11726-1&2

CAAGCTTTTTTTTTTTTTTAAAAAGTGTTAGCATTAAATGTTTTATTGTCACGCAGATGGCAACTGGGTTTATG
TCTTCATATTTTATATTTTGTAAATTAATAAATTACAAGTTTTAAATAGCCAATGGCTGGTTATATTTTTCAG
AAAACATGATTAGACTAATTCATTAATGGTGGCTTCAAGCTTTTCTTATTGGCTCCAGAAAATTCACCCACCT
TTTGTCCCTTCTTAAAAAACTGGAATGTTGGCATGCATTTGACTTCACACTCTGAAGCAACATCCTGACAGTCA
TCCACATCTACTTCAAGGAATATCACGTTGGAATACTTTTTCAGAGAGGGAATGAAAGAAAGGCTTGATCATT
GCAAGGCCACACCACGTGGCTGAGAAGTCACTACTACAAGTTTATCACCTGCAGCGTCCAAGGCTTCTGAA
AAGCAGTCTTGCTCTCGATCTGCTTACCATCTTGGCTGCTGGAGTCTGACGAGCGGCTGTAAGGACCGATGGA
AATGGATCCAAAGCACCAACAGAGCTTCAAGACTCGCTGCTTGGCTTGAATTCGGATCCGATATCGCCATGGC
CT

11727-1&2

AAGTGTTAGCATTAAATGTTTTATTGTCACGCAGATGGCAACTGGGTTTATGCTTCATATTTTATATTTTGT
AATTAATAAATTTMCAAGTTTTAAATAGCCAATGGCTGGTTATATTTTCAGAAAACATGATTAGACTAATTCAT
TAATGGTGGCTTCAAGCTTTTCTTATTGGCTCCAGAAAATTCACCCACCTTTTGTCCCTTCTTAAAAAACTGG
AATGTTGGCATGCATTTGACTTCACACTCTGAAGCAACATCCTGACAGTCATCCACATCTACTTCAAGGAATAT
CACGTTGGAATACTTTTTCAGAGAGGGAATGAAAGAAAGGCTTGATCATTTTGAAGGCCACACCACGTGGCTG
AGAAGTCACTACTACAAGTTTATCACCTGCAGCGTCCAAGGCTTCTGAAAAGCAGTCTTGCTCTCGATCTGC
TTCACCATCTTGGCTGCTGGAGTCTGACGAGCGGCTGTAAGGACCGATGGAAATGGATCCAAAGCACCAACAG
AGCTTCAAGACTCGCTGCTTGGCATGAATTCGGATCCGA

Fig. 15B

37/101

11728.1.40.19.19

TACAACTTTATTGAAACGCACACGCGCACACACACAAACACCCCTGTGGATAGGGAAAAGCACCTGGCCACAG
GGTCCACTGAAACGGGGAGGGGATGGCAGCTTGTAATGTGGCTTTGCCACAACCCCTTCTGACAGGGAAGGC
CTTAGATTGAGGCCCCACCTCCCATGGTGATGGGGAGCTCAGAATGGGGTCCAGGGAGAATTTGGTTAGGGGGA
GGTGCTAGGGAGGCATGAGCAGAGGGCACCCCTCGAGTGGGGTCCGAGGGCTGCAGAGTCTTCAGTACTGTCC
CTCACAGCAGCTGTCTCAAGGCTGGGTCCCTCAAAGGGGCGTCCAGCGCGGGGCTCCCTGCGCAAACACTTG
GTACCCCTGGCTGCGCAGCGGAAGCCAGCAGGACAGCAGTGGCGCGGATCAGCACACAGACGCCCTGGCGGTA
GGGACAGCAGGCCAGCCCTGTCGGTTGTCTCGGCAGCAGGTCTGGTTATCATGGCAGAAGTGTCTTCCCACA
CTTCACGTCCTTACACCCACGTGAXGGCTACXGGCCAGGAAG

11728.2.40.19.19

CCCGTGGGTGCCATCCACGGAGTTGTTACCTGATCTTTGGAAGCAGGATCGCCCGTCTGCACTGCAGTGGAAGC
CCCGTGGGCAGCAGTGATGGCCATCCCGCATGCCACGGCCTCTGGGAAGGGGCAGCAACTGGAAGTCCCTGAG
ACGGTAAAGATGCAGGAGTGGCCGGCAGAGCAGTGGGCATCAACCTGGCAGGGGCCACCCAGATGCCTGCTCAG
TGTTGTGGGCCATTTGTCCAGAAGGGGACGGCAGCAGCTGTAGCTGGCTCCTCCGGGGTCCAGGCAGCAGGCCA
CAGGGCAGAACTGACCATCTGGGCACCGGTTCCAGCCACCAGCCCTGCTGTTAAGGCCACCCAGCTCACCAGG
GTCCACATGGTCTGCCTGCGTCCGACTCCGCGGTCTTGGGCCCTGATGGTTCTACCTGCTGTGAGCTGCCAG
TGGGAAGTATGGCTGCTGCCAATGCCAACGCCACCTGCTGCTCCGATCACCTGCACTGCTGCCCAAGACACT
GTGTGTGACCTGATCCAGAGTAAGTGCCTCTCCAAGGAGAAGC

11730-1

GAATCACCTTTCTGGTTTAGCTAGTACTTTGTACAGAACAATGAGGTTTCCACAGCGGAGTCTCCCTGGGCTC
TGTTTGGCTCTCGGTAAGGCAGGCCTACACCTTTTCTCTCCTCTATGGAGAGGGGAATATGCATTAAGGTGAA
AAGTCACCTTCCAAAAGTGAGAAAGGGATTGATTGCTGCTTCAGGACTGTGGAATTAATTTGGAATGTTTTACA
AATGGTTGCTACAAAACAACAAAAAGGTAATTACAAAATGTGTACATCACAACATGCTTTTTAAAGACATTAT
GCATTGTGCTCACATTCCTTAAATGTTGTTTCCAAAGGTGCTCAGCCTCTAGCCAGCTGGATTCTCCGGGAA
GAGGCAGAGACAGTTTGGCGAAAAAGACACAGGGAAGGAGGGGTGGTGAAAGGAGAAAGCAGCCTTCCAGTTA
AAGATCAGCCCTCAGTTAAAGGTCAGCTTCCCGCAXGCTGGCCTCAXGCGGAGTCTGGGTGAGAGGGAGGAGCA
GCAGCAGGGTGGGACTGGGGCGT

11730-2

AACCGGAGCGCGAGCAGTAGCTGGGTGGGCACCATGGCTGGGATCACCACCATCGAGGCGGTGAAGCGCAAGAT
CCAGGTTCTGCAGCAGCAGGCAGATGATGCAGAGGAGCGAGCTGAGCGCCTCCAGCGAGAAGTTGAGGGAGAAA
GGCGGGCCCCGGGAACAGGCTGAGGCTGAGGTGGCCTCCTTGAACCGTAGGATCCAGCTGGTTGAAGAAGAGCTG
GACCGTGCTCAGGAGCGCCTGGCCACTGCCCTGCAAAAGCTGGAAGAAGCTGAAAAAGCTGCTGATGAGAGTGA
GAGAGGTATGAAGTTATTGAAAACCGGGCCTTAAAGATGAAGAAAAGATGGAATCCAGGAAATCCAACCTCA
AAGAAGCTAAGCACATTGCAGAAGAGGCAGATAGGAAGTATGAAGAGGTGGCTCGTAAGTTGGTGATCATTGAA
GGAGACTTGGAACGCACAGAGGAACGAGCTGAGCTGGCAGAGTCCGTTGCCGAGAGATGGATGAGCAGATTAG
ACTGATGGACCAGAACCTGAAGTGTCTGAGTGC

Fig. 15C

38/101

11732.1contig

GAGAACTTGGCCTTTATTGTGGGCCAGGAGGGCACAAAGGTGAGGAGGCCAAGGGAGGGATCTGGTTTTCTG
GATAGCCAGGTATAGCATGGGTATCAGTAGGAATCCGCTGTAGCTGCACAGGCCTCACTTGCTGCAGTTCCGG
GGAGAACACCTGCACTGCATGGCGTTGATGACCTCGTGGTACACGACAGAGCCATTGGTGCAGTGAAGGGCAC
GCGCATGGGCTCCGTCTCGAGGGCAGGCAGCAGGAGCATTGCTCCTGCACATCCTCGATGTCAATGGAGTACA
CAGCTTTGCTGGCACACTTTCCTGGCAGTAATGAATGTCCACTTCCTCTTGGGACTTACAATCTCCCACTTTG
ATGTACTGCACCTTGGCTGTGATGTCTTTGCAATCAGGCTCCTCACATGTGTACAGCAGGTGCCTGGAATTTT
CACGATTTTGCTCCTTCAGCCAGACACTTGTGTTCAATGGTGGGCAGCCGTGACCCTCTTCTCCAGA
TGTA CTCTCTCT

11732.2contig

GCCTGGACCTTGCCGGATCAGTGCCACACAGTGACTTGCTTGGCAAATGGCCAGACCTTGCTGCAGAGTCATCG
TGTC AATTGTGACCATGGACCCCGGCTTCATGTGCCAACAGCCAGTCTCCTGTTCCGGGTGGAGGAGACGTGTG
GCTGCCGCTGGACCTGCCCTTGTTGTGTGCACGGGCAGTTCCTCGGCACATCGTCACCTTCGATGGGCAGAAT
TTCAAGCTTACTGGTAGCTGCTCCTATGTCATCTTTCAAACAAGGAGCAGGACCTGGAAGTGCTCCTCCACAA
TGGGGCCTGCAGCCCCGGGGCAAAACAAGCCTGCATGAAGTCCATTGAGATTAAGCATGCTGGCGTCTCTGCTG
AGCTGCACAGTAACATGGAGATGGCAGTGGATGGGAGACTGGTCTTGCCCCGTACGTTGGTGAACATGGAA
GTCAGCATCTACGGCGCTATCATGTATGAAGTCAGGTTACCCATCTTGGCCACATCTCACATACACCGCCXC
AAAACAACGAGTT

11735-1-2

AGATCAACCTCTGCTGGTCAGGAGGAATGCCTTCCTTGCTTGGATCTTTGCTTTGACGTTCTCGATAGTRWCA
aCTKKRYTSRAMSKMAAGKGYRATGRWMTTKSYWGWASYKTMWMMRSGRARAYTTaGaCAYCCCMCCTCWgAG
aCGSAGKACCARGTGCAgAgGTGGACTCTTTCTGGATGTTGTAGTCAGACAGGGTGCGTCCATCTTCAGCTGT
TTCCCAGCAAAGATCAACCTCTGCTGATCAGGAGGGATGCCTTCCTTATCTTGGATCTTTGCCCTTGACATTCTC
GATGGTGTCACTGGGCTCCACCTCGAGGGTGATGGTCTTACCAGTCAGGGTCTTCACGAAGATYTGATCCAC
CTCTGAGACGGAGCACCAGGTGCAGGGTRGACTCTTTCTGGATGTTGTAGTCAGACAGGGTGCGYCCATCTTCC
AGCTGcTTTCCSaGCAAAGATCAACCTCTGCTGGTCAGGAGGRATGCCTTCCTTGTCYTGGATCTTTGCTTTGA
CRTTCTCRATGGTGTCACTCGGCTCCACTTCGAGAGTGATGGTCTTACCAGTCAGGGTCTTCACGAAGATCTGC
ATCCCACCTCTAA

11740.2.contig

AAGTCACAAACAGACAAAGATTATTACCAGCTGCAAGCTATATTAGAAGCTGAACGAAGAGACAGAGGTCATGA
TTCTGAGATGATTGGAGACCTTCAAGCTCGAATTACATCTTTACAAGAGGAGGTGAAGCATCTCAAACATAATC
TCGAAAAAGTGGAAGGAGAAAAGAAAGAGGCTCAAGACATGCTTAATCACTCAGAAAAAGAAAAGAATAATTTA
GAGATAGATTTAACTACAACTTAAATCATTACAACAACGGTTAGAACAAGAGGTAAATGAACACAAAGTAAC
CAAAGCTCGTTTAACTGACAAACATCAATCTATTGAAGAGGCAAAGTCTGTGGCAATGTGTGAGATGGAAAAA
AGCTGAAAGAAGAAAGAGAAGCTCGAGAGAAGGCTGAAAATCGGGTTGTTGAGATTGAGAAACAGTGTTCCATG
CTAGACGTTGATCTGAAGCAATCTCAGCAGAACTAGAACATTTGACTGGAAATAAAGAAAGGATGGAGGATGA
AGTTAAGAATCTA

Fig. 15D

39/101

11765.2&64.2.contig

CGCCTCCACCATGTCCATCAGGGTGACCCAGAAGTCTACAAGGTGTCCACCTCTGGCCCCGGGCTTCAGCA
GCCGCTCCTACACGAGTGGGCCCCGTTCCCGCATCAGCTCCTCGAGCTTCTCCCGAGTGGGCAGCAGCAACTTT
CGCGGTGGCCTGGGCGGCGGCTATGGTGGGGCCAGCGGCATGGGAGGCATACCGCAGTTACGGTCAACCAGAG
CCTGCTGAGCCCCCTTGTCTGGAGGTGGACCCCAACATCCAGGCCGTGCGCACCCAGGAGAAGGAGCAGATCA
AGACCCTCAACAACAAGTTTGCCTCCTTCATAGACAAGGTACGGTTCCTGGAGCAGCAGAACAAGATGCTGGAG
ACCAAGTGGAGCCTCCTGCAGCAGCAGAAGACGGCTCGAAGCAACATGGACAACATGTTGAGAGCTACATCAA
CARCCTTAGGCGGCAGCTGGAGACTCTGGGCCAGGAGAAGCTGAAGCTGGAGGCGGAGCTTGGCAACATGCAGG
GGCTGGTGGAGGACTTCAAGAACAAGTATGAGGATGAGATCAATAAGCGTACAGAGATGGAGAACGAATTTGTC
CTCATCAAGAAGGATGTGGATGAAGCTTACATGAACAAGGTAGAGCTGGAGTCTCGCCTGGAAGGGCTGACCGA
CGAGATCAACTTCCTCAGGCAGCTGTATGAAGAGGAGATCCGGGAGCTGCAGTCCAGATCTCGGACACATCTG
TGGTGTGTCCATGGACAACAGCCGCTCCCTGGACATGGACAGCATCATTGCTGAGGTCAAGGCACAGTACGAG
GATATTGCCAACCAGCCGGGCTGAGGCTGAGAGCATGTACCAGGTCAAGTATGAGGAGCTGCAGAGCCTGGC
TGGGAAGCACGGGGATGACCTGCGGCGCACAAAGACTGAGATCTCTGAGATGAACCCGGAACATCAGCCCGGCT
XCAGGCTGAGATTGAGGGCCTCAAAGGCCAGAXGGCTTXCCTGGAXGCCGCCAT

11767.2.contig

CCCGGAGCCAGCCAACGAGCGGAAAATGGCAGACAATTTTTGCTCCATGATGCGTTATCTGGGTCTGGAAACC
CAAACCTCAAGGATGGCCTGGCGCATGGGGGAACAGCCTGCTGGGGCAGGGGGCTACCCAGGGGCTTCCTAT
CCTGGGGCTACCCCGGCAGGCACCCCCAGGGGCTTATCCTGGACAGGCACCTCCAGGCGCTACCTGGAGC
ACCTGGAGCTTATCCCGAGCACCTGCACCTGGAGTCTACCCAGGGCCACCCAGCGGCCCTGGGGCTACCCAT
CTTCTGGACAGCCAAGTGCCACCGAGCCTACCTGCCACTGGCCCTATGGCGCCCTGCTGGGCCACTGATT
GTGCCTTATAACCTGCCTTTGCCTGGGGGAGTGGTGCCTCGCATGCTGATAACAATTCTGGGCACGGTGAAGCC
CAATGCAAACAGAATTGCTTTAGATTTCAAAGAGGGAATGATGTTGCCTTCACTTTAACCACGCTTCAATG
AGAACAACAGGAGAGTCATTGGTTGCAATACAAAGCTGGATAA

11768-1&2

GGGAATGCAACAACCTTTATTGAAAGGAAAGTGCAATGAAATTTGTTGAAACCTTAAAGGGGAAACTTAGACAC
CCCCCTCRAgCGMAGKACCARGTGCARAgTGGACTCTTCTGGATGTTGTAGTCAGACAGGGTRCGWCCATC
TTCCAGCTGTTTYCCRGCAAAGATCAACCTCTGCTGATCAGGAGGRATGCCTTCCTTATCTTGGATCTTGCCT
TGACATTCTCGATGGTGTCACTGGGCTCCACCTCGAGGGTGATGGTCTTACCAGTCAGGGTCTTCACGAAGATY
TGCATCCACCTCTGAGACGGAGCACCAGGTGCAGGGTRGACTCTTCTGGATGTTGTAGTCAGACAGGGTGCG
YCCATCTCCAGCTGcTTTCCSaGCAAAGATCAACCTCTGCTGGTCAGGAGGRATGCCTTCCTTGTCTGTGGATC
TTTGCYTTGACRTTCTCAATGGTGTCACTCGGCTTCACTTCGAGAGTGATGGTCTTACCAGTCAGGGTCTTCAC
GAAGATCTGCATCCACCTCTAAGACGGAGCACCAGGTGCAGGGTGGACTCTTCTGGATGgTTGTAGTCAGAC
AGGGTGCGTCCATCTTCCAGCTGTTTCCAGCAAAGATCAACCT

Fig. 15E

40/101

11768-182-11735-182

AGGTTGATCTTTGCTGGGAAACAGCTGGAAGATGGACGCACCCTGTCTGACTACAACCATCCAGAAAGAGTCCA
CCCTGCACCTGGTGCTCCGTCTTAGAGGTGGGATGCAGATCTTCGTGAAGACCCTGACTGGTAAGACCATCACT
CTCGAAGTGGAGCCGAGTGACACCATTGAGAAAGTCAARGCAAAGATCCARGACAAGGAAGGCATYCCTCCTGA
CCAGCAGAGGTTGATCTTTGCTSGGAAAGCAGCTGGAAGATGGRCGCACCCTGTCTGACTACAACATCCAGAAA
GAGTCYACCCTGCACCTGGTGCTCCGTCTCAGAGGTGGGATGCARATCTTCGTGAAGACCCTGACTGGTAAGAC
CATCACCTCGAGGTGGAGCCAGTGACACCATCGAGAATGTCAAGGCAAAGATCCAAGATAAGGAAGGCATCC
CTCCTGATCAGCAGAGGTTGATCTTTGCTGGGAAACAGCTGGAAGATGGACGCACCCTGTCTGACTACAACATC
CAGAAAGAGTCCACcTYTGACYTGGTMCTBCgtCTYaGAGGKGGGRTGcaaTCTWMGTKWagaCaCtCaCTK
KYAAGRYYaTCAMCMWtgAKKTCgAKYSCASTKWCaCTWTCRAKAAMGTYRWGCAWagaTCCMAGACAAGGAA
GGCATTCTCTGACCAGCAGAGGTTGATCT

11769.1.contig

ATGGAGTCTCACTCTGTCCAGGCTGGAGCGCTGTGGTGGGATATCGGCTCACTGCAGTCTCCACTTCCTGG
GTTCAAGCGATCCTCCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGCAGGCGTCACCATAATTTTTGTATT
TTTAGTAGAGACATGGTTTCGCCATGTTGGCTGGGCTGGTCTCGAACTCCTGACCTCAAGTGATCTGTCTGGC
CTCCCAAAGTGTGGGATTACAGGCGAAAGCCAACGCTCCCGGCCAGGGAACAACCTTTAGAATGAAGGAAATAT
GCAAAAGAACATCACATCAAGGATCAATTAATTACCATCTATTAATTACTATATGTGGGTAATTATGACTATTT
CCCAAGCATTCTACGTTGACTGCTTGAGAAGATGTTTGTCTGCATGGTGGAGAGTGGAGAAGGGCCAGGATTC
TTAGGTT

11769.2.contig

AGCGCGGTCTTCGGCGCGAGAAAGCTGAAGGTGATGTGGCCGCCCTCAACCGACGCATCCAGCTCGTTGAGGA
GGAGTTGGACAGGGCTCAGGAACGACTGGCCACGGCCCTGCAGAAGCTGGAGGAGGCAGAAAAAGCTGCAGATG
AGAGTGAGAGAGGAATGAAGGTGATAGAAAACCGGGCCATGAAGGATGAGGAGAAGATGGAGATTCAGGAGATG
CAGCTCAAAGAGGCCAAGCACATTGCGGAAGAGGCTGACCGCAAATACGAGGAGGTAGCTCGTAAGCTGGTCAT
CCTGGAGGGTGAGCTGGAGAGGGCAGAGGAGCGTGCGGAGGTGTCTGAACTAAAATGTGGTGACCTGGAAGAAG
AACTCAAGAATGTTACTAACAATCTGAAATCTCTGGAGGCTGCATCTGAAAAGTATTCTGAAAAGGAGGACAAA
TATGAAGAAGAAATTAACCTTCTGTCTGACAACTGAAAGAGGCTGAGACCCGTGCTGAATTTGCAGAGAGAAC
GGTTGCAAACTGGAAGACAATTGATGACCTGGAAGAGAAACTTGCCAGC

11770.1.contig

GTGCACAGGTCCCATTTATTGTAGAAAATAATAATAATTACAGTGATGAATAGCTCTTCTTAAATTACAAAACA
GAAACCACAAAGAAGGAAGAGGAAAAACCCAGGACTTCCAAGGGTGAAGCTGTCCCCTCCTCCCTGCCACCCT
CCCAGGCTCATTAGTGCTTGGAAAGGGGCAGAGGACTCAGAGGGGATCAGTCTCAGGGGCCCTGGGCTGAAG
CGGGTGAGGCAGAGAGTCTGAGGCCACAGAGCTGGGCAACCTGAGCCGCCCTCTCTGGCCCCCTCCCCACCAC
TGCCCAAACCTGTTTACAGCACCTTCGCCCTCCCTCTAAACCGTCCATCCACTCTGCACTTCCAGGCAGG
TGGGTGGGCCAGGCCCTAGCCATACTCTGGGCGCGGGTTTCGGTGAGCAAGGCACAGTCCAGAGGTGATATC
AAGGCCT

Fig. 15F

41/101

11770.2.contig

GCAAGGAAC TGGTCTGCTCACACTTGCTGGCTTGCGCATCAGGACTGGCTTTATCTCCTGACTCACGGTGCAAA
GGTGCACTCTGCGAACGTTAAGTCCGTCCCCAGCGCTTGAATCCTACGGCCCCACAGCCGGATCCCCTCAGC
CTTCAGGTCCTCAACTCCCGTGGACGCTGAACAATGGCCTCCATGGGGCTACAGGTAATGGGCATCGCGCTGG
CCGTCTGGGCTGGCTGGCCGTATGCTGTGCTGCGCGCTGCCATGTGGCGCGTGACGGCCTTCATCGGCAGC
AACATTGTCACCTCGCAGACCATCTGGGAGGGCCTATGGATGAACTGCGTGGTGCAGAGCACC GGCCAGATGCA
GTGCAAGGTGTACGACTCGCTGCTGGCACTGCCGAGGACCTGCAGGCGGCCCGGCCCTCGTCATCATCA

11773.1.contig

TGCAAAAGGGACACAGGGGTTCAAAAATAAAAATTTCTCTTCCCCCTCCCCAACCTGTACCCAGCTCCCCGA
CCACAACCCCTTCTCCCCGGGGAAGCAAGAAGGAGCAGGTGTGGCATCTGCAGCTGGGAAGAGAGAGGCC
GGGGAGGTGCCGAGCTCGGTGCTGGTCTCTTTCCAAATATAAATACXTGTGTGCAACTGGAAAATCCTCCAGC
ACCCACCACCAAGCACTCTCCGTTTTCTGCCGTGTTTGGAGAGGGGCGGGGGCAGGGGCGCCAGGCACCGG
CTGGCTGCGGTCTACTGCATCCGCTGGGTGTGCACCCCGCGAGCCTCCTGCTGCTCATTGTAGAAGAGATGACA
CTCGGGGTCCCCCGGATGGTGGGGGCTCCCTGGATCAGCTTCCCGGTGTTGGGGTTCACACACCAGCACTCCC
CACGCTGCCCGTTCAGAGACATCTTGCAGTGTGAGGTTGTACAGGCCATGCTTGTACAGTTG

11778.1.contig

GGGTTGGAGGGAAGTGGTTCTTTATTTCAAAAAGACACTTGTCAATATTCAGTATCAAAACAGTTGCACTATTGA
TTTCTCTTTCTCCCAATCGGCCCCAAAGAGACCACATAAAAGGAGGTACATTTTAAGCCAATAAGCTGCAGGA
TGTACACCTAACAGACCTCCTAGAAACCTTACCAGAAAATGGGGACTGGGTAGGGAAGGAACTTAAAGATCA
ACAAACTGCCAGCCACGGACTGCAGAGGCTGTACAGCCAGATGGGGTGGCCAGGGTGCCACAAACCCAAAGC
AAAGTTTCAAAATAATATAAAATTTAAAAAGTTTGTACATAAGCTATTCAAGATTTCTCCAGCACTGACTGAT
ACAAAGCACAATTGAGATGGCACTTCTAGAGACAGCAGCTTCAAACCCAGAAAAGGGTGTAGATGAGTTTCA
CATGGCTAAATCAGTGGCAAAAACACAGTCTTCTTTCTTTCTTTCTTTCAAGGAGGCAGGAAAGCAATTAAGTG
GTCACCTCAACATAAGGGGGACATGATCCATTCTGTAAGCAGTTGTGAAGGGG

11778-2&30-2

CAGGAACCGGAGCGCGAGCAGTAGCTGGGTGGGCACCATGGCTGGGATCACCACCATCGAGGCGGTGAAGCGCA
AGATCCAGGTTCTGCAGCAGCAGGCAGATGATGCAGAGGAGCGAGCTGAGCGCCTCCAGCGAGAAGTTGAGGGA
GAAAGGCGGGCCCGGAACAGGCTGAGGCTGAGGTGGCCTCCTTGAACCGTAGGATCCAGCTGGTTGAAGAAGA
GCTGGACCGTGCTCAGGAGCGCCTGGCCACTGCCCTGCAAAAGCTGGAAGAAGCTGAAAAGCTGCTGATGAGA
GTGAGAGAGGTATGAAGTTATTGAAAACCGGGCCTTAAAGATGAAGAAAAGATGGAAGCTCAGGAAATCCAA
CTCAAAGAAGCTAAGCACATTGCAGAAGAGGCAGATAGGAAGTATGAAGAGGTGGCTCGTAAGTTGGTGATCAT
TGAAGGAGACTTGAACGCACAGAGGAACGAGCTGAGCTGGCAGAGTCCCGTTGCCGAGAGATGGATGAGCAGA
TTAGACTGATGGACCAGAACCTGAAGTGTCTGAGTGC

Fig. 15G

42/101

11782.1.contig

ATCTACGTCATCAATCAGGCTGGAGACACCATGTTCAATCGAGCTAAGCTGCTCAATATTGGCTTTCAAGAGGC
CTTGAAGGACTATGATTACAACTGCTTTGTGTTCACTGATGTGGACCTCATTCCGATGGACGACCGTAATGCCT
ACAGGTGTTTTTCGCAGCCACGGCACATTTCTGTTGCAATGGACAAGTTCGGGTTTAGCCTGCCATATGTTTCAG
TATTTTGGAGGTGTCTCTGCTCTCAGTAAACAACAGTTTCTTGCCATCAATGGATTCCCTAATAATTATTGGGG
TTGGGGAGGAGAAGATGACGACATTTTTAACAGATTAGTTCATAAAGGCATGTCTATATCACGTCCAAATGCTG
TAGTAGGGAGGTGTCAATGATCCGGCATTCAAGAGACAAGAAAAATGAGCCCAATCCTCAGAGGTTTGACCGG
ATCGCACATACAAAGGAAACGATGCGCTTCGATGGTTTGAACCTCACTTACCTACAAGGTGTTGGATGTCAGAGA
TACCGTTATATACCCAAATCAC

11782.2.contig

CTAGACCTCTAATTAAGGACACAATCATGCTGGAGAATGAACAGTCTGACCCCGAGGGCCACAGCGAATTTTA
GGGAAGGAGGCAAAGAGGTGAGAAGGGAAGGAAGGAAGGAGAACAATAAGAACTGGAGACGTTGG
GTGGGTGAGGGAGTGTGGTGGAGGCTCGGAGAGATGGTAAACAAACCTGACTGCTATGAGTTTTCAACCCATA
GTCTAGGGCCATGAGGGCGTCAGTTCTGGTGGCTGAGGGTCTTCCACCCAGCCACCTGGGGGAGTGGAGTG
GGGAGTTCTGCCAGGTAAGCAGATGTTGTCTCCAAGTTCTTGACCCAGATGTCTGGCAGGATAACGCTGACCT
GTTCCCTCAACAAGGGACCTGAAAGTAATTTTGCTCTTTAC

11783-1 & 2

CCGAATTCAGCGTCAACGATCCYTCCCTTACCATCAAATCAATTGGCCACCAATGGTACTGAACCTACGAGTA
CACCGACTACGGGGGACTAATCTTCAACTCCTACATACTTCCCCATTATTCCTAGAACCAGGCGACCTGCGA
CTCCTTGACGTTGACAATCGAGTAGTACTCCGATTGAAGCCCCATTCTGATAATAATTACATCACAAGACGT
CTTGCACTCATGAGCTGTCCACATTAGGCTTAAAAACAGATGCAATTCCTGGACGTCTAAGCCAAACCACTT
TCACCGCTACACGACCGGGGGTATACTACGGTCAATGCTCTGAAATCTGTGGAGCAAACCACAGTTTCATGCCC
ATCGTCTAGAAATTAATCCCCATAAAATCTTTGAAATAGGGCCCGTATTTACCCTATAGCACCCCTCTACCC
CCTCTAG

11786.1.contig

GCTCTTCACACTTTTATTGTTAATTCTCTTCACATGGCAGATACAGAGCTGTGCTCTTGAAGACCACCACTGAC
CAGGAAATGCCACTTTTACAAAATCATCCCCCTTTTCATGATTGGAACAGTTTTCTGACCGTCTGGGAGCGT
TGAAGGGTGACCAGCACATTTGCACATGCAAAAAAGGAGTGACCCCAAGGCCTCAACCACACTTCCCAGAGCTC
ACCATGGGCTGCAGGTGACTTGCCAGGTTTGGGGTTCGTGAGCTTTCTTGCTGCTGCGGTGGGGAGGCCCTCA
AGAAGTGAAGAGGCCGGGTATGCTTCATGAGTGTTAACATTTACGGGACAAAAGCGCATCATTAGGATAAGGAA
CAGCCACAGCACTTCATGCTTGTGAGGGTTAGCTGTAGGAGCGGGTGAAAGGATTCCAGTTTATGAAAATTTAA
AGCAACAACGGTTTTTAGCTGGGTGGGAAACAGGAAACTGTGATGTCGGCCAATGACCACCATTTTTCTGCC
CATGTGAAGGTCCCATGAAACC

Fig. 15H

43/101

11786.2.contig

CAAGCGCTTGGCGTTTGGACCCAGTTCAGTGAGGTTCTTGGGTTTTGTGCCTTTGGGGATTTTGGTTTGACCCA
GGGGTCAGCCTTAGGAAGGTCTTCAGGAGGAGGCCGAGTTCCCCTTCAGTACCACCCTCTCTCCCCACTTTCC
CTCTCCCGGCAACATCTCTGGGAATCAACAGCATATTGACACGTTGGAGCCGAGCCTGAACATGCCCTCGGCC
CCAGCACATGGAAAACCCCTTCTTGCCTAAGGTGTCTGAGTTTCTGGCTCTTGAGGCATTTCCAGACTTGAA
ATTCTCATCAGTCCATTGCTCTTGAGTCTTTCAGAGAACCTCAGATCAGGTGCACCTGGGAGAAAGACTTTGT
CCCCACTTACAGATCTATCTCCTCCCTTGGGAAGGGCAGGAATGGGGACGGTGTATGGAGGGGAAGGGATCTC
CTGCGCCCTTCATTGCCACACTTGGTGGGACCATGAACATCTTTAGTGTCTGAGCTTCTCAAATTACTGCAATA
GGA

13691.1&2

AGCGTCAAATCAGAATGGAAAAGACTCAAACCATCATCAACACCAAGATCAAAGGACAAGRATCCTTCAAGA
AACAGGAAAAAACTCCTAAACACCAAAAGGACCTAGTTCTGTAGAAGACATTAAAGCAAAAATGCAAGCAAGT
ATAGAAAAAGGTGGTTCTTCCCAAAGTGAAGCCAAATTCATCAATTATGTGAAGAATTGCTTCCGGATGAC
TGACCAAGAGGCTATTCAAGATCTCTGGCAGTGGAGGAAGTCTCTTAAGAAAATAGTTTAAACAATTTGTAA
AAAATTTCCGTCTTATTTTCAATTTCTGTAAACAGTTGATATCTGGCTGTCTTTTTATAATGCAGAGTGAGAACT
TTCCCTACCGTGTGTTGATAAATGTTGTCCAGGTTCTATTGCCAAGAATGTGTTGTCCAAAATGCCTGTTTAGTT
TTTAAAGATGGAACCCACCCTTTGCTTGGTTTAAAGTATGTATGGAATGTTATGATAGGACATAGTAGTAGCG
GTGGTCAGACATGGAAATGGTGGGSMGACAAAAATATACATGTGAAATAA

13692.1&2

TCCGAATTCGAAGCGAATTATGGACAAACGATTCCCTTTAGAGGATTACTTTTTCAATTCGGTTTTAGTAAT
CTAGGCTTTGCCGTGTAAGAATACAACGATGGATTTTAAATACTGTTTGTGGAATGTGTTTAAAGGATTGATTC
TAGAACCTTTGTATATTTGATAGTATTTCTAACTTTTCAATTTCTTTACTGTTTGCAGTTAATGTTTATGTTCTGC
TATGCAATCGTTTATATGCAGTTTCTTTAATTTTTTAGATTTTCTGGATGTATAGTTTAAACAACAAAAAG
TCTATTTAAACTGTAGCAGTAGTTTACAGTTCTAGCAAAGAGGAAAGTTGTGGGGTTAACTTTGTATTTCT
TTCTTATAGAGGCTTCTAAAAAGGTATTTTATATGTTCTTTTAAACAAATATTGTGTACAACCTTTAAACAT
CAATGTTTGGATCAAAACAAGACCCAGCTTATTTTCTGC

13693.2

TGTGGTGGCGGGGCTGAGGTGGAGGCCAGGACTCTGACCCTGCCCTGCCTTCAGCAAGGCCCCGGCAGCG
CCGGCCACTACGAAGTCCCGTGGGTGAAAAATATAGGCCAGTAAAGCTGAATGAAATTGTCGGGAATGAAGAC
ACCGTGAGCAGGCTAGAGGTCTTTGCAAGGAAGGAAATGTGCCCAACATCATATTGCGGGCCCTCCAGGAAC
CGGCAAGACCACAAGCATTCTGTGCTTGGCCCGGGCCTGCTGGGCCAGCACTCAAAGATGCCATGTTGGAAC
TCAATGCTTCAAATGACAGGGGCATTGACGTTGTGAGGAATAAAATTTAAATGTTTCTCAACAAAAAGTCACT
CTTCCCAAAGGCCGACATAAGATCATATTCTGGATGAAGCAGACAGCATGACCGACGGAGCCGCAAGCCTT
GAGGAGAACCATGGAAATCTACTCTAAACCACTCGTTGCGCCTTGTGTAATGCTTCGGATAAGATCATCGA
GCC

Fig. 15I

44/101

13696.1-13744.1

CTTTGCAAAGCTTTTATTTTCATGTCTGCGGCATGGAATCCACCTGCACATGGCATCTTAGCTGTGAAGGAGAAA
GCAGTGCACGAGAAGGAATGAGTGGGCGGAACCAACGGCCTCCACAAGCTGCCTTCAGCAGCCTGCCAAGGCC
ATGGCAGAGAGAGACTGCAACAAACACAAGCAAACAGAGTCTCTTCACAGCTGGAGTCTGAAAGCTCATAGTG
GCATGTGTGAATCTGACAAAATTTAAAGTGTGCATAGTCCATTACATGCATAAAACACTAATAATAATCCTGTT
TACACGTGACTGCAGCAGGCAGGTCCAGCTCCACCACTGCCCTCCTGCCACATCACATCAAGTGCCATGGTTTA
GAGGGTTTTTCATATGTAATTCTTTTATTCTGTAAAAGGTAACAAATATACAGAACAAAACCTTCCCTTTTAA
AACTAATGTTACAAATCTGTATTATCACTTGGATATAAATAGTATATAAGCTGATC

13700.1

CAAGGGATATATGTTGAGGGTACRGRGTGACACTGAACAGATCACAAAGCACGAGAAACATTAGTTCTCTCCCT
CCCCAGCGTCTCCTTCGTCTCCCTGGTTTTCCGATGTCCACAGAGTGAGATTGTCCCTAAGTAACTGCATGATC
AGAGTGCTGKCTTTATAAGACTCTTCATTACGCGTATCCAATTCAGCAATTGCTTCATCAAATGCCGTTTTTGC
CAGGCTACAGGCCTTTTCAGGAGAGTTTGAATCTCATAGTAAAAGACTGAGAAATTTAGTGCCAGACCAAGAC
GAATTGGGTGTGTAGGCTGCATTNCTTTCTTACTAATTTCAAATGCTTCCTGGTAAGCCTGCTGGGAGTTCGAC
ACAAGTGGTTTGTGTTGCTCCAGATGCCACTTCAGAAAGATACCTAAATAATCTCCTTTTCAATTTCAAAGT
AGAACAC

13700.2

TCCGGAGCCGGGGTAGTCGCCGCCGCCGCCGCCGGTGCAGCCACTGCAGGCACCGCTGCCGCCGCCCTGAGTAGT
GGGCTTAGGAAGGAAGAGGTCTCTCGCTCGGAGCTTCGCTCGGAAGGGTCTTTGTTCCCTGCAGCCCTCCAC
GGGAATGACAATGGATAAAAGTGAGCTGGTACAGAAAGCCAAACTCGCTGAGCAGGCTGAGCGATATGATGATA
TGGCTGCAGCCATGAAGGCAGTCACAGAACAGGGGCATGAACTCTCCAACGAAGAGAGAAATCTGCTCTCTGTT
GCCTACAAGAATGTGGTAAGGCCGCCGCCGCTCTTCTGGCGTGTCTCTCCAGCATTGAGCAGAAAAACAGAG
AGGAATGAGAAGAAGCAGCAGATGGGCAAAGAGTACCGTGAGAAGATAGAGGCAGAACTGCAGGACATCTGCAA
TGATGTTCTGGAGCTTGTGGACAAATATCTTATTCCAATGCTACACAACCCAGAAA

13701.1

AAAAAGCAGCARGTTCAACACAAAATAGAAATCTCAAATGTAGGATAGAACAAAACCAAGTGTGTGAGGGGGGA
AGCAACAGCAAAAGGAAGAAATGAGATGTTGCAAAAAGATGGAGGAGGGTTCCCTCTCCTCTGGGGACTGAC
TCAAACACTGATGTGGCAGTATACCAATTCAGAGTCAGGGGTGTTCACTCTTTTTTGGGAGTAAGAAAAGGT
GGGGATTAAGAAGACGTTTCTGGAGGCTTAGGGACCAAGGCTGGTCTCTTTCCCCCTCCCAACCCCTTGATC
CCTTTCTCTGATCAGGGGAAAGGAGCTCGAATGAGGGAGGTAGAGTTGGAAGGGAAAGGATTCCACTTGACAG
AATGGGACAGACTCCTTCCCA

Fig. 15J

45/101

13701.2

TGGCAATAGCACAGCCATCCAGGAGCTCTTCARGCGCATCTCGGAGCAGTTCACTGCCATGTTCCGCCGGAAGG
CCTTCCTCCACTGGTACACAGGCGAGGGCATGGACGAGATGGAGTTCACCGAGGCTGAGAGCAACATGAACGAC
CTCGTCTCTGAGTATCAAGCAGTACCAGGATGCCACCGCAGAAGAGGAGGAGGATTTCCGGTGAAGAGGCCGAAG
AGGAGGCCTAAGGCAGAGCCCCATCACCTCAGGCTTCTCAGTTCCTTAGCCGTCTTACTCAACTGCCCCTTT
CCTCTCCCTCAGAAATTTGTGTTTGCTGCCTCTATCTTGTGTTTTTCTTCTGGGGGGGTCTAGAACAGT
GCCTGGCACATAGTAGGCGCTCAATAAATACTTGGTTGNTGAATGTCTCCT

13702.2

AGCTGGCGCTAGGGCTCGGTTGTGAAATACAGCGTRGTAGCCCTTGCGCTCAGTGTAGAAACCCACGCCTGTA
AGGTGGTCTTCGTCCATCTGCTTTTTCTGAAATACACTAAGAGCAGCCACAAAACCTGTAACCTCAAGGAAAC
CATAAAGCTTGGAGTGCCTTAATTTTAACCAAGTTTCCAATAAAACGGTTTACTACCT

13704.2-13740.2

GGAGATGAAGATGAGGAAGCTGAGTCAGCTACGGGCARGCGGGCAGCTGAAGATGATGAGGATGACGATGTCTGA
TACCAAGAAGCAGAAGACCGACGAGGATGACTAGACAGCAAAAAAGGAAAAGTTAAA

13706.1

GATGAAAATTAATACTTAATTAATCAAAAGGCACTACGATACCACCTAAAACCTACTGCCTCAGTGGCAGTA
KGCTAAKGAAGATCAAGCTACAGSACATYATCTAATATGAATGTTAGCAATTACATAKCARGAAGCATGTTTGC
TTTCCAGAAGACTATGGNACAATGGTCATTWGGGCCAAGAGGATATTTGGCCNGGAAAGGATCAAGATAGATN
AANGTAAAG

13706.2

GAGTAGCAACGCAAAGCGCTTGGTATTGAGTCTGTGGGSGACTTCGGTTCGGTCTCTGCAGCAGCCGTGATCG
CTTAGTGGAGTGCTTAGGGTAGTTGGCCAGGATGCCGAATATCAAAATCTTCAGCAGGCAGCTCCCACCAGGAC
TTATCTCASAAAATTGCTGACCGCCTGGGCTGGAGCTAGGCAAGGTGGTACTAAGAAATTCAGCAACCAGGA
GACCTGTGTGGAATTTGGTGAAAGTGTACCGTGGAGAGGATGTCTACATTGTTGAGAGTGGNTGTGGCGAAATC
AATGACAATTTAATGGAGCTTTTGATCATGATTAATGCCTGCAAGATTGCTTCAGCCAGCCGGGTTACTGCAGT
CATCCCATGCTTCCCTTATGCCCCGGCAGGATAAGAAAGATNAGAGCCGGGCCGCAATCTCAGCCAAGCTTGG
TGCAATATGCTATCTGTAGCAGTGCAGATCATATTATCACCATGGACCTACATGCTTCTCAAATTCANGGCTT
TTT

Fig. 15K

46/101

13707.3

ATGCAAAAGGGGACACAGGGGTTCAAAAATAAAAATTTCTCTTCCCCCTCCCCAACCTGTACCCAGCTCCC
CGACCACAACCCCTTCTCCCCCGGGGAAAGCAAGAAGGAGCAGGTGTGGCATCTGCAGCTGGGAAGAGAGAG
GCCGGGGAGGTGCCGAGCTCGGTGCTGGTCTCTTTCCAAATATAAATACGTGTGTGAGAACTGGAAAATCCTCC
AGCACCACACCCCAAGCACTCTCCGTTTTCTGCCGGTGTGGAGAGGGGCGGNGGGCAGGGGCGCCAGGCAC
CGGCTGGCTGCGGTCTACTGCATCCGCTGGGTGTGCACCCCGCA

13710.2

AGGTTGGAGAAGGTGCAGGTGCAGATTGTCCAGGSKCAGCCACAGGGTCAAGCCCAACAGGCCAGAGTGG
CACTGGACAGACCATGCAGGTGATGCAGCAGATCATCTAACACAGGAGAGATCCAGCAGATCCCGGTGCAGC
TGAATGCCGGCCAGCTGCAGTATATCCGCTTAGCCCAGCCTGTATCAGGCACTCAAGTTGTGCAGGGACAGATC
CAGACACTTGCCACCAATGCTCAACAGATTACACAGACAGAGGTCCAGCAAGGACAGCAGAGTTCAAGCCAGT
TCACAAGATGGACAGCAGCTCTACCAGATCCAGCAAGTCAACATGCCTGCCGGCCANGACCTCGCCAGCCCATG
TTCATCCAGTCAAGCCAACAGCCCTTCNACGGGCAGGCCCCCAGGTGACCGGCGACTGAAGGGCCTGAGCTG
GCAAGGCCAANGACACCCAACACAATTTTTGCCATACAGCCCCCAGGCAATGGGCACAGCCTTTCTTCCAGAG
GAC

13710-1

TGAGATTTATTGCATTTTCATGCAGCTTGAAGTCCATGCAAAGGRGACTAGCACAGTTTTTAATGCATTTAAAAA
ATAAAAGGGAGGTGGGCAGCAAACACACAAAGTCTAGTTTCTTGGGTCCCTGGGAGAAAAGAGTGTGGCAATG
AATCCACCCACTCTCCACAGGGAATAAATCTGTCTCTTAAATGCAAAGAATGTTTCCATGGCCTCTGGATGCAA
ATACACAGAGCTCTGGGGTCAGAGCAAGGGATGGGGAGAGGACCACGAGTGAAAAAGCAGCTACACACATTAC
CTAATTCATCTGAGGGCAAGAACAACGTGGCAAGTCTTGGGGGTAGCAGCTGTT

13711.1

TCCAGACATGCTCCTGTCTAGGCGGGGAGCAGGAACCAGACCTGCTATGGGAAGCAGAAAGAGTTAAGGGAAG
GTTTCCTTTCATTCTGTTCTTCTCTTTGCTTTTGAACAGTTTTTAAATATACTAATAGCTAAGTCATTTGC
CAGCCAGGTCCCGGTGAACAGTAGAGAACAAAGGAGCTTGCTAAGAATTAATTTTGTGTTTTTCAACCCATTCA
AACAGAGCTGCCCTGTTCCCTGATGGAGTTCATTCTGCCAGGGCACGGCTGAGTAACACGAAGCCATTCAAG
AAAGGCGGGTGTGAAATCACTGCCACCCCATGGACAGACCCCTCACTCTTCTTCTTAGCCGACGCGCTACTTA
ATAAATATATTTATACTTTGAAATTATGATAACCGATTTTTCCCATGCCGCATCCTAAGGGCACTTGCCAGCTC
TTATCCGGACAGTCAAGCACTGTTGTTGGACAACAGATAAAGGAAAAGAAAAAGAAGAAAAACAACCGCAACTTC
TGT

Fig. 15L

47/101

13711.2

TGAGACGGACCACTGGCCTGGTCCCCCTCATKTGCTGTGCTAGGACCTGACATGAAACGCAGATCTAGTGGCA
GAGAGGAAGATGATGAGGAACCTCTGAGACGTCGGCAGCTTCAAGAAGAGCAATTAATGAAGCTTAAGTCAGGC
CTGGGACAGTTGATCTTGAAAGAAGAGATGGAGAAAGAGAGCCGGGAAAGGTCATCTCTGTTAGCCAGTCGCTA
CGATTCTCCCATCAACTCAGCTTCACATATTCATCATCTAAACTGCATCTCTCCCTGGCTATGGAAGAAATG
GGCTTCACCGGCCTGTTTCTACCGACTTCGCTCAGTATAACAGCTATGGGGATGTCAGCGGGGAGTGCGAGAT
TACCAGACACTTCCAGATGGCCACATGCCTGCAATGAGAATGGACCGAGGAGTGTCTATGCCAACATGTTGGA
ACCAAGATATTTCCATATGAAATGCTCATGGTGACCAACAGAGGGCCGAAACCAATCTCAGAGAGGTGGACA
GAA

13713.1&2

TCACTTTATTTTTCTTGATATAAAACCCTATGTTGTAGCCACAGCTGGAGCCTGAGTCCGCTGCACGGAGACTC
TGGTGTGGGTCTTGACGAGGTGGTCAGTGAACCTCTGATAGGGAGACTTGGTGAATACAGTCTCCTCCAGAGG
TCGGGGGTCAGGTAGCTGTAGGTCTTAGAAATGGCATCAAAGGTGGCCTTGCGAAGTTGCCAGGTGGCAGT
GCAGCCCCGGGTGAGGTGTAGCAGTCATCGATACCAGCCATCATGAG

13715.4

CTGGAATATAGACCCGTGATCGACAAAACCTTTGAACGAGGCTGACTGTGCCACCGTCCCGCCAGCCATTGCTC
CTACTGATGAGACAAGATGTGGTGATGACAGAATCAGCTTTTGTATTATGTATAATAGCTCATGCATGTGTCC
ATGTCATAACTGTCTTCATACGCTTCTGCACTCTGGGAAGAAGGAGTACATTGAAGGGAGATTGGCACCTAGT
GGCTGGGAGCTTGCCAGGAACCCAGTGGCCAGGGAGCGTGGCACTTACCTTTGTCCCTTGCTTCATTCTTGTA
GATGATAAACTGGGCACAGCTCTTAAATAAAATATAAATGAACA

13717.1&2

TGAATGGGGAGGAGCTGACCCAGGAAATGGAGCTTGNGGAGACCAGGCCTGCAGGGGATGGAACCTTCCAGAAG
TGGGCATCTGTGGTGGTGCCTCTTGGGAAGGAGCAGAAGTACACATGCCATGTGGAACATGAGGGGCTGCCTGA
GCCCCCTACCCCTGAGATGGGGCAAGGAGGAGCCTCCTTCATCCACCAAGACTAACACAGTAATCATTGCTGTTT
CGGTTGTCTTGGAGCTGTGGTCATCCTTGGAGCTGTGATGGCTTTTGTGATGAAGAGGAGGAGAAACACAGGT
GGAAAAGGAGGGGACTATGCTCTGGCTCCAGGCTCCAGAGCTCTGATATGTCTCTCCAGATTGTAAAGTGTG
AAGACAGCTGCCTGGTGTGGACTTGGTGACAGACAATGTCTTCACACATCTCCTGTGACATCCAGAGACCTCAG
TTCTCTTTAGTCAAGTGTCTGATGTTCCCTGTGAGTCTGCGGGCTCAAAGTGAAGAACTGTGGAGCCAGTCCA
CCCCCTGCACACCAGGACCCTATCCCTGCACTGCCCTGTGTTCCCTTCCACAGCCAACCTTGCTGCTCCAGCCAA
ACATTGGTGGACATCTGCAGCCTGTGAGCTCCATGCTACCCTGACCTTCAACTCCTCACTTCCACACTGAGAAT
AATAATTTGAATGTGGGTGGCTGGAGAGATGGCTCAGCGCTGACTGCTCTTCCAAAGGTCCTGAGTTCAAATCC
CAGCAACCACATGGTGGCTCACAACCATCTGTAATGGGATCTAATACCCTCTTCTGCAGTGTCTGAAGACASCT
ACAGTGTACTTACATATAATAATAAATAAG

Fig. 15M

48/101

13719.1&2

GGCCGGGCGCGCGCCCCGCCACGCGCGCGGGCGTGCCAGTTTATAAAGGGAGAGAGCAAGCAGCGAGT
CTTGAAGCTCTGTTTGGTGCTTTGGATCCATTTCCATCGGTCTTACAGCCGCTCGTCAGACTCCAGCAGCCAA
GATGGTGAAGCAGATCGAGAGCAAGACTGCTTTTCAGGAAGCCTTGGACGCTGCAGGTGATAAACTTGTAGTAG
TTGACTTCTCAGCCACGTGGTGTGGGCCTTGCAAAATGATCAAGCCTTTCTTTCATTCCCTCTCTGAAAAGTAT
TCCAACGTGATATTCCTTGAAGTAGATGTGGATGACTGTGAGGATGTTGCTTCAGAGTGTGAAGTCAAATGCAT
GCCAACATTCCAGTTTTTTAAGAAGGGACAAAAGGTGGGTGAATTTTCTGGAGCCAATAAGGAAAAGCTTGAAG
CCACCATTAATGAATTAGTCTAATCATGTTTTCTGAAAATATAACCAGCCATTGGCTATTTAAACTTGTAAAT
TTTTTAATTTACAAAAATATAAAATATGAAGACATAAACCCMGTTGCCATCTGCGTGACAATAAACATTAATG
CTAACACTT

13721.1

TCACATAAGAAATTTAAGCAAGTTACRCTATCTTAAAAACACAACGAATGCATTTTAAATAGAGAAACCCTTCC
CTCCCTCCACCTCCCTCCCCACCCTCCTCATGAATTAAGAATCTAAGAGAAGAAGTAACCATAAAACCAAGTT
TTGTGGAATCCATCATCCAGAGTGCTTACATGGTGATTAGGTTAATATTGCCTTCTTACAAAATTTCTATTTTA
AAAAAAATTATAACCTTGATTGCTTATTACAAAAAAATTCAGTACAAAAGTTCAATATATTGAAAATGCTTTT
CCCCTCCCTCACAGCACCGTTTTATATATAGCAGAGAATAATGAAGAGATTGCTAGTCTAGATGGGGCAATCTT
CAAATTACACCAAGACGCACAGTGGTTTATTTACCCTCCCCTTCTCATAAG

13721.2

GGAAAGGATTCAAGAATTAGAGGACTTGCTTGCTRRAGAAAAAGACAACCTCTCGTCGCATGCTGACAGACAAAG
AGAGAGAGATGGCGGAAATAAGGGATCAAATGCAGCAACAGCTGAATGACTATGAACAGCTTCTTGATGTAAAG
TTAGCCCTGGACATGGAAATCAGTGCTTACAGGAACTCTTAGAAGGCGAAGAAGAGAGGTTGAAGCTGTCTCC
AAGCCCTTCTTCCCGTGTGACAGTATCCCGAGCATCCTCAAGTCGTAGTGTACCGTACAACCTAGAGGAAAGCGG
AAGAGGGTTGATGTGGAAGAATCAGAGGCGAAGTAGTAGTGTTAGCATCTCTCATTCCGCCTCAACCACTGGAA
ATGTTTGCATCGAAGAAATTGATGTTGATGGGAAATTTATCCCGCTTGAAGAACACTTCTGAACAGGATCAACC
AATGGGAAGGCTTGGGAGATGATCAGAAAAATTGGAGACACATCAGTCAGTTATAAATATACCTCAA

13723.1

CATGGGTTTCACCAGGTTGGCCAGGCTGCTCTTGAACTSCTGACCTCAGGTGATCCACCCGCCTCGGCCTCCCA
AAGTGCTGGGATTACAGGCGTGAGCCACCACGCCCGGCCCCAAAGCTGTTTCTTTTGTCTTTAGCGTAAAGCT
CTCCTGCCATGCAGTATCTACATAACTGACGTGACTGCCAGCAAGCTCAGTCACTCCGTGGTCTTTTTCTCTTT
CCAGTTCTTCTCTCTCTTCAAGTTCTGCCTCAGTGAAAGCTGCAGGTCCCAGTTAAGTGATCAGGTGAGGG
TTCTTTGAACCTGGTTCTATCAGTCGAATTAATCCTTCATGATGG

Fig. 15N

49/101

13723.2

GATGTGTTGGACCCTCTGTGTCAAAAAAACCTCACAAAGAATCCCCTGCTCATTACAGAAGAAGATGCATTTA
AAATATGGGTTATTTTCAACTTTTTATCTGAGGACAAGTATCCATTAATTATTGTGTGAGAAGAGATTGAATAC
CTGCTTAAGAAGCTTACAGAAGCTATGGGAGGAGGTTGGCAGCAAGAACAATTTGAACATTATAAAATCAACTT
TGATGACAGTAAAAATGGCCTTTCTGCATGGGAACCTATTGAGCTTATTGGAAATGGACAGTTTAGCAAAGGCA
TGGACCGGCAGACTGTGTCTATGGCAATTAATGAAGTCTTTAATGAACCTATATTAGATGTGTTAAAGCAGGGT
TACATGATGAAAAAGGGCCACAGACGGAAAACTGGACTGAAAGATGGTTTGTACTAAAACCCAACATAATTC
TTACTATGTGAGTGAGGATCTGAAGGATAAGAAAGGAGACATTCTCTTGATGAAAATTGCTGTGTAGAAGTCC
TTGCCTGACAAAAGATGGAAAGAAATGCCTTTT

13725.1

GACTGGTTCTTTATTTCAAAAAGACACTTGTCAATATTCAGTRTCAAAACAGTTGCACTATTGATTTCTCTTTC
TCCAATCGGCCCCAAAGAGACCACATAAAAGGAGAGTACATTTTAAGCCAATAAGCTGCAGGATGTACACCTA
ACAGACCTCTAGAAACCTTACCAGAAAATGGGGACTGGGTAGGGAAGGAACTTAAAGATCAACAACTGCC
AGCCACGGACTGCAGAGGCTGTACAGCCAGATGGGGTGGCCAGGGTGCCACAAACCCAAAGCAAAGTTTCAA
AATAATATAAAATTTAAAAAGTTTTGTACATAAGCTATTCAAGATTTCTCCAGCACTGACTGATACAAAGCACA
ATTGAGATGGCACTTCTAGAGACAGCAGCTTCAAACCCAGAAAAGGGTGATGAGATGAAGTTTACATGGCTAA
ATCAGTGGCAAAAACACAGTCTTCTTTCTTTCTTTCTTTCAAGGANGCAGGAAAGCAATTAAGTGGTCACCTTA
ACATAAGGGGGAC

13725.2

TGGGTGGGCACCATGGCTGGGATCACCACCATCGAGGCGGTGAAGCGCAAGATCCAGGTTCTGCAGCAGCAGGC
AGATGATGCAGAGGAGCGAGCTGAGCGCTCCAGCGAGAAGTTGAGGGAGAAAGGCGGGCCGGGAACAGGCTG
AGGCTGAGGTGGCCTCCTTGAACCGTAGGATCCAGCTGGTTGAAGAAGAGCTGGACCGTGTCTCAGGAGCGCCTG
GCCACTGCCCTGCAAAAGCTGGAAGAAGCTGAAAAAGCTGCTGATGAGAGTGAGAGAGGTATGAAGGTTATTGA
AAACCGGGCCTTAAAGATGAAGAAAAGATGGAACCTCAGGAAATCCAACCTCAAAGAAGCTAAGCACATTGCAG
AAGAGGCAGATAGGAAGTATGAAGAGGTGGCTCGTAAGTTGGTGATCATTGAAGGAGACTTGAACCGCACAGA
AGGAACGAGCTTGAGCTTGGCAAAAGTCCCGTTGCCAGAGATGGGATGAACCAGATTAGACTGATGGACCANA
ACC

13726.1&2

AGGGGCNGCGGGTGCGTGGGCCACTGGGTGACCGACTTAGCCTGGCCAGACTCTCAGCACCTGGAAGCGCCCG
AGAGTGACAGCGTGAGGCTGGGAGGGAGGACTTGGCTTGAGCTTGTTAACTCTGCTCTGAGCCTCCTTGTGCG
CTGCATTTAGATGGCTCCCGCAAAGAAGGGTGGCGAGAAGAAAAAGGCGGTCTGCCATCAACGAAGTGGTAA
CCCGAGAATACACCATCAACATTCACAAGCGCATCCATGGAGTGGGCTTCAAGAAGCGTGACCTCGGGCACTC
AAAGAGATTCGGAATTTGCCATGAAGGAGATGGGAACCTCAGATGTGCGCATTGACACCAGGCTCAACAAAGC
TGTCTGGGCCAAAGGAATAAGGAATGTGCCATACCGAATCCGGTGTGCGGCTGTCCAGAAAACGTAATGAGGAT
GAAGATTCACCAAATAAGCTATATACTTTGGTTACCTATGTACCTGTTACCACTTTCAAAAATCTACAGACAGT
CAATGTGGATGAGAACTAATCGCTGATCGTCAGATCAAATAAAGTTATAAAAT

Fig. 150

50/101

13727.1

TCGGGAGCCACACTTGGCCCTCTTCCTCTCCAAAGSGCCAGAACCTCCTTCTCTTTGGAGAATGGGGAGGCCTC
TTGGAGACACAGAGGGTTTCACCTTGGATGACCTCTAGAGAAATTGCCAAGAAGCCCACCTTCTGGTCCCAAC
CTGCAGACCCACAGCAGTCAGTTGGTCAGGCCCTGCTGTAGAAGGTCACTTGGCTCCATTGCCTGCTTCCAAC
CAATGGGCAGGAGAGAAGGCCTTTATTTCTCGCCACCCATTCTCCTGTACCAGCACCTCCGTTTTCAGTCAG
TGTTGTCCAGCAACGGTACCGTTTACACAGTCACCTCAGACACACCATTTCACCTCCCTTGCCAAGCTGTTAGC
CTTAGAGTGATTGCAGTGAACACTGTTTACACACCGTGAATCCATTCCCATCAGTCCATTCCAGTTGGCACCAG
CCTGAACCATTGGTACCTGGTGTAACTGGAGTCCTGTTTACAAGGTGGAGTCGGGGCTTGCTGACTTCTCTT
CATTTGAGGGCAC

13727.2

ACCTAGACAGAAGGTGGGTGAGGGAGGACTGGTAGGAGGCTGAGGCAATTCCTTGGTAGTTTGTCTGAAACCC
TACTGGAGAAGTCAGCATGAGGCACCTACTGAGAGAAGTGCCAGAACTGCTGACTGCATCTGTTAAGAGTTA
ACAGTAAAGAGGTAGAAGTGTTTCTGAATCAGAGTGGAAGCGTCTCAAGGGTCCCACAGTGAGAGTCCCTGA
GCTACCTCCCTTCCGTGAGTGGGAAGAGTGAAGCCCATGAAGAACTGAGATGAAGCAAGGATGGGGTTCCTGGG
CTCCAGGCAAGGGCTGTGCTCTCTGCAGCAGGGAGCCCCACGAGTCAGAAGAAAAGAACTAATCATTTGTTGCA
AGAAACCTTGCCCGGATACTAGCGGAAAAGTGGAGGCGNGGTGGGGGCACAGGAAAGTGAAGTGATTTGATG
GAGAGCAGAGAAGCCTATGCACAGTGGCGGAGTCCACTTGTAAGTG

13728.1&2

TTCAAGCAATTGTAACAAGTATATGTAGATTAGAGTGAGCAAAATCATATACAATTTTCATTTCCAGTTGCTAT
TTTCCAAATTGTTCTGTAATGTCGTTAAATTAATAAAGCCAAAAATTATATTTATGACAAGA
AAGCCATCCCTACATTAATCTTACTTTTCCACTCACCAGCCCATCTCCTTCTCTTTTCTTAACATATGCCATT
AAAAGTGTCTACTGGGCCGGCGTGTGGCTCATGCTGTAAATCCAGCATTTTGGGAGGCCAAGGCAGGCGGA
TCATGAGGTCAAGAGATTGAGACCATCTGGCCAACATGGTGAAACCCCGCTCGACTAAGAATACAAAAATTA
GCTGGGCATGGTGGCGCATGCCTGTAGTCTCAGTACTCGGGAGGCTGAGGCAGAAGATCGCTTGAACCCGGG
AGGCAGAGGATGCAGTGAGCCCCGATCGCGCCACTGCACTCTAGCCTGGGCGACAGACTGAGACTCTGCTC

13731.1&2

TGTGCCAGTCTACAGGCCTATCAGCAGCGACTCCTTCAGCAACAGATGGGGTCCCCTGTTTCAGCCCAACCCCAT
GAGCCCCAGCAGCATATGCTCCCAAATCAGGCCAGTCCCCACACCTACAAGGCCAGCAGATCCCTAATTCTC
TCTCAATCAAGTGCCTCTCCCCAGCCTGTCCCTTCTCCAGGCCACAGTCCCAGCCCCCCTCCAGTCTCCT
TCCCCAAGGATGCAGCCTCAGCCTTCTCCACACCAGTTTCCCCACAGACAAGTTCCCCACATCCTGGACTGGT
AGTTGCCCAGGCCAACCCCATGGAACAAGGGCATTGTCAGCC

Fig. 15P

51/101

13734.1&2

TGTA AAAA ACTTGT TTTTAATTTTGTATAAAATAAAGGTGGTCCATGCCACGGGGGCTGTAGGAAATCCAAGCA
GACCAGCTGGGGTGGGGGGATGTAGCCTACCTCGGGGACTGTCTGTCTCAAAACGGGCTGAGAAGGCCCGTC
AGGGGCCAGGTCCACAGAGAGGCCTGGGATACTCCCCAACCCGAGGGGCAGACTGGGCAGTGGGGAGCCCC
CATCGTGCCCCAGAGGTGGCCACAGGCTGAAGGAGGGCCTGAGGCACCGCAGCCTGCAACCCCCAGGGCTGCA
GTCCACTAACTTTTACAGAATAAAAGGAACATGGGGATGGGGAAAAAGCACCAGGTGAGGCAGGGCCCCGAGG
GCCCCAGATCCAGGAGGGCCAGGACTCAGGATGCCAGCACCACCCTAGCAGCTCCACAGCTCCTGGCACAGG
AGGCCGCCACGATTGGCACAGGCCGCTGCTGGCCATCACGCCACATTGGAGAACTTGCCGACAGAGGTCA
GCTCGGAGGAGCTCCTCGTGGGCACACACTGTACGAACACAGATCTCCTTGTTAATGACGTACACACGGCGGAG
GCTGCGGGGACAGGGCACGGGAGGTCTCAGCCCCACTT

13736.2

ATGGCTGCTGGATTTAGGTGGTAATAGGGGCTGTGGGCCATAAATCTGAAGCCTTGAGAACCTTGGGTCTGGAG
AGCCATGAAGAGGGAAGGAAAAGAGGGCAAGTCTGAACCTAACCAATGACCTGATGGATTGCTCGACCAAGAC
ACAGAAGTGAAGTCTGTGTCTGTGCACTTCCACAGACTGGAGTTTTTGGTGCTGAATAGAGCCAGTTGCTAAA
AAATTGGGGGTTTGGTGAAGAAATCTGATTGTTGTGTGATTCAATGTGTGATTTAAAAATAAACAGCAACAA
CAATAAAAACCTGACTGGCTGTTTTTCCCTGTATTCTTTACAACATTTTTTGACCCTCTGAAAATTATTAT
ACTTCACCTAAATGGAAGACTGCTGTGTTTGTGGAATTTTGAATTTTTAATTTATTTTATTCTCTCTCCTT
TTTATTTTGCCTGCAGAATCCGTTGAGAGACTAATAAGGCTTAATATTTAATTGATTGTTTAATATGTATATA
AAT

13744.2-13696.2

GGCATGCGAGCGCACTCGGCGGACGCAAGGGCGGGGAGCACACGGAGCACTGCAGGCGCCGGGTTGGGACA
GCGTCTTCGCTGCTGCTGGATAGTCGTGTTTTCGGGGATCGAGGATACTCACCAGAAACCGAAAATGCCGAAAC
CAATCAATGTCCGAGTTACCACCATGGATGCAGAGCTGGAGTTTGCAATCCAGCCAAATACAACCTGAAAAACAG
CTTTTTGATCAGGTGGTAAAGACTATCGGCCCTCCGGGAAGTGTGGTACTTTGGCCTCCACTATGTGGATAATAA
AGGATTTCTACCTGGCTGAAGCTGGATAAGAAGGTGTCTGCCAGGAGGTGAGGAAGGAGAATCCCTCCAGT
TCAAGTTCGGGGCAAAGTTCTACCCTGAAGATGTGGCTGAGGAGCTCATCCAGGACATCACCAGAACTTTT
CTTCCTTCAAGTGAAGGAAGGAATCCTTAGCGATGAGATCTACTGCCCCCTTGARACTGCCGTGCTCTTGGG
TCCTACGCTTGTGCATGCCAAGTTTGGGACTACCACCAAGAAG

13746.1&2-13720.1&2

GAAGGAGTCGGGATACTCAGCATTGATGCACCCCAATTTCAAAGCGGCATTCTCGGCAGGTCTCTGGGACAAT
CTCTAGGGTCACTACCTGGAACTCGTTAGGGTACAACCTGAATGCTGAAAGGAAAGAACCTGCAGAACCGGA
CAGAAATTCACCCGGCGATCAGCTGATTGATCTCGGTGACCCAGAAAGTCATGGCTAAAGATGACGAGGACGTT
GTCAATTCCTGGGCTTTTCAAGTGAGTCCAGCAGCAGTCTGAGGTATTCGGGCCGGTTATGCACCTGGACCA
CCAGCACCAGCTCCCGGGGGGCCAGGTGCCAGCCTTATCTACATTCCTCAGGGTCTGATCAAAGTTCAGCTGG
TACACCAGGGACCGGTACCGCAGCGTCAGGTTGTCCGCTCGGGCTGGGGACCGCCGGGACCGGAAGCCGCC
GACACGTTGGAGACCCTGCGGATGCCACAGCCACAGAGGGGTGGTCCCCACCGCGGCCCGCGGACCCCGCGC
GGGTTGCGCGTCCAGCAACGGTGGGGCGAGGGCCTCGTTCTTCTTTGTGCCCCATTGCTGCTCCAGAGGACGA
AGCCGCAGGCGGCCACCACGAGCGTCAGGATTAGCACCTTCCGTTTGTAGATGCGGAACCTCATGGTCTCCAGG
GCCGGGAGCGCAGCTACAGCTCGAGCGTCGGCGCCGCGCTAGGAGCCGCGGCTCGGCTTCGTCTCGTCTCT
CCATTACGACCAACGGGTCCCGGAAAAAGCTCAGCCSCGGTCCCAACCGCACCTAGCTTCGTTACCTGCGCCT
CGCTTG

Fig. 15Q

52/101

14347.1

CAGATTTTATTTGCAGTCGTCAGTGGGGCCGTTTCTTGCTGCTTATTTGTCTGCTAGCCTGCTCTTCCAGCTG
CATGGCCAGGCGCAAGGCCTTGATGACATCTCGCAGGGCTGAGAAATGCTTGGCTTGCTGGGCCAGAGCAGATT
CCGCTTTGTTACAAAGGTCTCCAGGTCATAGTCTGGCTGCTCGGTATCTCAGAGAGCTCAAGCCAGTCTGGT
CCTTGCTGTATGATCTCCTTGAGCTCTTCCATAGCCTTCTCCTCCAGCTCCCTGATCTGAGTCATGGCTTCGTT
AAAGCTGGACATCTGGGAAGACAGTTCCTCCTCTTCTGGATAAATTGCCTGGAATCAGCGCCCGTTAGAGC
AGGCTTCCATCTCTTCTGTTTCCATTTGAATCAACTGCTCTCCACTGGGCCCACTGTGGGGGCTCAGCTCCTTG
ACCCTGCTGCATATCTTAAGGGTGTAAAGGATATTACAGGAGCTTATGCCTGGT

14347.2

CTCCTCTTGGTACATGAACCAAGTTGAAAGTGGACTTAACAAAGTATCTGGAGAACCAAGCATTCTGCTTTGA
CTTTGCATTTGATGAAACAGCTTCGAATGAAGTTGTCTACAGGTTACAGCAAGGCCACTGGTACAGACAATCT
TTGAAGGTGGAAGCAACTTGTTTTGCATATGGCCAGACAGGAAGTGGCAAGACATACTATGGGCGGAGAC
CTCTCTGGGAAAGCCAGAATGCATCCAAAGGGATCTATGCCATGGCCTTCCGGGACGTCTTCTTCTGAAGAAT
CAACCCTGCTACCGGAAGTTGGGCCTGGAAGTCTATGTGACATTCTTCGAGATCTACAATGGGAAGCTGTTTGA
CCTGCTCAACAAGAAGGCCAAGCTTGCGCTGCTGGAAGACGGCAAGCAACAGGTGCAAGTGGTGGGGGCTTGC
AGGAACATCTGGNTAACTCTGCTTGATGATGGCANTCAAGATGATCGACATGGGCAGCGCCTGCAGA

14348.2&14350.1&2

TCCGAATTCAAGCGACAAATTGGAWAGTGAAATGGAAGATGCCTATCATGAACATCAGGCAAATCTTTTGGCG
CAAGATCTGATGAGACGACAGGAAGAATTAAGACGCATGGAAGAACTTCACAATCAAGAAATGCAGAAACGTAA
AGAAATGCAATTGAGGCAAGAGGAGGAACGACGTAGAAGAGAGGAAGAGATGATGATTCGTCAACGTGAGATGG
AAGAACAAATGAGGCGCCAAAGAGAGGAAAGTTACAGCCGAATGGGCTACATGGATCCACGGGAAAGAGACATG
CGAATGGGTGGCGGAGGAGCAATGAACATGGGAGATCCCTATGGTTCAGGAGGCCAGAAATTTCCACCTCTAGG
AGGTGGTGGTGGCATAGGTTATGAAGCTAATCCTGGCGTTCCACCAGCAACCATGAGTGGTCCATGATGGGAA
GTGACATGCGTACTGAGCGCTTTGGGCAGGGAGGTGCGGGGCTGTGGGTGGACAGGGTCTAGAGGAATGGGG
CCTGGAATCCAGCAGGATATGGTAGAGGGAGAGAAGAGTACGAAGGC

14349.1&2

TTCGTGAAGACCCTGACTGGTAAGACCATCACTCTGAAGTGGAGCCCGAGTGACACCATTGAGAATGTCAAGG
CAAAGATCCAAGACAAGGAAGGCATCCCTCCTGACCAGCAKAGGTTGATCTTTGCTGGGAAACAGCTGGAAGAT
GGACGCACCCTGTCTGACTACAACATCCAGAAAGAGTCCACCCTGCACCTGGTGCTCCGTCTCAGAGGTGGGAT
GCAATCTTCGTGAAGACCCTGACTGGTAAGACCATCACCCTCGAGGTGGAGCCAGTGACACCATCGAGAATG
TCAAGGCAAGATCCAAGATAAGGAAGGCATCCCTCCTGATCAGCAGAGGTTGATCTTTGCTGGGAAACAGCTG
GAAGATGGACGCACCCTGTCTGACTACAACATCCAGAAAGAGTCCACTCTGCACTTGGTCTGCGCTTGAGGGG
GGGTGTCTAAGTTTCCCTTTTAAGGTTTCAACAAATTTTATTGCACTTTCCCTTTCAATAAAGTTGTTGCATTCT

Fig. 15R

53/101

14352.1&2

GCGCGGGTGCGTGGGCCACTGGGTGACCGACTTAGCCTGGCCAGACTCTCAGCACCTGGAAGCGCCCCGAGAGT
GACAGCGTGAGGCTGGGAGGGAGGACTTGGCTTGAGCTTGTTAACTCTGCTCTGAGCCTCCTTGTGCGCTGCA
TTTAGATGGCTCCCGCAAAGAAGGGTGGCGAGAAGAAAAAGGGCCGTTCTGCCATCAACGAAGTGGAACCCGA
GAATACACCATCAACATTCACAAGCGCATCCATGGAGTGGGCTTCAAGAAGCGTGCACCTCGGGCACTCAAAGA
GATTCGGAAATTTGCCATGAAGGAGATGGGAACTCCAGATGTGCGCATTGACACCAGGCTCAACAAAGCTGTCT
GGGCCAAAGGAATAAGGAATGTGCCATACCGAATCCGTGTGCGGCTGTCCAGAAAACGTAATGAGGATGAAGAT
TCACCAAATAAGCTATATACTTTGGTTACCTATGTACCTGTTACCACTTTCAAAAATCTACAGACAGTCAATGT
GGATGAGAACTAATCGCTGATCGT

14353.1

AATTCTTTATTTAAATCAACAACTCATCTTCCTCAAGCCCCAGACCATGGTAGGCAGCCCTCCCTCTCCATCC
CCTCACCCACCCCTTAGCCACAGTGAAGGAATGGAAATGAGAAGCCACGAGGGCCCTGCCAGGGAAGGCT
GCCCCAGATGTGTGGTGAGCACAGTCAGTGCAGCTGTGGCTGGGGCAGCAGCTGCCACAGGCTCCTCCCTATAA
ATTAAGTTCCTGCAGCCACAGCTGTGGGAGAAGCATACTTGTAGAAGCAAGGCCAGTCCAGCATCAGAAGGCAG
AGGCAGCATCAGTGACTCCCAGCCATGGAATGAACGGAGGACACAGAGCTCAGAGACAGAACAGGCCAGGGGGA
AGAAGGAGAGACAGAATAGGCCAGGGCATGGCGGTGAGGGA

14353.2

TGATGAATCTGGGTGGGCTGGCAGTAGCCCGAGATGATGGGCTCTTCTCTGGGGATCCCACTGGTTCCTAAG
AAATCCAAGGAGAATCCTCGGAACCTCTCGGATAACCAGCTGCAAGAGGGCAAGAACGTGATCGGGTTACAGAT
GGGCACCAACCGCGGGGCGTCTCANGCAGGCATGACTGGCTACGGGATGCCACGCCAGATCCTCTGATCCCACC
CCAGGGCTTGCCCTGCCCTCCACGAATGGTTAATATATATGTAGATATATATTTTAGCAGTGACATTCACAG
AGAGCCCCAGAGCTCTCAAGCTCCTTTCTGTACGGGTGGGGGTTCAAGCCTGTCTGTACCTCTGAAGTGCC
TGCTGGCATCCTCTCCCCATGCTTACTAATACATTCCCTTCCCCATAGCC

17182.1&2

AGCGGAGCTCCCTCCCCTGGTGGCTACAACCCACACAGCCAGGCTCAGGCATCGAGCAGAACTCCAGCGACTG
GGTAACCACTGACATTCAGGTGAAGGTGCGGGACACCTACCTGGATACACAGGTGGTGGGACAGACAGGTGTCA
TCCGCAGTGTACGGGGGGCATGTGCTCTGTGTACCTGAAGGACAGTGAGAAGGTTGTGAGCATTTCAGTGAG
CACCTGGAGCCTATCACCCCAACAAGAACAAGGTGAAAGTGATCCTGGGCGAGGATCGGGAAGCCACGGG
CGTCTACTGAGCATTGATGGTGAGGATGGCATTGTCCGTATGGACCTTGATGAGCAGCTCAAGATCCTCAACC
TCCGCTTCCTGGGGAAGCTCCTGGAAGCCTGAAGCAGGCAGGGCCGGTGACTTCGTGGATGAAGAGTGATCC
TCCTTCCTTCCTGGCCCTTGCTGTGACACAAGATCCTCCTGCAGGGCTAGGCGGATTGTTCTGGATTTCTT
TTGTTTTCTTTTAGGTTTCCATCTTTTCCCTCCCTGGTGCTCATTGGAATCTGAGTAGAGTCTGGGGGAGGG
TCCCCACCTTCCTGTACCTCCTCCCCACAGCTTGCTTTTGTGTACCGTCTTTCAATAAAAAGAGCTGTTTGG
TCTA

Fig. 15S

54/101

17183.2

GGTTCACAGCACTGCTGCTTGTGTGTTGCCGGCCAGGAATTCCAGGCTCACAAGGCTATCTTAGCAGCTCGTTC
TCCGGTTTTTAGTGCCATGTTTGAACATGAAATGGAGGAGAGCAAAAAGAATCGAGTTGAAATCAATGATGTGG
AGCCTGAAGTTTTTAAGGAAATGATGTGCTTCATTTACACGGGGAAGGCTCCAAACCTCGACAAAATGGCTGAT
GATTTGCTGGCAGCTGCTGACAAGTATGCCCTGGAGCGCTTAAAGGTCATGTGTGAGGATGCCCTCTGCAGTAA
CCTGTCCGTGGAGAACGCTGCAGAAATTCTCATCCTGGCCGACCTCCACAGTGCAGATCAGTTGAAAACCTCAGG
CAGTGGATTTTCATCAACTATCATGCTTCGGATGTCTTGGAGACCTCTTGGG

17186.1&2

TCGTAGCCATTTTTCTGCTTCTTTGGAGAATGACGCCACACTGACTGCTCATTGTGCTTGGTTCCATGCCAATT
GGTGAAATAGAACCTCATCCGGTAGTGGAGCCGGAGGGACATCTTGTCATCAACGGTGATGGTGCGATTTGGAG
CATACCAGAGCTTGGTGTTCTCGCCATACAGGGCAAAGAGGTTGTGACAAAGAGGAGAGATACGGCATGCCTGT
GCAGCCCTGATGCACAGTTCCTCTGCTGTGTACTCTCCACTGCCAGCCGGAGGGGCTCCCTGTCCGACAGATA
GAAGATCACTTCCACCCCTGGCTTG

17187.1&2

TGGCACACTGCTCTTAAGAACTATGAWGATCTGAGATTTTTTTGTGTATGTTTTTGA CTCTTTTGAGTGGTAA
TCATATGTGTCTTTATAGATGTACATACCTCCTTGACACAAATGGAGGGGAATTCATTTTCATCACTGGGAGTGT
CCTTAGTGATAAAAACCATGCTGGTATATGGCTTCAAGTTGTAAAAATGAAAGTGACTTTAAAGAAAAATAGG
GGATGGTCCAGGATCTCCACTGATAAGACTGTTTTTAAGTAACTTAAGGACCTTTGGGTCTACAAGTATATGTG
AAAAAATGAGACTTACTGGGTGAGGAAATTCATTGTTTAAAGATGGTCGTGTGTGTGTGTGTGTGTGTGTGTG
TTGTGTTGTGTTTTGTTTTTAAGGGAGGGGAATTTATTATTTACCGTTGCTTGAAATTACTGKGTAATATATG
TYTGATAATGATTTGCTYTTTGVMCTAAATAGGVCTGTATAAGTWCTARATGCMTCCCTGGGKGTGATY
TTCCMAGATATTGATGATAMCCCTTAAATGTAAACCYGCCTTTTCCCTTGCTYTCMATTAAAGTCTATTCM
AAAG

17191.1&89.1

GGGGGTAGGCTCTTTATTAGACGGTTATTGCTGTACTACAGGGTCAGAGTGCAGTGTAAGCAGTGTGAGAGGCC
CGCGTTACAGCCAAGAATGTGGATTTTCTCTCCCTATTGATCACAGTGGGTGGGTTTCTTCAGAAAAGCCCCAG
AGGCAGGGACCAGTGAGCTCCAAGGTTAGAAGTGGAAGTGGAAAGGCTTCAGTCACATGCTGCTTCCACGCTTCC
AGGCTGGGCAGCAAGGAGGAGATGCCATGACGTGCCAGGTCTCCCATCTGACACCAGTGAAGTCTGGTAGGA
CAGCAGCCGCACGCTGCCTCTGCCAGGAGGCCAATCATGGTAGGCAGCATTGCAGGGTCAGAGGTCTGAGTCC
GGAATAGGAGCAGGGGCAGGTCCCTGCGGAGAGGCACCTTCTGGCCTGAAGACAGCTCCATTGAGCCCCCTGCAGT
ACAGGYGTAGTGCCTTGGACCAAGCCACAGCCTGGTAAGGGGCGCCTGCCAGGGCCACGGCCAGGAGGCA

Fig. 15T

55/101

17192.1&2

TAATTTCTTAGTCGTTTGAATCCTTAAGCATGCAAAAGCTTTGAACAGAAGGGTTACAAAAGGAACCAGGGTT
GTCTTATGGCATCCAGTTAAGCCAGAGCTGGGAATGCCTCTGGGTCATCCACATCAGGAGCAGAAGCACTTGAC
TTGTCGGTCTGCTGCCACGGTTTGGGCGCCACCACGCCACGTCCACCTCGTCTCCCTGCCGCCACGTCC
TGGGCGGCCAAGGTCTCCAAAATTGATCTCCAGCTGAGACGTTATATCATTTGCTGGCTCCGGAATGATGGT
CCATAACCGAATCTTCAGCATGAGCCTCTTCACTCTTTGATTTATGAAGAACAAATCCCTTCTTCCACTGCCCA
TCAGCACCTTCATTTGGTTTTCGGATATTAAATTCTACTTTTGCCCGGTCCTATTTTGAATAGCCTTCCACTC
ATCCAAAGTCATCTCTTTTGGACCTCCTCTTTTACCTCTTCAACTTCATTCTCCTTATTTTCAAGTGTCTGCCA
CTGGATGATGTTCTTCACCTTCAGGTGTTTCTCAGTCACATTTGATTGATCCAAGTCAGTTAATTCGTCTTTG
ACAGTTCCCCAGTTGTGAGATCCGCTACCTCCAGTTTGTCTCGTGTTCAGGCCAGATCTATCACTTCCACT
ATGCCTATCAAATTCACGTTTGCACGAGAATCAAATCCATCTCCTCGGCCATTCCACGTCCACGGCCCCCTC
GACCTCTTCCAAGACCACCACGACCTCGAATAGGTGGTCAATAATCGGTCTATCAACTGAAAATTCGCCTCCT
TCACCTTTTCTTCAAGTGGCTTTTGAATCTTCGTTACGAGGTGGTCGCTTTCTGGTCTTCTATCAATTAT
TTCCCTTACCCTGAAGTTGTTGATCAGGTCTTCTTCCAACCTCGTGC

17193

AAGCGGATGGACCTGAGTCAGCCGAATCCTAGCCCCCTTCCCTTGGGCCTGCTGTGGTGCTCGACATCAGTGACA
GACGGAAGCAGCAGACCATCAAGGCTACGGGAGGCGCGGGGCGCTTGCGAAGATGAAGTTTGGCTGCCTCTCCT
TCCGGCAGCCTTATGCTGGCTTTGTCTTAAATGGAATCAAGACTGTGGAGACGCGCTGGCGTCTCTGCTGAGC
AGCCAGCGGAAGTGTACCATCGCCGTCCACATTGCTCACAGGGACTGGGAAGCGGATGCCTGTCTGGGAGCTGCT
GGTGGAGAGACTCGGGATGACTCCTGCTCAGATTCAAGGCTTGTCTCAGGAAAGGGGAAAAGTTTGGTCGAGGAG
TGATAGCGGACTCGTTGACATTGGGGAACTTTGCAATGCCCGAAGACTTAACTCCCGATGAGGTTGTGGAA
CTAGAAAATCAAGCTGCACTGACCAACCTGAAGCAGAAGTACCTGACTGTGATTTCAAACCCAGGTGGTTACT
GGAGCCCATACCTAGGAAAGGAGGCAAGGATGTATTCCAGGTAGACATCCAGAGCACCTGATCCCTTTGGGGC
ATGAAGTGTGACAAGTGTGGGCTCCTGAAAGGAATGTTCCRGAGAAACCAGCTAAATCATGGCACCTTCAATTT
GCCATCGTGACGCAGACCTGTATAAATTAGGTTAAAGATGAATTTCCACTGCTTTGGAGAGTCCACCCACTAA
GCACTGTGCATGTAAACAGGTTCTTTGCTCAGATGAAGGAAGTAGGGGGTGGGCTTTCTTGTGTGATGCCT
CCTTAGGCACACAGGCAATGTCTCAAGTACTTTGACCTTAGGGTAGAAGGCAAAGCTGCCAGTAAATGTCTCAG
CATTGCTGCTAATTTTGGTCTGCTAGTTTCTGGATTGTACAAATAAATGTGTTGTAGATGA

Fig. 15U

56/101

16443.1.edit

TCGAGCGGCCGCCGGGCAGGTGTCGGAGTCCAGCACGGGAGGCGTGGTCTTGTAGTTGTTCTCCGGCTGCCCA
TTGCTCTCCCACTCCACGGCGATGTCGCTGGGATAGAAGCCTTTGACCAGGCAGGTCAAGCTGACCTGGTTCTT
GGTCATCTCCTCCCGGATGGGGCAGGGTGTACACCTGTGGTTCTCGGGGCTGCCCTTTGGCTTTGGAGATGG
TTTTCTCGATGGGGCTGGGAGGGCTTTGTTGGAGACCTTGCACTTGTACTCCTTGCCATTCAACCAGTCCTGG
TGCANGACGGTGAGGACGCTNACCACACGGTACGNGCTGGTGTACTGCTCCTCCCGCGGCTTTGTCTTGGCATT
ATGCACCTCCACGCCGTCCACGTACCAATTGAACTTGACCTCAGGGTCTTCGTGGCTCACGTCCACCACCACGC
ATGTAACCTCAAANCTCGGNCGGANACGC

16443.2.edit

AGCGTGGTCGCGGCCGAGGTCTGAGGTTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT
TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG
TACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTC
CAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
ACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTGACCTGACCTGCCTGGTCAAAGGCTTCTAT
CCCAGCGACATCGCCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCTCCCGTGC
TGGACTCCGACACCTGCCGGGCGGCCGCTCGA

16444.2.edit

AGCGTGGTTNCGGCCGAGGTCCCAACCAAGGCTGCANCCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACT
GGTGAGACCTGCGTGTACCCCACTCAGCCAGTGTGGCCAGAAGAACTGGTACATCAGCAAGAACCCCAAGGA
CAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGACC
CTGCCGATGTGGACCTGCCGGGCGGNCGCTCGA

16445.1.edit

AGCGTGGTCGCGGCCGAGGTCAAGAACCCCGCCGACCTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAA
GAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGA
CTGGTGAGACCTGCGTGTACCCCACTCAGCCAGTGTGGCCAGAAGAACTGGTACATCAGCAAGAACCCCAAG
GACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGA
CCCTGCCGATGTGGACCTGCCGGGCGGCCGCTCGA

Fig. 15V

57/101

16445.2.edit

TCGAGCGGTGCCCCGGGCAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATC
GGNCATGCTCTCGCCGAACCAGACATGCCTCTTGNCCTTGGGGTTCTTGCTGATGTACCAGNTCTTCTGGGCCA
CACTGGGCTGAGTGGGGTACACGCAGGTCTCACCANTCTCCATGTTGCANAAGACTTTGATGGCATCCAGGTTG
CAGCCTTGGTTGGGGTCAATCCAGTACTCTCCACTCTTCAGACAGAGTGGCACATCTTGAGGTCACGGCAGGT
GCGGGCGGGGTTCTTGACCTCGGTGCGGACCACGCT

16446.1.edit

TCGAGCGGCCGCCCCGGGCAGGTCTCCTCAGAGCGGTAGCTGTTCTTATTGCCCCGGCAGCCTCCATAGATNAA
GTTATTGCANGAGTTCCTCTCCACGTCAAAGTACCAGCGTGGGAAGGATGCACGGCAAGGCCAGTGACTGCGT
TGGCGGTGCAGTATTCTTCATAGTTGAACATATCGCTGGAGTGGACTTCAGAATCCTGCCTTCTGGGAGCACTT
GGGACAGAGGAATCCGCTGCATTCTGCTGGTGGACCTCGGCCGCGACCACGCT

16446.2.edit

AGCGTGGTCGCGGCCGAGGTCCACCAGCAGGAATGCAGCGGATTCTCTGTCCCAAGTGCTCCAGAAGGCAGG
ATTCTGAAGACCACTCCAGCGATATGTTCAACTATGAAGAATACTGCACCGCCAACGCAGTCACTGGGCCTTGC
CGTGCATCCTTCCCACGCTGGTACTTTGACGTGGAGAGGAACCTCCTGCAATAACTTCATCTATGGAGGCTGCCG
GGGCAATAAGAACAGCTACCGCTCTGAGGAGGACCTGCCCGGGCGGCCGCTCGA

16447.1.edit

TCGAGCGGCCGCCCCGGGCAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATC
GGTCATGCTCTCGCCGAACCAGACATGCCTCTTGTCCTTGGGGTTCTTGCTGATGTACCAGTTCTTCTGGGCCA
CACTGGGCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGGTTG
CAGCCTTGGTTGGGGTCAATCCAGTACTCTCCACTCTTCAGCCAGAATGGCACATCTTGAGGTCACGGCANGT
GCGGGCGGGGTTCTTGACCTCGGCCGCGACCACGCT

Fig. 15W

58/101

16447.2.edit

AGCGTGGTCGCGGCCGAGGTCAAGAAACCCGCGCCGACCTGCCGTGACCTCAAGATGTGCCACTCTGGCTGGA
AGAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAG
ACTGGTGAGACCTGCGTGTACCCCACTAGCCCAAGTGTGGCCGAGAAGAACTGGTACATCAGCAAGAACCCCAA
GGACAAGAGGCATGTCTGGCTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCG
ACCCTGCCGATGTGGACCTGCCCGGGCGGCCGCTCGA

16449.1.edit

AGCGTGGTCGCGGCCGAGGTCCTGTGACAGTGGCACTGGTAGAAGNTCCAGGAACCCCTGAACTGTAAGGGTTCT
TCATCAGTGCCAACAGGATGACATGAAATGATGTAAGTGTCTGNAATGGGGCCCATGANATGGTTGN
CTGAGAGAGAGCTTCTTGCTTACATTGCGCGGGTATGGTCTTGGCCTATGCCTTATGGGGGTGGCCGTTGNGG
GCGGTGNGGTCCGCCTAAAACCATGTTCTCAAAGATCATTTGTTGCCAACACTGGGTTGCTGACCANAAGTG
CCAGGAAGCTGAATACCATTTCCAGTGTACATCCAGGGTGGGTGACGAAAGGGGTCTTTTGAAGTGTGGAAGG
AACATCCAAGATCTCTGNTCCATGAAGATTGGGGTGTGGAAGGGTTACAGTTGGGGAAGCTCGCTGTCTTTT
CCTTCCAATCANGGGCTCGCTCTTCTGAATATTCTTCAGGGCAATGACATAAATTGTATATTCGGTTCCCGGT
CCAGGCCAG

16450.1.edit

TCGAGCGGCCGCGCGGGCAGGTCCACCACACCCAATTCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGAT
TACCGGTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCCCGCCCTGGTG
TCACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATTTATGTCATTGCCCTGAAGAATAAT
CAGAAGAGCGAGCCCTGATTGGAAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCTTCCACACCCCAA
TCTTCATGGACCAGAGATCTTGGATGTTCTTCCACAGTTCAAAGACCCCTTTGTCACCCACCCTGGGTATG
ACACTGGAATGGTATTGAGCTTCTGGCACTTCTGGTCAGCAACCCAGTGTGGGCAACAAATGATCTTTGAN
GAACATGGNTTTAGGCGGACCACACCGGCCACAACGGGCACCCCCATAAGGCATAGGCCAAGAACATAACCGNC
GAATGTAGGACAAGAAGCTCTNTCTCANACAANCATCTCATGGGCCCCATTCCANGACACTTCTGAGTACATCA
NTTCATGGCATCCTGGTGGCACTGATAAAAACCTTACAGTTA

16450.2.edit

AGCGTGGTCGCGGGCGAGGTCTGTGACAGTGGCACTGGTAGAAGTTCCAGGAACCCCTGAACTGTAAGGGTTCT
TCATCAGTGCCAACAGGATGACATGAAATGATGTAAGTGTCTGGAATGGGGCCCATGAGATGGTTGT
CTGAGAGAGAGCTTCTTGCTTACATTGCGCGGGTATGGTCTTGGCCTATGCCTTATGGGGGTGGCCGTTGTGG
GCGGTGTGGTCCGCCTAAAACCATGTTCTCAAAGATCATTTGTTGCCAACACTGGGTTGCTGACCAGAAGTG
CCAGGAAGCTGAATACCATTTCCAGTGTACATCCAGGGTGGGTGACGAAAGGGGTCTTTTGAAGTGTGGAAGG
AACATCCAAGATCTCTGGTCCATGAAGATTGGGGTGTGGAAGGGTTACAGTTGGGGAAGCTCGTCTGTCTTTT
TCCTTCCAATCANGGGCTCGCTCTTCTGATTATTCTTCAGGGCAATGACATAAATTGTATATTCGGNTCCCGG
TNCAGCCAATAATAAACCCTCTGTGACACCANGGCGGGCCGAAGGANCAT

Fig. 15X

59/101

16451.1.edit

AGCGTGGTCGCGGCCGAGGTCCTCACCAGAGGTACCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGCA
GAGGCATAAGGTTGCGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACGGATG
ACTCGTGCTTTGACCCCTACACAGTTTCCCATTATGCCGTTGGAGATGAGTGGGAACGAATGTCTGAATCAGGC
TTTAAACTGTTGTGCCAGTGCTTANGCTTTGGAAGTGGTCATTTAGATGTGATTCATCTAGATGGTGCCATGA
CAATGGTGTGAACTACAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGACCTGCCCGGGCGGCCGCTC
GA

16451.2.edit

TCGAGCGGCCGCCCGGGCAGGTCCATTTCTCCCTGACGGTCCCACTTCTCTCCAATCTTGTAGTTCACACCAT
TGTCATGGCACCATCTAGATGAATCACATCTGAAATGACCACTTCCAAAGCCTAAGCACTGGCACAACAGTTTA
AAGCCTGATTCAGACATTCGTTCCCACTCATCTCCAACGGCATAATGGGAACTGTGTAGGGGTCAAAGCACGA
GTCATCCGTAGGTTGGTTCAAGCCTTCGNTGACAGAGTTGCCACGGTAACAACCTTCTCCGAACCTTATGCC
TCTGCTGGTCTTTCAGTGCCTCCACTATGATGTTGTAGGTGGTACCTCTGGTGAGGACCTCGGCCGCGACCAG
CT

16452.1.edit

AGCGTGGCCGCGGCCGAGGTCCATTGGCTGGAACGGCATCAACTTGAAGCCAGTGATCGTCTCAGCCTTGGTT
CTCCAGCTAATGGTGATGGNGGTCTCAGTAGCATCTGTACACGAGCCCTTCTTGGTGGGCTGACATTCTCCAG
AGTGGTGACAACACCCTGAGCTGGTCTGCTTGTCAAAGTGTCTTAAGAGCATAGACACTCACTTCATATTTGG
CGNCCACCATAAGTCCTGATACAACCACGGAATGACCTGTCAGGAAC

16452.2.edit

TCGAGCGGCCGCCCGGGCAGGTCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGACGATGAT
ATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCTGCACCAACTGACCTGAAGTTCACTCAGGT
CACACCCACAAGCCTGAGCGCCAGTGGACACCACCAATGTTCAAGTCACTGGATATCGAGTGGGGTGACCC
CCAAGGAGAAGACCGGACCAATGAAAGAAATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTT
ATGGCGGCCACCAATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGTGT
TGTCACCACTCTGGAGAATGTCAGCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGAGACCACCATCACCA
TTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGATGCCGTTCCAGCCAATGGACCTCGGCCG
CGACCACGCTT

Fig. 15Y

60/101

16453.1.edit

AGCGTGGTCGCGGCCGAGGTCTGGCCGAACTGCCAGTGTACAGGGAAGATGTACATGTTATAGNTCTTCTCGAA
GTCCCGGGCCAGCAGCTCCACGGGGTGGTCTCCTGCCTCCAGGCGCTTCTCATTCTCATGGATCTTCTTCACCC
GCAGCTTCTGCTTCTCAGTCAGAAGGTGTGTCTCATCCCTCTCATACAGGGTGACCAGGACGTTCTTGAGC
CAGTCCCGCATGCGCAGGGGGAATTCGGTCAGCTCAGAGTCCAGGCAAGGGGGGATGTATTTGCAAGGCCGAT
GTAGTCCAAGTGGAGCTTGTGGCCCTTCTTGGTGCCTCCAAGGTGCACTTTGTGGCAAAGAAGTGGCAGGAAG
AGTCGAAGGTCTTGTGTGCTGCTGCACACCTTCTCAAACCTGCCAATGGGGGCTGGGCAGACCTGCCCGGGC
GGCCGCTCGA

16453.2.edit

TCGAGCGGCCCGCCGGGCAGGTCTGCCCAGCCCCATTGGCGAGTTTGAGAAGGNGTGCAGCAATGACAACAAG
ACCTTCGACTCTTCTGCCACTTCTTTGCCACAAAGTGACCCCTGGAGGGCACCAAGAAGGGCCACAAGCTCCA
CCTGGACTACATCGGGCCTTGCAAATACATCCCCCTTGCTGGACTCTGAGCTGACCGAATTCCCCCTGCGCA
TGCGGGACTGGCTCAAGAACGTCCTGGTCACCCTGTATGAGAGGGATGAGGACAACAACCTTCTGACTGAGAAG
CANAAGCTGCGGGTGAAGAANATCCATGAGAATGANAAGCGCTGNAGGCANGAGACCACCCCGTGGAGCTGCT
GGCCCGGGACTTCGAGAAGAACTATAACATGTACATCTTCCCTGTACACTGGCAGTTGCGCCAGACCTCGGCCG
CGACCAGCT

16454.1.edit

AGCGTGGNTGCGGACGACGCCACAAAGCCATTGTATGTAGTTTTANTTCAGCTGCAAANAATACCNCCAGCAT
CCACCTTACTAACCAGCATATGCAGACA

16454.2.edit

TCGAGCGGTGCCCCGGGCAGGTCTGGGCGGATAGCACCGGGCATATTTTGGAATGGATGAGGTCTGGCACCCCTG
AGCAGCCCAGCGAGGACTTGGTCTTAGTTGAGCAATTTGGCTAGGAGGATAGTATGCAGCACGGTTCTGAGTCT
GTGGGATAGTGCCATGAAGNAACCTGAAGGAGGCGCTGGCTGGTANGGGTTGATTACAGGGCTGGGAACAGCT
CGTACACTTGCCATTCTCTGCATATACTGGNTAGTGAGGCGAGCCTGGCGCTCTTCTTTCGCTGAGCTAAAGC
TACATAAATGGCTTTGNGGACCTCGGCCGCGACACGCTT

Fig. 15Z

61/101

16455.1.edit

TCGAGCGGCCGCCGGGCAGGTCCATTTCTCCCTGACGGTCCCACTTCTCTCCAATCTTGTAGTTCACACCAT
TGTCATGACACCATCTAGATGAATCACATCTGAAATGACCACTTCAAAGCCTAAGCACTGGCACAACAGTTTA
AAGCCTGATTCAGACATTGTTCCCACTCATCTCCAACGGCATAATGGGAACTGTGTAGGGTCAAAGCACGA
GTCATCCGTAGGTTGGTTCAAGCCTTCGTTGACAGAAGTTGCCACGGTAACAACCTTTCCGAACCTTATGC
CTCTGCTGGTCTTTCAAGTGCTCCACTATGATGTTGTAGGTGGCACCTCTGGTGAGGACCTCGGCCGCGACCA
CGCT

16455.2.edit

AGCGTGGTTTGGGCCGAGGTCTCACCANAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGC
AGAGGCATAAGGTTGCGGAAGAGGTTGTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACGGAT
GACTCGTGCTTTGACCCCTACACAGNTTCCCATTATGCCGTTGGAGATGAGTGGGAACGAATGTCTGAATCAGG
CTTTAACTGTTGTGCCAGTGCTTANGCTTTGGAAGTGGTCATTTGAGATGTGATTCATCTANATGGTGTGATG
ACAATGGTGNGAACTACAAGATTGGAGAGAAGTGGNACCGTCAGGGGANAAAATGGACCTGCCCGGGCGGCNCG
CTCGA

16456.1.edit

AGCGTGGTCGCGGCCGAGGTCTGGCTTCTGCTCANGTGATTATCCTGAACCATCCAGGCCAAATAAGCGCCGG
CTATGCCCTGNATTGGATTGCCACACGGCTCACATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATTGATC

16456.2.edit

TCGAGCGGCCGCCGGGCAGGTCCAATTGAAACAAACAGTTCTGAGACCGTTCTCCCACTGATTAAGAGTG
GGNGGCGGGTATTAGGGATAATATTCATTTAGCCTTCTGAGCTTTCTGGGCAGACTTGGTGACCTTGCCAGCT
CCAGCAGCCTTCTGGTCCACTGCTTTGATGACACCCACCGCAACTGTCTGTCTCATATCACGAACAGCAAAGCG
ACCCAAAGGTGGATAGTCTGAGAAGCTCTCAACACACATGGGCTTGCCAGGAACCATATCAACAATGGGCAGCA
TCACCAGACTTCAAGAATTTAAGGGCCATCTTCAGCTTTTACCAGAACGGCGATCAATCTTTCTTCAGCT
CAGCAAACCTGCATGCAATGTGAGCCG

Fig. 15AA

62/101

16459.1.edit

TCGAGCGGCCGCCGGGCAGGTCCAGAGGGCTGTGCTGAAGTTTGCTGCTGCCACTGGAGCCACTCCAATTGCT
GGCCGCTTCACTCCTGGAACCTTCACTAACCAGATCCAGGCAGCCTTCCGGGAGCCACGGCTTCTTGTTGNTAC
TGACCCAGGGCTGACCACCAGCCTCTCACGGAGGCATCTTATGTTAACCTACCTACCATTGCGCTGTGTAACA
CAGATTCTCCTCTGCGCTATGTGGACATTGCCATCCATGCAACAACAAGGGAGCTCACTCAGNNGGGTTTGAT
GTGGTGGATGCTGGCTCGGGAAGTTCTGCGCATGCGTGGCACCATTTCCTGTGAACACCCATGGGANGNCATGC
CTGATCTGGACTTCTACAGAGATCCTGAAGAGATTGAAAAAGAAGAACAGGCTGNTTGCTGANAAGCAAGTGA
CCAAGGANGAAATTCANGGGTGAAANGGACTGCTCCCGCTCCTGAATCACTGCTACTCAACCTGANGNTGCA
GACTGGTCTTGAAGNGNACANGGGCCCTCTGGGCCTATTTAAGCANCTTCGGTCGCGAACACGNT

16459.2.edit

AGCGTGNGTCGCGGCCGAGGTGCTGAATAGGCACAGAGGGCACCTGTACACCTTCAGACCAGTCTGCAACCTCA
GGCTGAGTAGCAGTGAACCTCAGGAGCGGGAGCAGTCCATTACCCCTGAAATTCCTCCTTGNCACCTGCCTTCTC
AGCAGCAGCCTGCTCTTCTTTTTCAATCTCTTCAGGATCTCTGTAGAAGTACAGATCAGGCATGACCTCCCATG
GGTGTTACGGGAAATGGTGCCACGCATGCGCAGAACTTCCCGAGCCAGCATCCACCACATCAAACCCACTGAG
TGAGCTCCCTTGTTGTTGCATGGGATGGGCAATGTCCACATAGCGCAGAGGAGAATCTGTGTTACACAGCGCAA
TGGTAGGTAGGTTAACATAAGATGCCTCCGCGAGAAGCTGGTGGTCAGCCCTGGGGTCAAGTAACCACAAGAAG
CCGTGGCTCCCGGAAGGCTGCCTGGATCTGGTTAGTGAAGGNTCCAGGAGTGAAGCGGCCAACAAATTGGAGTGG
CTTCAGTGGCAAGCAGCAAACTTCAGCACAAAGCCCTCTGGACCTGCCCGGCGGCCGCTCGA

16460.1.edit

TCGAGCGGCCGCCGGGCAGGTCCATTTTCTCCCTGACGGNCCCCTTCTCTCCAATCTTGTAGTTCACACCAT
TGTCATGGCACCATCTAGATGAATCACATCTGAAATGACCACTTCCAAAGCCTAAGCACTGGCACAACAGTTTA
AAGCCTGATTGAGACATTCGTTCCCACTCATCTCCAACGGCATAATGGGAACTGTGTAGGGGTCAAAGCACGA
GTCATCCGTAGGTTGGTTCAAGCCTTCGTTGACAGAGTTGCCACGGTAACAACCTCNTCCCGAACCTTATGC
CTCTGCTGGGCTTTCAGNGCCTCCACTATGATGNTGTAGGGGGGCACCTCTGGNGANGACCTCGGCCGCGACCA
CGCT

16460.2.edit

AGCGTGGTCGCGGCCGAGGTCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGCA
GAGGCATAAGGCTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACGGATG
ACTCGTGCTTTGACCCCTACACAGTTTCCATTATGCCGTTGGAGATGAGTGGGAACGAATGTCTGAATCAGGC
TTTAACTGTTGTGCCAGTGCTTANGCTTTGGAAGTGGGTCAATTCAGATGTGATTCATCTAGATGGTGCCATG
ACAATGGNGNGAACTACAAGATTGGAGAGAAGTGGNACCGNCAGGGAGAAAATGGACCTGCCCGGGCGGCCGCT
CGA

Fig. 15BB

63/101

16461.1.edit

AGCGTGGTCGCGGCCGAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATCGG
TCATGCTCTGCGCGAACCAGACATGCCTCTTGTCCTTGGGGTTCTTGCTGATGTACCAAGTCTTCTGGGCCACA
CTGGGCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGGNTGCA
ACCTTGGTTGGGGTCAATCCAGTACTCTCCACTCTTCCAGCCAGAGTGGCACATCTTGAGGTACCGGCAGGTGC
GGNCGGGGNTTTTGCGGCTGCCCTCTGGNCTTCGGNTGTNCTCNATCTGCTGGCTCA

16461.2.edit

TCGAGCGGCCGCCCGGGCAGGTCTCGCGGTGCACTGGTGATGCTGGTCCTGTTGGTCCCCCGGCCCTCCTGG
ACCTCCTGGCCCCCTGGTCCTCCAGCGCTGGTTTCGACTTCAGCTTCCTGCCCCAGCCACCTCAAGAGAAGG
CTCAGGATGGTGGCCGCTACTACCGGGCTGATGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACC
ACCCTCAAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCCAGAGGGCAGNCGCAAGAACCCCGCCGCAC
CTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGAGTACTGGATTGACCCCAACCAAGCTGCAA
CCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCCAGTGTGG
CCCAAAAGAACTGGTACATCAGCAAGAACCCCAAGGACAAGAAGCATGTCTGGTTGCGCGAGAACATGACCGAT
GGATTCCAGTTCGAGTATGGCGGGCAGGGCTCCGACCCTGCCGATGGGGACCTTGCCCGCAACACGCT

16463.1.edit

AGCGTGGNNGCGGCCGAGGTATAAATATCCAGNCCATATCCTCCCTCCACACGCTGANAGATGAAGCTGTNCAA
AGATCTCAGGGTGGANAAAACCAT

16463.2.edit

TCGAGCGGCCGCCCGGGCAGGTCTTCAGACTTGGACTGTGTCACTGCCAGGCTTCCAGGGCTCCAATTGC
AGACGGCCTGTTGTGGGACAGTCTCTGTAATCGCGAAAGCAACCATGGAAGACCTGGGGGAAAACCATGGTT
TTATCCACCCTGAGATCTTTGAACAACCTCATCTCTCAGCGTGCGGAGGGAGGCTCTGGACTGGATATTTCTAC
CTCGGCCGCGACCACGCT

Fig. 15CC

64/101

16464.1.edit

CGAGCGGGCGACCGGGCAGGTNCAGACTCCAATCCANANAACCATCAAGCCAGATGTCAGAAGCTACACCATCA
CAGGTTTACAACCAGGCACTGACTACAAGANCTACCTGCACACCTTGAATGACAATGCTCGGAGCTCCCCTGTG
GTCATCGACGCCTCCACTGCCATTGATGCACCATCCAACCTGCGTTTCCTGGCCACCACACCCAATTCTTGCT
GGTATCATGGCAGCCGCCACGTGCCAGGATTACCGGTACATCATCNAGTATGANAAGCCTGGGCCTCCTCCCAG
AGAAGNGGTCCCTCGGCCCCGCCCTGNTGTCCANAGNCTACTATTACTGNGCCNGCAACCGGCAACCGATATC
NATTTTGNCAATTGGCCTTCAACAATAATTA

16464.2.edit

AGCGTGGTTCGCGGCCGANGTCTGTGAGAGTGGCACTGGTAGAAGTTCAGGAACCTGAACTGTAAGGGTTC
TTCATCAGNGCCAACAGGATGACATGAAATGATGTACTCAGAAAGTGCCTGGAATGGGGCCCATGAGATGGTTG
TCTGAGAGAGAGCTTCTTGNCTGTCTTTTTCTTCCAATCAGGGGCTCGCTCTTCTGATTATTCTTCAGGGCA
ATGACATAAATTGTATATTCGGGTCCCGGNTCCAGGCCAGTAATAGTANCCTCTGTGACACCAGGGCGGNGCCG
AGGGACCACTTCTCTGGGAGGAGACCCAGGCTTCTCATACTTGATGATGTAACCGGTAATCCTGGCACGTGGCG
GCTGCCATGATACCAGCAAGGAATTGGGGTGTGGTGGCCAGGAAACGCAGGTTGGATGGNGCATCAATGGCAGT
GGAGGCCGTCGATGACCACAGGGGGAGCTCCGACATTGTCAATTCAAGGTG

16465.1.edit

AGCGTGGNCGCGGCCGAGGTGCAGCGCGGGCTGTGCCACCTTCTGCTCTCTGCCCAACGATAAGGAGGGTNCCT
GCCCCAGGAGAACATTAACNTNTCCCAGCTCGGCCTCTGCCGG

16465.2.edit

TCGAGCGGCCGCCCGGGCAGGTTTTTTTTGCTGAAAGTGGNTACTTTATTGGNTGGGAAAGGGAGAAGCTGTGG
TCAGCCCAAGAGGGAATACAGAGNCCGAAAAAGGGGAGGGCAGGTGGGCTGGAACCAGACGCAGGGCCAGGCA
GAACTTTCTCTCTCACTGCTCAGCCTGGTGGTGGCTGGAGCTCANAAATTGGGAGTGACACAGGACACCTTC
CCACAGCCATTGCGGCGGCATTTCTCTGGCCAGGACACTGGCTGTCCACCTGGCACTGGTCCGACAGAAGCC
CGAGCTGGGGAAAGTTAATGTTACCTGGGGGCAGGAACCTCCTTATCATTGNGCAGAGAGCAGAAGGTGGCA
CAGCCCGCGCTGCACCTCGGCCGCGACCACGCT

16466.2.edit

TCGAGCGGCCGCCCGGGCAGGTCCACCATAAGTCTGATACAACCACGGATGAGCTGTCAGGAGCAAGGTTGAT
TTCTTTCATTGGTCCGGNCTTCTCCTTGGGGGNCACCCGCACTCGATATCCAGTGAGCTGAACATTGGGTGGCG
TCCACTGGGCGCTCAGGCT

16467.2.edit

TCGAGCGGTTGCCCCGGGCAGGTCCACCACACCCAATTCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGA
TTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGCGGTCCCTCGGCCCCGCCCTGGT
GTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATTTATGTCATTGNCCTGAAGAATAA
TCANNAANAGCGANCCCTGATTGGAAGGA

Fig. 15DD

01 16469.edit

02 16469.edit

03 16470.edit

04 16470.edit

05 16471.edit

Fig. 15EE

66/101

06_16471.edit

AGCGTGGTCGCGGCCGAGGTCTGCTGCTTCAGCGAAGGGTTTCTGGCATAACCAATGATAAGGCTGCCAAAGAC
TGTTCCAATACCAGCACCAGAACCAGCCACTCCTACTGTTGCAGCACCTGCACCAATAAATTTGGCAGCAGTAT
CAATGTCTCTGCTGATTGCACTGGTCTGAAACTCCCTTTGGATTAGCTGAGACACACCATTTCTGGGCCCTGATT
TTCCTAAGATAGAACTCCAACCTCTTTGCCCTCTAGCACATAGCCATCTGCTCGGTACACTGTCCCGGCCCTTGA
AGCGATGCACGCAAGAAGCTTGCCCTGCTGGAAGTCTCCTCCAGGAGACTGCTGATTTTGGCATTCTTTTTCC
TTTCATCATATTTCTTCTGAATTTTTTAGATCGTTTTTGTTTAAAATCTCTTCTTCTCAGGAGTCAGCTTG
GCCCCCGCCGCATCCACACAGTCCGTGTGCGGGGAGGTAACAAGAAATACCGTGCCCTGAGGTTGGACGTGGGG
AATTTCTCCTGGGGCTCAGAGTGGTGTACTCGTAAACAAGGATCATCGATGGTGNCTACAATGCATCTAATAA
CGAGCTGGGTGCGACCCAAAGAACCTGGNGAANAATGGATCGNCTCATCGACAGGACACCGTACCCGACAGGG
GNACGANTCCCACTATGCGCTTGCCCTGGGCGCAANAAAGGAAAACCTGCCCGGGCGGCCNTCGAAAGCCCAA
TTNTGGAAAAAATCCATCACACTGGNGGCCNGTCGAGCATGCATNTANAGGGGCCCATCCCCCTNANN

07_16472.edit

TCGAGCGGCCGCGCGGCCGAGGTCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAG
ACTGGTGAGACCTGCGTGTACCCCACTCAGCCAGTGTGGCCAGAAGAAGTGGTACATCAGCAAGAACCCCAA
GGACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCG
ACCCTGCCGATGTGGACCTCGGCCGCGACCACGCT

08_16472.edit

AGCGTGGTCGCGGCCGAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATCGG
TCATGCTCTCGCCGAACCAGACATGCCTCTTGTCTTGGGGTTCTTGCTGATGTACCAGTTCTTCTGGGCCACA
CTGGGCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGGTTGCA
GCCTTGGTTGGGGACCTGCCCGGGCGGCCGCTCGA

09_16473.edit

TCGAGCGGCCGCGCGGCCGAGGTCCACCACACCAATTCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGAT
TACCGGTACATCATCAAGTATGAGAAGCTGGGTCTCCTCCAGAGAAGTGGTCCCTCGGCCCGCCCTGGTG
TCACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATTTATGTATTGCCCTGAAGAATAAT
CAGAAGAGCGAGCCCTGATTGGAAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCTTCCACACCCCAA
TCTTCATGGACCAGAGATCTTGGATGTTCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGGGTATG
ACACTGGAATGGTATTAGCTTCTTGGCACTTCTGGTCAGCAACCCAGTGTGGGCAACAAATGATCTTTGAG
GAACATGGNTTTAGGCGGACCACACCGCCACAACGGCCACCCCCATAAGGCATAGGCCAAGACCATAACCGCC
GAATGTAGGACAAGAAGCTNTNTNCANACACCATNTNATGGGCCCCATTCCAGGACACTTCTGAGTACATCAT
TTATGNCATCTGTGGCACTTGATGAAAACCTTACAGTTACAGGTTCTGGAACCTTTACCAGGCCNTTACAGG
ACTNGGCCGGACNCCTTAAGCCNATTNCACCTGGGGCGTTCTANGGTCCCACTCGNNCACTGGNGAAAATGGC
TACTGTN

Fig. 15FF

67/101

11_16474.edit

AGCGTGGTCGCGGCCGAGGTCCACTAGAGGTCTGTGTGCCATTGCCAGGCAGAGTCTCTGCGTTACAACTCC
TAGGAGGGCTTGCTGTGCGGAGGGCCTGCTATGGTGTGCTGCGGTTTCATCATGGAGAGTGGGGCCAAAGGCTGC
GAGGTTGTGGTGTCTGNGAACTCCNAGGACANGAGGGCTAAATTCCATGAAGTTTGTGGATGGCCTGATGATC
CACAAATCGGAGACCCTGTTAACTACTACCGTCTNACCNCCTGCTGTNCNCCCCNTTTCTGCTNAANACATNGG
GNTNNTNCTTGNCNTCCTTGGGTNGAANATNNAATNGCCTNCCCNTTCTANCNCTACTNGNTCCANANTTGG
CCTTTAAANAATCCNCCTTGCCCTNNNCACTGTTCANNTNTTTNNTCGTAAACCTATNANTTNNATTANATNN
TNNNNNCTCACCCCCCTCATTNANCCNATANGCTNNNAANTCCTTNANNCTCCNCCCCNTTNCNCTCCT
ACTNANTNCTTCTNNCCATTACNAGCTCTTCTNTTAAANATAATGNNGCCNNGCTCTNCATNTCTACNATNT
GNNNAATNCCCCNCCCCNANGNNTTTTGACCTNNNAACCTCCTTCTCCTTCCCTNCNNAATTTNCNNAN
TTCCNCNTTCCNNCNTTTTCGNTNNTCCCATNCTTCCANNCTTCANTCTANCNCNCTNCAACTTATTTTCT
NTCATCCCTTNTTCTTTACANNCCCCCTNNTCTACTCNCNNTTNCATTANATTTGAAACTNCCACNNCTANTT
NCCTCNCCTACNNTTTTATTTTNCGNTCNCCTCTACNTAATANTTTAATNANTTNTCN

12_16474.edit

TCGAGCGGCCGCGCCGGGCAGGTCTGCCAAGGAGACCCTGTTATGCTGTGGGGACTGGCTGGGGCATGGCAGGCG
GCTCTGGCTTCCCACCCTTCTGTTCTGAGATGGGGTGGTGGGCAGTATCTCATCTTTGGGTTCCACAATGCTC
ACGTGGTCAGGCAGGGGCTTCTTAGGGCCAATCTTACCAGTTGGGTCCCAGGGCAGCATGATCTTACCTTGAT
GCCCAGCACACCCTGTCTGAGCAACACGTGGCGCACAAGCAGTGTCAACGTAGTAAGTTAACAGGGTCTCCGCT
GTGGATCATCAGGCCATCCACAACTTCATGGATTTAGCCCTCTGTCCTCGGAGTTTCCCAGACACCACAACCT
CGCAGCCTTTGGCCCCACTCTCCATGATGAACCGCAGCACACCATAGCAGGCCCTCGGCACAAGCAAGCCCTCC
TAAGAATTTGTAACGCANANACTCTGCTGGCAATGGCACACAAACCTCTAGTGGACCTCGGNCGGGACCACGC

13_16475.edit

TCGAGCGGCCGCGCCGGGCAGGTCTGGTCCAGGATAGCCTGCGAGTCTCCTACTGCTACTCCAGACTTGACATC
ATATGAATCATACTGGGGAGAATAGTTCTGAGGACCAGTAGGGCATGATTCACAGATTCAGGGGGGCCAGGAG
AACCAGGGGACCCTGGTTGTCTGGAATACCAGGGTCACCATTTCTCCAGGAATACCAGGAGGGCCTGGATCT
CCCTTGGGGCCTTGAGGTCTTGACCATTAGGAGGGCGAGTAGGAGCAGTTGGAGGCTGTGGGCAAACTGCACA
ACATTCTCCAAATGGAATTTCTGGGTGGGGCAGTCTAATTCTTGATCCGTACATATTATGTCATCGCAGAGA
ACGGATCCTGAGTCACAGACACATATTTGGCATGGTTCTGGCTTCCAGACATCTCTATCCGNCATAGGACTGAC
CAAGATGGGAACATCCTCTTCAACAAGCTTNTGTTGTGCCAAAAATAATAGTGGGATGAAGCAGACCGAGAA
GTANCCAGCTCCCCTTTTGCACAAAGCNCATCATGTCTAAATATCAGACATGAGACTTCTTTGGGCAAAAAA
GGAGAAAAAGAAAAAGCAGTTCAAAGTANCCNCCATCAAGTTGGTTCCTTGCCNNTCAGCACCCGGGCCCGT
TATAAACACCTNGGGCCGGACCCCCCTT

Fig. 15GG

68/101

14_16475.edit

AGCGTGGTCGCGGCCGAGGTGTTTTATGACGGGCCCGGTGCTGAAGGGCAGGGAACAACCTGATGGTGCTACTT
TGAAGTGTCTTTCTTTCTCCTTTTGCACAAAGAGTCTCATGTCTGATATTTAGACATGATGAGCTTTGTGCA
AAAGGGGAGCTGGCTACTTCTCGCTCTGCTTCATCCCACTATTATTTTGGCACAACAGGAAGCTGTTGAAGGAC
GATGTTCCCATCTTGGTCAGTCCTATGCGGATAGAGATGTCTGGAAGCCAGAACCATGCCAAATATGTGTCTGT
GACTCAGGATCCGTTCTCTGCGATGACATAATATGTGACGATCAAGAATTAGACTGCCCCAACCCAGAAATTCC
ATTTGGAGAATGTTGTGCAGTTTGCCACAGCCTCCAAGTCTCTACTCGCCCTCCTAATGGTCAAGGACCTC
AAGGCCCAAGGGAGATCCAGGCCCTCTGGTATTCTGGGAGAAATGGTGACCCTGGTATTCAGGACAACCA
GGGTCCCCTGGTTCTCCTGGCCCCCTGGAATCNGGNGAATCATGCCCTACTGGTCTCAAATATTCTCCAN
ATGATTCATATGATGTCAAGTCTGGGATAGCNAGTANGGANGGACTCGCAGGCTATTCTGGACCANACCTGCC
GGGGGGCGTTCGAAAGCCGAATCTGCANANNTNCNTTCACACTGGCGGCCGTGAGCTGCTTTAAAGGGCCA
TTCNCCTTTAGNGNGGGGGANTACAATTACTNGCGCGGCTTTANANCGCGNGNCTGGGAAAT

15_16476.edit

AGCGTGGTCGCGGCCGAGGTCCACATCGGCAGGGTGGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATCG
TCATGCTCTCGCGAACCAGACATGCCTCTTGCTCTGGGGTTCTTGCTGATGTACCAGTTCTTCTGGGCCACA
CTGGGCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGGTTGCA
GCCTTGGTTGGGGTCAATCCAGTACTCTCCACTCTTCAGTCAGAGTGGCACATCTTGAGGTACGGCAGGTGC
GGGCGGGTCTTGCGGCTGCCCTCTGGGCTCCGGATGTTCTCGATCTGCTGGCTCAGGCTCTTGAGGGTGGT
TCCACCTCGAGGTACGGTCACGAACCACATTGGCATCATCAGCCCGGTAGTAGCGGCCACCATCGTGAGCCTT
CTCTTGANGTGGCTGGGGCAGGAAGTGAAGTGAACCAGCGCTGGGAGGACCAGGGGGACCAANAGGTCCAG
AAGGGCCCGGGGGGACCAACAGGACCAGCATCACCAGTGCGACCCGCGAGAACCTGCCCGCCGNCCTGCTC
AA

16_16476.edit

TCGAGCGNCCGCGGGCAGGTCTCGCGGTGCACTGGTGATGCTGGTCTGTTGGTCCCCCGGCCCTCCTGC
ACCTCCTGGTCCCCCTGGTCTCCAGCGCTGGTTTCGACTTCAGCTTCTGCCCCAGCCACCTCAAGAGAAGE
CTCACGATGGTGGCCGCTACTACCGGCTGATGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACC
ACCCTCAAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCCAGAGGGCAGCCGCAAGAACCCCGCCGCAC
CTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCA
ACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCAGTGTE
GCCCAGAAGAACTGGTACATCAGCAAGAACCCCAAGGACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGA
TGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCACCCTGCCGATGTGGACCTCCGGCCGCGACACCCTT

Fig. 15HH

69/101

17_16477.edit

TNGAGCGGCCGCCGGGCAGGNTGNNAACGCTGGTCTGCTGGTCTCTGGCAAGGCTGGTGAAGATGGTCAC
CCTGGAACCCGGACGACCTGGTGAGAGAGGAGTTGTTGGACCACAGGGTGCTCGTGGTTTCCCTGGAATCC
TGGACTTCCTGGCTTCAAAGGCATTAGGGGACACAATGGTCTGGATGGATTGAAGGGACAGCCGGTGCTCCTG
GTGTGAAGGGTGAACCTGGTGCCCTGGTGAAAATGGAATCCAGGTCAAACAGGAGCCCGTGGGCTTCTGGT
GAGAGAGGACCGTGTGGTGCCCTGGCCANACCTCGGCCGCGACACGCTAAGCCGAATTTCCAGCACACT
GGNGGCCGTTACTANTGGATCCGAGCTCGGTACCAAGCTTGGCGTAATCATGGTCATAGCTGTTTCTGNGTGA
AATTGTTATCCGCTCACAATTTACACANCATACGAAGCCGGAAGCATAAAGTGTAAGCCTTGGGGTGCTAA
TGAGTGAGCTAACTCNCATTAAATTGCGTTGCGCTCACTGCCGCTTTTCCANNNGGAAACNTGGCNTNGCC
NGCTTGCNTTAANTGAAATCCGCCNACCCCGGGGAAAAGNCGGTTTGCNGTATTGGGGCNCCTTTTCCCTTTC
CTCGGNTTACTTGANTTANTGGGCTTTGGNCGNTTCGGGTTGNGGCGANCNGTTCAACNTCACNCCAAAGNG
GNAANACGGTTTTCCANAATCCGGGGGNTANCCCAANGNAAAACATNNGNCNAANGGGCT

18_16477.edit

AGCGTGGTTNGCGGCCGAGGTCTGGGCCAGGGGCACCAACACGTCCTCTCTCACCAGGAAGCCACGGGCTCCT
GTTTGACCTGGAGTTCATTTTACCAGGGGCACCGAGTTACCCTTCACACCAGGAGACCGGGCTGTCCCTT
CAATCCATNCAGACATTGTGNCCTTAATGCCTTTGAAGCCAGGAAGTCCAGGAGTTCAGGGAAACACCGA
GCACCTGTGGTCCAACAACCTCTCTCACCAGGTCTCGGGTTTTCCAGGTGACCATCTTACCAGCCTT
GCCAGGAGGACGACGAGGACGCGTTACCAACCTGCCGGGCGGCGCTCGA

21_16479.edit

TCGAGCGGCCGCCGGGCAGGTCCATTTTCTCCCTGACGGTCCCACTTCTCTCCAATCTTGTAGTTCACACCAT
TGTCATGGCACCATCTAGATGAATCACATCTGAAATGACCACTTCCAAAGCCTAAGCACTGGCACAACAGTTTA
AAGCCTGATTGAGACATTCGTTCCCACTCATCTCAACGGCATAATGGGAACTGTGTAGGGGTCAAAGCACGA
GTCATCCGTAGGTTGGTTCAAGCCTTCGTTGACAGAGTTGCCACGGTAACAACCTCTTCCGAACCTTATGCC
TCTGCTGGTCTTTCAGTGCTCCACTATGATGTTGTAGGTGGCACCTCTGGTGAGGACCTCGGCCGCGACACG
CT

22_16479.edit

AGCGTGGTTCGCGGCCGAGGTCTCACCAGAGGTGCCACCTACAACATCATAGTGAGGCACTGAAAGACCAGCA
GAGGCATAAGGTTGCGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACGGATG
ACTCGTGCTTTGACCCCTACACAGTTTCCATTATGCCGTTGGAGATGAGTGGGAACGAATGTCTGAATCAGGC
TTTAACTGTTGTGCCAGTGCTTAGGCTTTGGAAGTGGTCATTTCAAGATGTGATTCTAGATGGTGCCATG
ACAATGGTGTGAACATAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGACCTGCCCGGGCCGGCCG
TCGA

Fig. 15II

70/101

24_16480.edit

TCGAGCGNCGCCCGGGCAGGTCCAGTAGTGCCTTCGGGACTGGGTTACCCCCAGGTCTGCGGCAGTTGTCAC
AGCGCCAGCCCCGCTGGCCTCCAAAGCATGTGCAGGAGCAAATGGCACCGAGATATTCCTTCTGCCACTGTTCT
CCTACGTGGTATGTCTTCCCATCATCGTAACAGTTGCCTCATGAGGGTCACACTTGAATTCCTTTTCCGTT
CCCAAGACATGTGCAGCTCATTTGGCTGGCTCTATAGTTTGGGGAAAGTTTGTGAAACTGTGCCACTGACCTT
TACTTCCTCCTTCTCTACTGGAGCTTTCGTACCTTCCACTTCTGCTGTTGGTAAATGGTGGATCTTCTATCAA
TTTCATTGACAGTACCCACTTCTCCCAAACATCCAGGGAAATAGTGATTTAGAGCGATTAGGAGAACCAAATT
ATGGGGCAGAAATAAGGGGCTTTTCCACAGGTTTCTTTGGAGGAAGATTTAGTGCTGACTTTAAAAGAATA
CTCAACAGTGTCTTCATCCCATAGCAAAGAAGAAACNGTAAATGATGGAANGCTTCTGGAGATGCCNNCATT
TAAGGGACNCCCAGAACTTCACCATCTACAGGACCTACTTCAGTTTACANNAAGNCACATANTCTGACTCANAA
AGGACCCAAGTAGCNCATGGNCAGCACTTTCAGCCTTTCCTTGGGGGAAAANNTTACNTTCTTAAANCCTNGG
CCNNGACCCCTTAAGNCCAAATTNTGGAAAANTTCNTNCCNCTGGGGGGCNGTTCNACATGCNTTTAAGGG
CCCAATTNCCCCNT

25_16481.edit

TCGAGCGGCCCGCCCGGGCAGGTGTGCGAGTCCAGCACGGGAGGCGTGGTCTTGTAGTTGTTCTCCGGCTGCCCA
TTGCTCTCCCACTCCACGGCGATGTGCTGGGATAGAAGCCTTTGACCAGGCAGGTGAGGCTGACCTGGTTCTT
GGTCATCTCCTCCCGGATGGGGCAGGGGTGTACACCTGTGGTTCTCGGGGCTGCCCTTTGGCTTTGGAGATGG
TTTTCTCGATGGGGGCTGGGAGGGCTTTGTTGGAGACCTTGCACTTGTAATCCTTGCCATTAGCCAGTCCTGG
TGCAGGACGGTGAGGACGCTGACCACACGGTACGTGCTGTTGTACTGCTCCTCCCGCGGCTTTGTCTTGGCATT
ATGCACCTCCACGCGTCCACGTACCAGTTGAACCTGACCTCAGGGTCTTCGTGGCTCACGTCCACCACCACGC
ATGTAACCTCAGACCTCGGCCGCGACACGCT

26_16481.edit

AGCGTGGTCGCGGCCGAGGTCTGAGGTTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT
TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG
TACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTCAAGGTCTC
CAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCAAAGCCAAAGGGCAAGCCCCGAGAACACAGGTG
TACACCTGCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTA
TCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAATAACAAGACCAGCCTCCCGTGC
TGGACTCCGACACCTGCCCGGGCGGCGCTCGA

27_16482.edit

TCGAGCGGCCCGCCCGGGCAGGTTGAATGGCTCCTCGCTGACCACCCCGGTGCTGGTGGTGGGTACAGAGCTCCG
ATGGGTGAAACCATTGACATAGAGACTGTCCCTGTCCAGGGTGTAGGGGCCAGCTCAGTGATGCCGTGGGTCA
GCTGGCTCAGTTCCAGTACAGCGCTCTCTGTCCAGTCCAGGGCTTTTGGGGTCAGGACGATGGGTGCAGACA
GCATCCACTCTGGTGGCTGCCCCATCCTTCTCAGGCCTGAGCAAGGTGAGTCTGCAACCAGAGTACAGAGAGCT
GACACTGGTGTCTTGAACAAGGGCATAAGCAGACCCTGAAGGACACCTCGGCCGCGACACGCT

Fig. 15JJ

71/101

28_16482.edit

AGCGTGGTCGCGGCCGAGGTGTCCTTCAGGGTCTGCTTATGCCCTTGTTCAAGAACACCAGTGTCAGCTCTCTG
TACTCTGGTTGCAGACTGACCTTGCTCAGGCCTGAGAAGGATGGGGCAGCCACCAGAGTGGATGCTGTCTGCAC
CCATCGTCCTGACCCAAAAGCCCTGGACTGGACAGAGAGCGGCTGTACTGGAAGCTGAGCCAGCTGACCCACG
GCATCACTGAGCTGGGCCCTACACCCTGGACAGGGACAGTCTCTATGTCAATGGTTTCACCCATCGGAGCTCT
GTACCCACCACCAGCACCAGGGGTGGTCAGCGAGGAGCCATTCAACCTGCCCGGGCGGCCGCTCGA

29_16483.edit

AGCGTGGTCGCGGCCGAGGTGCTGTGTCAGAGTGGCACTGGTAGAAGTTCAGGAACCCTGAACTGTAAGGGTTCT
TCATCAGTGCCAACAGGATGACATGAAATGATGTACTCAGAAGTGCTTGGGAATGGGGCCCATGAGATGGTTGT
CTGAGAGAGAGCTTCTTGTCTACATTGCGCGGGTATGGTCTTGGCCTATGCCTTATGGGGGTGGCCGTTGTGG
GCGGTGTGGTCCGCCTAAAACCATGTTCTCAAAGATCATTTGTTGCCAACACTGGGTGCTGACCAGAAGTG
CCAGGAAGCTGAATACCATTTCAGTGTACATCCAGGGTGGGTGACGAAAGGGGTCTTTTGAAGTGTGGAAGG
AACATCCAAGATCTCTGGTCCATGAAGATTGGGGTGTGGAAGGGTTACCAGTTGGGGAAGCTCGTCTGTCTTTT
TCCTTCCAATCAGGGGCTCGCTCTTCTGATTATTCTTCAGGGCAATGACATAAATTGTATATTCGGTCCCGGTT
CCAGGCCAGTAATAGTAGCCTCTGTGACACCAGGGCGGGGCCGAGGGACCCCTTCTNTTGGGAAGAGACCAGCTTC
TCATACTTGATGATGAGNCCGGTAATCCTGGCACGTGGNGGTTGCATGATNCCACCAAGGAAATNGGNGGGGNG
GGACCTGCCCGGGCGGCCGTTTCAAAGCCCAATTCACACACTTGGNGGCCGTAATGGATCCCACTCNGTCCA
ACTTGGNGGAATATGGCATAACTTTT

31_16484.edit

TCGAGCGGCCGCCCGGGCAGGTCTTGACCTTTTCAGCAAGTGGGAAGGTGTAATCCGTCTCCACAGACAAGGC
CAGGACTCGTTTGTACCCGTTGATGATAGAATGGGGTACTGATGCAACAGTTGGGTAGCCAATCTGCAGACAGA
CACTGGCAACATTGCGGACACCCTCCAGGAAGCGAGAATGCAGAGTTTCTCTGTGATATCAAGCACTTCAGGG
TTGTAGATGCTGCCATTGTGGAACACCTGCTGGATGACCAGCCCAAAGGAGAAGGGGGAGATGTTGAGCATGTT
CAGCAGCGTGGCTTCGCTGGCTCCCACTTTGTCTCCAGTCTTGATCAGACCTCGGCCGCGACCACGCT

37_16487.edit

AGCGTGGTCGCGGCCGAGGTCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCT
CCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCAGCAACACCAAGGTGGACAAGAGA
GTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGTC
AGTCTTCTCTTCCCCGCATCCCCCTTCAAACCTGCCCGGGCGGCCGCTCG

Fig. 15KK

72/101

38_16487.edit

CGAGCGGCCGCCCGGGCAGGTTTGAAGGGGGATGCGGGGGAAGAGGAAGACTGACGGTCCCCCAGGAGTTCA
GGTGCTGGGCACGGTGGGCATGTGTGAGTTTTGTCACAAGATTTGGGCTCAACTCTCTTGTCCACCTTGGTGTT
GCTGGGCTTGTGATCTACGTTGCAGGTGTAGGTCTGGGTGCCGAAGTTGCTGGAGGGCAGGTCACCACGCTGC
TGAGGGAGTAGAGTCCTGAGGACTGTAGGACAGACCTCGGCCGCGACCACGCT

39_16488.edit

NGGNNGGTCCGGNCNGNCAGGACCACTCNTCTTCGAAATA

41_16489.edit

AGCGTGGTCGCGGCCGAGGTCCTCACTTGCCCTCTGCAAAGCACCGATAGCTGCGCTCTGGAAGCGCAGATCTG
TTTTAAAGTCCTGAGCAATTTCTCGCACCAGACGCTGGAAGGGAAGTTTGCGAATCAGAAGTTCAGTGGACTTC
TGATAACGTCTAATTTACGGAGCGCCACAGTACCAGGACCTGCCCGGGCGGCGCTCGA

42_16489.edit

TCGAGCGGCCGCCCGGGCAGGTCCTGGTACTGNGGCGCTCCGTGAAATTAGACGTTATCAGAAGTCCACTGAAC
TTCTGATTCGCAAACCTCCCTTCAGCGTCTGGTGCGAGAAATTGCTCAGGACTTTAAACAGATCTGCGCTTC
CAGAGCGCAGCTATCGGTGCTTTGCAGGAGGCAAGTGAGGACCTCGGCCGCGACCACGCT

45_16491.edit

TCGAGCGGCCGCCCGGGCAGGTCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATC
GGTCATGCTCTCGCCGAACCAGACATGCCTCTTGCTTGGGGTTCTTGCTGATGTACCAGTTCTTCTGGGCCA
CACTGGGCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGGTTG
CAGCCTTGGTTGGGGTCAATCCAGTACTCTCACTCTTCCAGTCAGAGTGGCACATCTTGAGGTCACGGCAGGT
GCGGGCGGGGTTCTTGACCTCGGCCGCGACCACGCT

Fig. 15LL

73/101

46_16491.edit

GTGGGNTTGAACCCNTTTNANCTCCGCTTGGTACCGAGCTCGGATCCACTAGTAACGGCCGCCAGTGTGCTGGA
ATTCCGCTTAGCGTGGTCGCGGCCGAGGTCAAGAACCCCGCCGCACCTGCCGTGACCTCAAGATGTGCCACTC
TGACTGGAAGAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCA
ACATGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCAGTGTGGCCAGAAGAACTGGTACATCAGCAAG
AACCCCAAGGACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCA
GGGCTCCGACCCTGCCGATGTGGACCTGCCGGGCGGCCGCTCGA

47_16492.edit

AGCGTGGTCGCGGCCGAGGTCTGGGATGCTCCTGCTGTACAGTGAGATATTACAGGATCACTTACGGAGAAAC
AGGAGGAAATAGCCCTGTCCAGGAGTTCAGTGTGCTGGGAGCAAGTCTACAGCTACCATCAGCGGCTTAAAC
CTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCGCAAGCAGCAAGCCAATT
TCCATTAATTACCGAACAGAAATTGACAAACCATCCAGATGCAAGTGACCGATGTTCAAGACAACAGCATTAG
TGCAAGTGGCTGCCTTCAAGTTCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGAC
CAACAAAACTAAAAGTGCAGGTCCAGATCAACAGAAATGACTATTGAAGGCTTGAGCCACAGTGGAGTAT
GTGGTTAAGTGTCTATGCTCAGAATCCAAGCGGAGAGAAGTCAGCCTCTGGTTCAGACTGNAAGTAACCAACAT
TGATCGCCTAAAGGACTGGCATTCACTGATGNGGATGCCGATTCCATCAAAATTGNTTGGGAAAACCCACAGGG
GCAAGTTTNCANGTCNAGGNGGACCTACTCGAGCCCTGAGGATGGAATCCTTGACTNTTCTTNNCCTGATGGG
GAAAAAAAACCTTNAAACTTGAAGGACCTGCCGGGCGGCCGTNCAAAACCAATTCCACCCCTTGGGGGGG
TTCTATGGGNCCCACTCGGACCAAACTTGGGGTAAN

48_16492.edit

TCGAGCGGCCCGCCGGGCAGGTCTTGCAGCTCTGCAGTGTCTTCTTACCATCAGGTGCAGGAATAGCTCAT
GGATTCCATCCTCAGGGCTCGAGTAGGTACCCCTGTACCTGGAACTTGCCCTGTGGGCTTCCCAAGCAATT
TTGATGGAATCGGCATCCACATCAGTGAATGCCAGTCTTTAGGGCGATCAATGTTGGTTACTGCAGTCTGAAC
CAGAGGCTGACTCTCTCCGCTTGGATTCTGAGCATAGACATAACCACATACTCCACTGTGGGCTGCAAGCCTT
CAATAGTCATTTCTGTTTGATCTGGACCTGCAGTTTTAGTTTTGTTGGTCTGGTCCATTTTGGGAGTGGTG
GTTACTCTGTAACCAAGTAACAGGGGAACCTTGAAGGCAGCCACTTGACACTAATGCTGTTGCTGCTGCTGCGGGGCTTG
CACTTGCACTCTGGGATGGTTTGTCAATTTCTGTTGCGTAATTAATGGAATTTGGCTTGCTGCTTGCGGGGCTTG
TCTCCACGGCCAGTGACAGCATACAGTGATGGTATAATCAACTCCAGGTTTAAGCCGCTGATGGTAGCTGAA
ACTTTGCTCCAGGCACAAGTGAACCTCTGACAGGGCTATTTCTNCTGTTCTCCGTAAGTGATCCTGTAATATC
TCACTGGGACAGCAGGANGCATTCCAAAACCTTGGGCGNGACCCCTAAGCCGAATTNTGCAATATNCATCACA
CTGGCGGGCGCTCGANCATTCAATAAAGGCCAATCNCCTATAGGGAGTNTANTACAATTNG

Fig. 15MM

74/101

49_16493.edit

TCGAGCGGCCGCCCGGGCAGGTCACTTTTGGTTTTTGGTCATGTTGCGTTGGTCAAAGATAAACTAAGTTTG
AGAGATGAATGCAAAGGAAAAAATATTTTCAAAGTCCATGTGAAATTGTCTCCATTTTTTGGCTTTTGAG
GGGGTTCAGTTTGGGTTGCTTGTCTGTTCCGGGTTGGGGGAAAGTTGGTTGGGTGGGAGGGAGCCAGGTTGG
GATGGAGGGAGTTTACAGGAAGCAGACAGGGCCAACGTCG

55_16496.edit

AGCGTGGTCGCGGCCGAGGTCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGCA
GAGGCATAAGGTTGCGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACGGATG
ACTCGTGCTTTGACCCCTACACAGTTTCCATTATGCCGTTGGAGATGAGTGGGAACGAATGTCTGAATCAGGC
TTTAACTGTTGTGCCAGTGCTTAGGCTTTGGAAGTGGTCATTTAGATGTGATTATCTAGATGGTGCCATGA
CAATGGTGTGAACATAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGACCTGCCCGGGCGGCCGCTC
GA

56_16496.edit

TCGAGCGGCCGCCCGGGCAGGTCCATTTTCTCCCTGACGGTCCCACTTCTCTCCAATCTTGTTAGTTACACCAT
TGTCATGGCACCATCTAGATGAATCACATCTGAAATGACCACTTCCAAGCCTAAGCACTGGCACAACAGTTTA
AAGCCTGATTCAGACATTCGTTCCCACTCATCTCCAACGGCATAATGGGAACTGTGTAGGGGTCAAAGCACGA
GTCATCCGTAGGTTGGTTCAAGCCTTCGTTGACAGAGTTGCCACGGTAACAACCTCTTCCGAACCTTATGCC
TCTGCTGGTCTTTCAGTGCCTCCACTATGATGTTGTAGGTGGCACCTCTGGTGAGGACCTCGGCCGCGACCAG
CT

59_16498.edit

TCGAGCGGCCGCCCGGGCAGGTCCACCATAAGTCCTGATACAACCACGGATGAGCTGTCAGGAGCAAGGTTGAT
TTCTTTCATTGGTCCGGTCTTCTCCTTGGGGGTCAACCGCACTCGATATCCAGTGAGCTGAACATTGGGTGGTG
TCCACTGGGCGCTCAGGCTTGTGGGTGTGACCTGAGTGAACCTCAGGTGAGTTGGTGCAGGAATAGTGGTTACT
GCAGTCTGAACCAGAGGCTGACTCTCTCCGCTTGGATTCTGAGCATAGACACTAACCACATACTCCACTGTGGG
CTGCAAGCCTTCAATAGTCATTTCTGTTGATCTGGACCTGCAGTTTTAGTTTTTGTGGTCTGGTCCATTTT
TGGGAGTGGTGGTTACTCTGTAACCAGTAACAGGGGAACCTGAAGGCAGCCACTTGACACTAATGCTGTTGTCC
TGAACATCGGTCACTTGCATCTGGGATGGTTTGNCAATTTCTGTTCCGTAATTAATGGAATTTGGCTTGCTGCT
TGCGGGGCTGTCTCCACGGCCAGTGACAGCATACACAGNGATGGNATNATCAACTCCAAGTTTAAGGCCCTGAT
GGTAACTTTAAACTTGCTCCAGCCAGNGAACTTCCGGACAGGGTATTTCTTCTGGTTTTCCGAAAGNGANCCT
GGAATNNTCTCCTTGGANCAGAAGGANCNTCCAAACTTGGGCCGGAACCCCTT

Fig. 15NN

75/101

60_16473.edit

AGCGTGGTCGCGGCCGAGGTCCTGTCAGAGTGGCACTGGTAGAAGTTCAGGAACCTGAACTGTAAGGGTCT
TCATCAGTGCCAACAGGATGACATGAAATGATGTACTCAGAAGTGTCTGGAATGGGGCCCATGAGATGGTTGT
CTGAGAGAGAGCTTCTTGTCCTACATTGCGCGGGTATGGTCTTGGCCTATGCCCTATGGGGGTGGCCGTTGTGG
GCGGTGTGGTCCGCCTAAAACCATGTTCTCAAAGATCATTTGTTGCCAACACTGGGTTGCTGACCAGAAGTG
CCAGGAAGCTGAATACCATTTCCAGTGTATACCCAGGGTGGGTGACGAAAGGGGTCTTTTGAAGTGTGGAAGG
AACATCCAAGATCTCTGGTCCATGAAGATTGGGGTGTGGAAGGGTTACCAGTTGGGAAGCTCGTCTGTCTTTT
TCCTTCCAATCAGGGGCTCGCTCTTCTGATTATCTTCAGGGCAATGACATAAATTGTATATTCGGTTCGCGGT
TCCAGGCCAGTAATAGTAGCCTCTTGTGACACCAGCGGGGGCCANGGACCACTTCTCTGGGANGAGACCCAGC
TTCTCATACTTGATGATGTAACCCGGTAATCCTGCACGTGGCGGCTGNCATGATACCANCAAGGAATTGGGTGN
GGNGGACCTGCCCGCGGCCCTCNA

60_16498.edit

AGCGTGGTCGCGGCCGAGGTCGGGATGCTCCTGCTGTACAGTGAGATATTACAGGATCACTTACGGAGAAAC
AGGAGGAAATAGCCCTGTCCAGGAGTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCTTAAAC
CTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGAAGCAGCAAGCCAATT
TCCATTAATTACCGAACAGAAATTGACAAACCATCCAGATGCAAGTGACCGATGTTTCAAGACAACAGCATTAG
TGTCAGTGGCTGCCTTCAAGTTCCCTGTTACTGGTTACAGAGTAACCACCACTCCAAAAATGGACCAGGAC
CAACAAAACTAAAAGTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCACAGTGGAGTAT
GTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGACTGCAGTAACCACTATTCC
TGCACCAACTGACCTGAAGTTCACTCAGGTACACCCACAAGCCTGAGCCGCCAGTGGACACCACCCAATGTTCC
ACTCACTGGATATCGAGTGCGGGTGACCCCAAGGAGAAGACCCGGACCCATGAAAGAAATCAACCTTGCTCCT
GACAGCTCATCCGNGGGTGTATCAGGACTTATGGGGACTGCCCGGCGNGCCGNTCGAAANCGAATTNTGAA
TTTCCTTCNCACTGGGNGGCGNTTCGAGCTTNTTANANGGCCCAATTCNCCTNTAGNGGGTCTGN

61_16499.edit

AGCGTGGTCGCGGCCGAGGTCNAGGA

62_16483.edit

TCGAGCGGCCGCCCGGGCAGGTCCACCACACCCAATTCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGAT
TACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCCCGCCCTGGTG
TCACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATTTATGTCATTGCCCTGAAGAATAAT
CAGAAGAGCGAGCCCTGATTGGAAGGAAAAAGACAGACGAGCTTCCCAACTGGTAACCTTCCACACCCCAA
TCTTCATGGACCAGAGATCTTGATGTTCTTCCACAGTTCAAAAGACCCCTTCGTCACCCACCTGGGTATG
AACTGGAATGGTATTAGCTTCTGGCACTTCTGGTCAGCAACCCAGTGTGGGCAACAAATGATCTTTGAG
GAACATGGTTTTAGGCGGACCACACCGCCACAACGGGCACCCCATAGGNATAGGCAAGACCATACCCGC
CGAATGTAGGACAAGAAGCTCTNTCTCAACAACCATCTCATGGGCCCATTCAGGACACTTCTGAGTACATCA
TTTCATGTATCCTGGTGGGCACTTGATGAANAACCTTACAGTTCAGGGTCTGGAACCTTACCAGNGCCA
CTTCTGACAGGANCTTGGGCGNGACCACCT

Fig. 1500

76/101

63_16500.edit

AGCGTGGTCGCGGCCGAGGTCCATTTCTCCCTGACGGTCCCACTTCTCTCCAATCTTGTAGTTCACACCATTG
TCATGGCACCATCTAGATGAATCACATCTGAAATGACCACTTCCAAAGCCTAAGCACTGGCACAACAGTTTAAA
GCCTGATTCAGACATTCGTTCCCACTCATCTCCAACGGCATAATGGGAACTGTGTAGGGGTCAAAGCACGAGT
CATCCGTAGGTTGGTTCAAGCCTTCGTTGACAGAGTTGCCACGGTAACAACCTCTTCCCGAACCTTATGCCTC
TGCTGGTCTTTCAGTGCCTCCACTATGATGTTGTAGGTGGCACCTCTGGTGAGGACCTGCCCGGGCGGCCGCT
CGA

64_16493.edit

AGCGTGGTCGCGGCCGAGGTGTGCCCCAGACCAGGAATTCGGCTTCGACGTTGGCCCTGTCTGCTTCCTGTAAA
CTCCCTCCATCCCAACCTGGCTCCCTCCCACCCAACCAACTTCCCCCAACCCGGAAACAGACAAGCAACCCA
AACTGAACCCCTCAAAGCCAAAAAATGGGAGACAATTCACATGGACTTTGGAAAATATTTTTTCTTTG
CATTATCTCTCAAACCTAGTTTTATCTTTGACCAACCGAACATGACCAAAAACCAAAGTGACCTGCCCGGG
CGGCCGCTCGA

64_16500.edit

TCGAGCGGCCGCCCGGGCAGGTCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAG
CAGAGGCATAAGGTTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACGGA
TGACTCGTGCTTTGACCCCTACACAGTTTCCCATATGCCGTTGGAGATGAGTGGGAACGAATGTCTGAATCAG
GCTTTAACTGTTGTGCCAGTGCTTAGGCTTTGGAAGTGGTCATTTAGATGTGATTATCTAGATGGTGCCAT
GACAATGGTGTGAACCTACAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGACCTCGGCCGCGACCACG
CT

Fig. 15PP

77/101

16501.edit

TCGAGCGGCCGCCCCGGGCAGGTACCGGGGTGGTCAGCGAGGAGCCATTCACTGAACCTTACCATCAACAACC
TGCGGTATGAGGAGAACATGCAGCACCTGGCTCCAGGAAGTTCAACACCACGGAGAGGGTCCTTCAGGGCCTG
CTCAGGTCCCTGTTCAAGAGCACCAAGTGTGGCCCTCTGTAAGTCTGGCTGCAGACTGACTTTGCTCAGACCTGA
GAAACATGGGGCAGCCACTGGAGTGGACGCCATCTGCACCCTCCGCCCTTGATCCCACTGGTNCCTGGACTGGACA
NANAGCGGCTATACTTGGGAGCTGANCCNAACCTTTGGCGGNGACNCCNCTT

16501.2.edit

GAGGACTGGCTCAGCTCCCAGTATAGCCGCTCTCTGTCCAGTCCAGGACCAGTGGGATCAAGGCGGAGGGTGCA
GATGGCGTCCACTCCAGTGGCTGCCCATGTTTCTCAAGTCTGAGCAAAGNCAGTCTGCAGCCAGAGTACAGAG
GGCCAACACTGGTGCTCTTGAACAGGGACCTGAGCAGGCCCTGAAGGACCCTCTCCGTGGTGTGAACCTTCCTG
GAGCCAGGGTGCTGCATGTTCTCCTCATACCGCAGGTTGTTGATGGTGAAGTTCAGTGTGAATGGCTCCTCGCT
GACCACCC

16502.1.edit

AGCGTGGTCGCGGCCGAGGTCCACCACACCCAATTCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGATTA
CCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCAGAGAAGTGGTCCCTCGGCCCCGCCCTGGTGTC
ACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATTTATGTCATTGCCCTGAAGAATAATCA
GAAGAGCGAGCCCCGATTGGAAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCCTCCACACCCCAATC
TTCATGGACCANANANCTTGGATNGTCCTTTCACNGGTTNAAAAAACCTTTTCGCCCCCCCACCTTGGGGATT
AACCTTGGGAAANGGGGATTTNACCNTTCC

16502.2.edit

TCGAGCGGCCGCCCCGGGCAGGTCTGTGAGAGTGGCACTGGTAGAAGTTCAGGAACCCTGAACTGTAAGGGTT
CTTCATCAGTGCCAACAGGATGACATGAAATGATGTACTCAGAAGTGTCTGGAATGGGGCCCATGAGATGGTT
GTCTGAGAGAGAGCTTCTTGTCCTACATTGCGCGGGTATGGTCTTGGCCTATGCCCTATGGGGGTGGCGGTTGT
GGGCGGTGTGGTCCGCCTAAACCATGTTCTCAAAGATCATTTGTTGCCCAACACTGGGTTGCTGACCAGAAG
TGCCAGGAAGCTGAATACCATTTCCAGTGTATACCCAGGGNGGGTGACCAAAGGGGGTNTTTNGACCTGGNG
AAAGGAACCATCCAAAANCTCTGNCCCATG

Fig. 15QQ

78/101

16503.1.edit

AGCGTGGNCGCGGCCGAGGTCTGAGGATGTAACTCTTCCCAGGGGAAGGCTGAAGTGCTGACCATGGTGCTAC
TGGGTCCTTCTGAGTCAGATATGTGACTGATGNGAACTGAAGTAGGTACTGTAGATGGTGAAGTCTGGGTGTCC
CTAAATGCTGCATCTCCAGAGCCTTCCATCATTACCGTTTCTTCTTTGCTATGGGATGAGACACTGTTGAGTA
TTCTCTAAAGTCACCACTGAAATCTTCTCCAAAGGAAAACCTGTGGAAGGCCCTTATTCTGCCCCATAAT
TTGGTTCTCCTAATCCTCTGAAATCACTATTTCCCTGGAANGTTTGGGAAAAANNGGGCNACCTGNCANTGGA
AANTGGATANAAAGATCCCACCATTTTACCCAACNAGCAGAAAGTGGGAANGGTACCGAAAAGCTCCAAGTAAN
AAAAAGGAGGGAAGTAAAGGTCAAGTGGGCACCAAGTTTCAAACAAAACCTTCCCCAACTATANAACCCA

16503.2.edit

AAGCGGCCGCCCGGGCAGNNCAGNAGTGCCTTCGGGACTGGGNTCACCCCAGGTCTGCGGCAGTTGTCACAG
CGCCAGCCCCGCTGGCCTCCAAAGCATGTGCAGGAGCAATGGCACCGAGATATTCCTTCTGCCACTGTTCTCC
TACGTGGTATGTCTTCCCATCATCGTAACACGTTGCCTCATGAGGGTCACACTTGAATTCTCCTTTTCCGTTCC
CAAGACATGTGCAGCTCATTGGCTGGCTCTATAGTTTGGGGAAAGTTTGTGAACTGTGCCACTGACCTTTA
CTTCCTCCTTCTCTACTGGAGCTTTCGGTACCTTCCACTTCTGCTGNTGGNAAAAAGGGNGGAACNTCTTATCA
ATTTCAATTGGACAGTANCCCNCTTTCTNCCCAAACATNCAAGGGAAAATATTGATTNCNAGAGCGGATTAAGG
AACAACCCNAATTATGGGGGCCAGAAATAAAGGGGGCTTTTCCACAGGTNTTTTCT

16504.1.edit

TCGAGCGGCCGCCCGGGCAGGTCTGCAGGCTATTGTAAGTGTTCTGAGCACATATGAGATAACCTGGGCCAAGC
TATGATGTTGCATACGTTAGGTGTATTAATGCACTTTTGACTGCCATCTCAGTGGATGACAGCCTTCTCACTG
ACAGCAGAGATCTTCTCACTGTGCCAGTGGGCAGGAGAAAGAGCATGCTGCCACTGGACCTCGGCCGCGACCA
CGCT

16504.2.edit

AGCGTGGTGCAGGCCGAGGTCCAGTCGCAGCATGCTCTTTCTCCTGCCACTGGCACAGTGAGGAAGATCTCTG
CTGTCACTGAGAAGGCTGTCACTGAGATGGCAGTCAAAAGTGCAATTAATACACCTAACGTATCGAACAT
CATAGCTTGGCCAGGTTATCTCATATGTGCTCAGAACCTTACAATAGCCTGCAGACCTGCCCGGGCGGCCGC
TCGA

Fig. 15RR

79/101

16505.1.edit

CGAGCGGCCGCCCCGGGCAGGTCCAGACTCCAATCCAGAGAACCACCAAGCCAGATGTCAGAAGCTACACCATCA
CAGGTTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAATGACAATGCTCGGAGCTCCCTGTG
GTCATCGACGCCTCCACTGCCATTGATGCACCATCCAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCT
GGTATCATGGCAGCCGCCACGTGCCAGGATTACCGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCA
GAGAAGTGGTCCCTCGGCCCGCCCTGGTGNCACAGAAGCTACTATTACTGGCCTGGAACCGGGAACCGAATAT
ACAATTTATGTCATTGCCCTGAAGAATAATCANAGAGCGAGCCCCTGATTGGAAGG

16505.2.edit

AGCGTGGTCGCGGCCGAGGTCTGTGAGAGTGGCACTGGTAGAAGTTCAGGAACCCCTGAAGTGAAGGGTCT
TCATCAGTGCCAACAGGATGACATGAAATGATGTACTCAGAAGTGTCTGGAATGGGGCCCATGAGATGGTTGT
CTGAGAGAGAGCTTCTTGTCCTGTCTTTCTTCCAATCAGGGGCTCGCTCTTCTGATTATTCTTCAGGGCAA
TGACATAAATTGTATATTGCGTTCCCGTTCCAGGCCAGTAATAGTAGCCTCTGTGACACCAGGGCGGGGCCGA
GGGACCACTTCTCTGGGAGGAGACCCAGGCTTCTCATACTTGATGATGTANCCGGTAATCCTGGCACCGTGGCG
GCTGCCATGATACCAGCAAGGAATTGGGTGTGGTGGCAAGAAACGCAGGTTGGATGGTGCATCAATGGCAGTG
GAGGCGTCGATNACCACAGGGGAGCTCCGANCATTGTCATTCAAGGTGGACAGGTAGAATCTTGTAATCAGGTG
CCTGGTTTGTAACCTG

16506.1.edit

TCGAGCGGCCGCCCCGGGCAGGTTTCGTGACCGTGACCTCGAGGTGGACACCACCCTCAAGAGCCTGAGCCAGCA
GATCGAGAACATCCGGAGCCAGAGGGCAGCCGAAGAACCCCGCCGACCTGCCGTGACCTCAAGATGTGCC
ACTCTGACTGGAAGAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTC
TGCAACATGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCCAGTGTGGCCAGAAGAACTGGTACATCAG
CAAGAACCCCAAGGACAAGAAGCATGTCTGGTTCCGGCGAAAGCATGACCGATGGATTCCAGTTCGAGTATGGCG
GCCAGGGCTCCGACCCTGCCATGTGGACCTCGGCCGCGACCAGCTAAGCCCGAATTCAGCACACTGGCGGC
CGTTACTAGTGGGATCCGAGCTTCGGTACCAAGCTTGGCGTAATCATGGGNCATAGCTGTTTCTGNGTGAAAA
TGGTATTCGCTTCACAATTTCCAC

16506.2.edit

AGCGTGGTCGCGGCCGAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATCGG
TCATGCTCTCGCCGAACCAGACATGCCTCTTGCTCTGGGGTTCTTGCTGATGTACCAGTCTTCTGGGCCACA
CTGGGCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGGTTGCA
GCCTTGTTGGGGTCAATCCAGTACTCTCAGTCTTCCAGTCAGAGTGGCACATCTTGAGGTACGGCAGGTGC
GGGCGGGGTTCTTGCGGCTGCCCTCTGGGCTCCGATGTTCTCGATCTGCTGGCTCAAGCTCTGAAGGGTGGT
GTCCACCTCGAGGTACGGTCACGAAACCTGCCCGGGCGGCCGCTCGA

Fig. 15SS

80/101

16507.1.edit

AGCGTGGTCGCGGCCGAGGTCAAGAACCCCGCCCGCACCTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAA
GAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGA
CTGGTGAGACCTGCGTGTACCCCACTCAGCCCAGTGTGGCCAGAAGAACTGGTACATCAGCAAGAACCCCAAG
GACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTECAGTTCGAGTATGGCGGCCAGGGCTCCGA
CCCTGCCGATGTGGACCTGCCCGNGCCGNGCCGCTCGAAAAGCCCNAAATTTCCAGNCACACTTGGCCGGCCGTT
ACTACTG

16507.2.edit

TCGAGCGGCCGCCCCGGGCAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATC
GGTCATGCTCTCGCCGAACCAGACATGCCTCTTGCTTGGGGTCTTGCTGATGTACCAGTTCTTCTGGGCCA
CACTGGGCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGGTTG
CAGCCTTGTTGGGGTCAATCCAGTACTCTCCACTCTTCCAGTCAGAGTGGCACATCTTGAGGTCACGGCAGGT
GCGGGCGGGGTTCTTGACCTCGGCCGCGACACGCT

16508.1.edit

CGAGCGGCCGCCCCGGGCAGGTCCCCCCCCCTTT
TTTTTTTTTTTTTTTTTT

16508.2.edit

AGCGTGGTCGCGGCCGAGGTCTGGCATTCCCTCGACTTCTCTCCAGCCGAGCTTCCAGAACATCACATATCAC
TGCAAAATAGCATTGCATACATGGATCAGGCCAGTGGAATGTAAAGAAGGCCCTGAAGCTGATGGGGTCAAA
TGAAGGTGAATTCAAGGCTGAAGGAAATAGCAAATTCACCTACACAGTTCTGGAGGATGGTTGCACGAAACACA
CTGGGGAATGGAGCAAAACAGTCTTTGAATATCGAACACGCAAGGCTGTGAGACTACCTATTGTAGATATTGCA
CCCTATGACATTGGTGGTCCTGATCAAGAAATTTGGTGTGGACGTTGGCCCTGTTTGCTTTTATAAACCAAACCT
CTATCTGAAATCCCAACAAAAAAATTTAACTCCATATGTGNTCCTCTTGTTCTAATCTTGGCAACCAGTGCAA
GTGACCGACAAAATTCAGTTATTTATTTCCAAAATGTTTGGAAACAGTATAATTTGACAAAGAAAAAAGGATA
CTTCTCTTTTTTGGCTGGTCCACCAAATACAATTCAAAAGGCTTTTGGTTTTATTTTTTANCCAATTCCAA
TTTCAAAATGTCTCAATGGNGCTTATAATAAAATAAACTTTCACCCTNTTTTNTGAT

Fig. 15TT

81/101

16509.1.edit

AGCGTGGTCGCGGCCGAGGTCTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAAC
AGGAGGAAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCCTTAAAC
CTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGAAGCAGCAAGCCAATT
TCCATTAATTACCGAACAGAAATTGACAAACCATCCCAGATGCAAGTGACCGATGTTCAGGACAACAGCATTAG
TGTCAGTGGCTGCCCTCAAGTTCCTGTTACTGGTTACAGAAGTAACCACCACTCCCAAAAATGGACCAGGA
CCAACAAAACTAAACTGCAGGTCCAGATCAAACAGAAAATGGACTATTGAAGGCTTGACGCCACAGTGGAA
GTATGTGGNTAGNGTCTATGCTCAGAATCCCAAGCCGAGAAAGTCAGCCTTCTGGTTTAGACTGCAGTAACC
AACATTGATCGCCCTAAAGGACTGGNCATTCACTTGGATGGTGGATGTCCAATTC

16509.2.edit

TCGAGCGGCCGCCCGGGCAGGTCTTGCAGCTCTGCAGNGTCTTCTTCACCATCAGGTGCAGGGAATAGCTCAT
GGATTCCATCCTCAGGGCTCGAGTAGGTACCCTGTACCTGGAAACTTGCCCTGTGGGCTTTCCCAAGCAATT
TTGATGGAATCGACATCCACATCAGNGAATGCCAGTCTTTAGGGCGATCAATGTTGGTTACTGCAGTCTGAAC
CAGAGGCTGACTCTCTCCGCTTGGATTCTGAGCATAGACACTAACCACATACTCCACTGTGGGCTGCAAGCCTT
CAATAGTCATTTCTGTTTGATCTGGACCTGCAGTTTTAAGTTTTTGGTGGTCTGNCCATTTTTGGGAAGTGG
GGGGTTACTCTGTAACCAGTAACAGGGGAAGTTGAAGGCAGCCACTTGACACTAATGCTGTTGCTCTGAACATC
GGTCACTTGATCTGGGGATGGTTTTGACAATTTCTGGTTCGGCAAATTAATGGAAATTGGCTTGCTGCTTGGC
GGGGCTGNCTCCACGGGCCAGTGACAGCATAC

16510.1.edit

TCGAGCGGCCGCCCGGGCAGGTCTTGCAGCTCTGCAGTGTCTTCTTCACCATCAGGTGCAGGGAATAGCTCAT
GGATTCCATCCTCAGGGCTCGAGTAGGTACCCTGTACCTGGAAACTTGCCCTGTGGGCTTTCCCAAGCAATT
TTGATGGAATCGACATCCACATCAGTGAATGCCAGTCTTTAGGGCGATCAATGTTGGTTACTGCAGTCTGAAC
CAGAGGCTGACTCTCTCCGCTTGGATTCTGAGCATAGACACTAACCACATACTCCACTGTGGGCTGCAAGCCTT
CAATAGTCATTTCTGTTTGATCTGGACCTGCAGTTTTAAGTTTTTGGTGGNCTGNCCATTTTTGGGGAAGGG
GTGGTTACTCTTGTAAACAGTAACAGGGGAAGTTGAAGGCAGCCACTTGACACTAATGCTGGTGGCCTGAACATC
GGTCACTTGATCTGGGATGGTTTTGGTCAATTTCTGTTGCGTAATTAATGGGAAATTGGCTTACTGGCTTGGG
GGGCTGTCTCCACGGNCAGTGACAAGCATACACAGNGATGGGTATAATCAACTCCAGGTTTAAGGCCNCTGAT
GGTA

16510.2.edit

AGCGTGGTCGCGGCCGAGGTCTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAAC
AGGAGGAAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCCTTAAAC
CTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGAAGCAGTAAGCCAATT
TCCATTAATTACCGAACAGAAATTGACAAACCATCCCAGATGCAAGTGACCGATGTTCAGGACAACAGCATTAG
TGTCAGTGGCTGCCCTCAAGTTCCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGGACCAGGA
CCAACAAAACTAAACTGCANGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGACGCCACAGTGGAG
TATGTGGGTTAGTGTCTATGCTCAGAATNCCAAGCGGAGAGATCAGCCTCTGGTTACAGT

Fig. 15UU

82/101

16511.1.edit

TCGAGCGGCCGCCCGGGCAGGTCTCAGCGCTCTCAGGACGTACCACCATGGCCTGGGCTCTGCTCCTCCTACCC
TCCTCACTCAGGGCACAGGGTCTGGGCCAGTCTGCCCTGACTCAGCCTCCCTCCGCGTCCGGGTCTCTGGA
CAGTCAGTCACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGTGCTTATGAATTTGTCTCCTGGTACCAACA
ACACCCAGGCAAGGCCCCCAAACTCATGATTTCTGAGGTACTAAGCGGCCCTCAGGGGTCCCTGATCGTTCT
CTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCGTCTCTGGGCTCCANGCTGAGGATGANGCTGATTATTAC
TGGAAGCTCATATGCAGGCAACAACAATTGGGTGTTCCGGCGAAGGGACCAAGCTGACCGTNCTAAGGTCAAGC
CCAAGGCTTGCCCCCTCGGTCACTCTGTTCCACCCTCCTCTGAAGAAGCTTTCAAGCCAACAANGNCACACT
GGGTGTGTCTCATAAGTGGACTTTCTACCC

16511.2.edit

AGCGTGGTCGCGGCCGAGGTCTGTAGCTTCTGTGGGACTTCCACTGCTCAGGCGTCAGGCTCAGGTAGCTGCTG
GCCGCTACTTGTGTTGCTTTGNTTGGAGGGTGTGGTGGTCTCCACTCCCGCTTGACGGGGCTGCTATCTGC
CTTCCAGGCCACTGTACGGCTCCCGGTAGAAGTCACTTATGAGACACACCAAGTGTGGCTTGTGGCTTGAA
GCTCCTCAGAGGAGGGTGGGAACAGAGTGACCGAGGGGGCAGCCTTGGGCTGACCTAGGACGGTCAGCTTGGTC
CCTCCGCCGAACACCCAATTGTTGTTGCCTGCATATGAGCTGCAGTAATAATCAGCCTCATCCTCAGCCTGGAG
CCCAGAGACNGTCAAGGGAGGCCGTGTTTGCCAAGACTTGAAGCCAGANAAGCGATCAGGGACCCCTGAGGG
CCGCTTTACNGACCTCAAAAAATCATGAATTTGGGGGGCCTTTGCCTGGGNGTTGGTTGGTNACCAGNAAAAACA
AAATTTATAAAGCACCAACGTCACTGCTGGTTTCCAGTGCANGAANATGGTGAAGTGAANTGTCC

16512.1.edit

AGCGTGGTCGCGGCCGAGGTCCAGCATCAGGAGCCCCGCTTGCCGGCTCTGGTCATCGCCTTTCTTTTTGTGG
CCTGAAACGATGTCATCAATTCGCAGTAGCAGAACTGCCGTCTCCACTGCTGTCTTATAAGTCTGCAGCTTAC
AGCCAATGGCTCCCATATGCCAGTTCCTTCATGTCCACCAAAGTACCGTCTCACCATTACACCCAGGTCT
CACAGTTCTCCTGGGTGTGCTTGCCCCGAAGGGAGGTAAGTANACGGATGGTGCTGGTCCACAGTTCTGGATC
AGGGTACGAGGAATGACCTCTAGGGCCTGGGCNACAAGCCCTGTATGGACCTGCCCGGGCGGGCCGCTCGA

16512.2.edit

TCGAGCGGCCGCCCGGGCAGGTCCATACAGGGCTGTTGCCAGGCCCTAGAGGNATTCTTGTAACCTGATCC
AGAAGTGTGGGACCAGCACCATCCGTCTACTTACCTCCCTTCGGGCCAAGCACACCCAGGAGAACTGTGAGACC
TGGGGTGTAAATGGNGAGACGGGTACTTTGGTGACATGAAGGAACTGGGCATATGGGAGCCATTGGCTNGAA
GCTGCANACTTATAAGACAGCAGTGGAGACGGCAGTTCTGCTACTGCGAATTGATGACATCGTTTCAGGCCACA
AAAAGAAAGCGATGACCANAGCCGGCAAGCGGGGCTTCTGATGCTGGACCTCGGCCGCCGACACGCTT

Fig. 15VV

83/101

16514.1.edit

AGCGTGGTCGCGGCCGAGGTCCACTAGAGGTCTGTGTGCCATTGCCAGGCAGAGTCTCTGCGTTACAACTCC
TAGGAGGGCTTGCTGTGCGGAGGGCCTGCTATGGTGTGCTGCGGTTTCATCATGGAGAGTGGGGCCAAAGGCTGC
GAGGTTGTGGTGTCTGGGAACTCCGAGGACAGAGGGCTAAATCCATGAAGTTTGTGGATGGCCTGATGATCCA
CAGCGGAGACCTGTTAATACTACTGTTGACACTGCTGTGCGCCACGTGTTGCTCANACAGGGTGTGCTGGGCA
TCAAGGTGAAGATCATGCTGCCCTGGGACCCANCTGGCAAAAATGGCCCTTAAAAACCCCTTGCCNTGACCAG
TGAACCATTTGTGNGAACCCCAAGATGAANATACTTGCCACCACCCCCCATTC

16514.2.edit

TCGAGCGGCCGCCCCGGGCAGGTCTGCCAAGGAGACCCTGTTATGCTGTGGGACTGGCTGGGGCATGGCAGGCG
GCTCTGGCTTCCACCCCTTCTGTTCTGAGATGGGGTGGTGGGCAGTATCTCATCTTTGGGTTCCACAATGCTC
ACGTGGTCAGGCAGGGGCTTCTTAGGGCCAATCTTACCAGTTGGGTCCAGGGCAGCATGATCTTACCTTGAT
GCCAGCACACCCTGTCTGAGCAACACGTGGCGCACAGAGTGTCAACGTAGTAGTTAACAGGGTCTCCGCTGT
GGATCATCAGGCCATCCACAACTTCATGGATTTAGCCCTCTGTCTCGGAGTTTCCAAAACACCACAACCTC
GCCAGCCTTTGGGCCCCACTTCTTCATGAATGAAACCGCAGCACACCATTANCAAGGCCCTTCGCACAGGNAA
GCCCTTCTAAGGAGTTTTGTAAACGCAAAAACTCTTGCTGGGGCAATGGGCACACAGACCTNTANTNGGA
CCTTGGNCCGCGAACCCCGCTT

16515.1.edit

AGCGTGGTCGCGGCCGAGGTCTGGCCCTCCTGGCAAGGCTGGTGAAGATGGTCACCCTGGAAAACCCGGACGAC
CTGGTGAGAGAGGAGTTGTTGGACCACAGGGTGTCTGTTGGTTCCCTGGAACTCCTGGACTTCTGGCTTCAA
GGCATTAGGGGACACAATGGTCTGGATGGATTGAAGGGACAGCCGGTGCTCCTGGTGTGAAGGGTGAACCTGG
NGCCCTGGTGAAATGGAATCCAGGTCAACAGGAGCCGNGGGCTTCTGGNGAGAGAGGACGTGTTGGTG
CCCCTGGCCANACCTGCCGGGCGCCGCTCNAAGCCGAAATCCAGNACACTGGCGGCCGNTACTANTGGA
ATCCGAACCTTCGGTACCAAAGCTTGCCCGTAATCATGGCCATAGCTTGTTCCCTGGGNGGAAATTGGTATTCC
GCTNCCAATTCACACAACATACCGAACCCGGAAGCATTAAAGTGTAAGCCCTGGGGGGGCTAAATGANG
TGAGCNTAACTCNCATTTAATTGGCGTTGCGCTTCACTGCCCCGCTTTTCCAGTCCGGGNA

16515.2.edit

TCGAGCGGCCGCCCCGGGCAGGTCTGGGCCAGGGGCACCAACACGTCTCTCACCAGGAAGCCACGGGCTCC
TGTTTGACCTGGAGTTCCATTTTACCAGGGGCACCAGGTTTACCCTTCACACCAGGAGCACCGGGCTGTCCCT
TCAATCCATCCAGACCATTGTGNGCCCTAATGCCTTTGAAGCCAGGAAGTCCAGGAGTTCCAGGGAAACCACGA
GCACCCTGTGGTCCAACACTCCTCTCTCACCAGGTGTCGGGTTTTCCAGGGTGACCATCTTACCAGCCTT
GCCAGGAGGGCCAGACCTCGGCCGCGACCACGCT

Fig. 15WW

84/101

16516.1.edit

ANCGTGGTCGCGGCCGAGGTCCTCACCAGAGGTGNCACCTACAACATCATAGTGAGGCACTGAAAGACCANCA
GAGGCATAAGGTTCCGGGAAGAGG

16516.2.edit

TCGAGCGGCCGCCCCGGGCAGGTCCATTTTCTCCCTGACGGTCCCACTTCTCTCCAATCTTGTAGTTCACACCAT
TGTCATGGCACCATCTAGATGAATCACATCTGAAATGACCACTTCAAAGCCTAAGCACTGGCACAACAGTTTA
AAGCCTGATTAGACATTCGTTCCCACTCATCTCAAACGGCATAATGGGAACTGTGTAGGGGTCAAAGCACGA
GTCATCCGTAGGTTGGTTCAAGCCTTCGTTGACAGAGTTGTCCACGGTAACAACCTCTTCCCGAACCTTATGCC
TCTGCTGGTCTTTCAGTGCCTCCACTATGATGTTGTAGGTGGCACCTCTGGTGAGGACCTCNGNCCNGAACAAC
GCTTAAGCCCGNATTCTGCAGAATAATCCCATCACACTTGGCGGCCGCTTCGANCATGCATCNTAAAAGGGGCC
CCAATTTCCCTTATAAGNGAANCCGTATTTNCCAATTTCACTGGNCCCGCGNTTTTACAAACGNCGGTGAA
CTGGGGAAAAACCTGGCGGTTACCCAACCTTAATCGCCNTTGGCAGCACAATCCCCCTTTTCGNCCANCNTG
GGCGTAAATAACCGAAAA

16517.1.edit

ANCGNGGTCGCGGCCGANGTNTTTTTCTTNTTTTTT

16518.1.edit

AGCGTGGTCGCGGCCGAGGTCTGAGGTTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT
TCAACTGGTACGTGGACGGCGTGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG
TACCGGGNGGTGAGCGTCTCACCCTCCTGCACCAGAATTGGTTGAATGGCAAGGAGTACAAGNCAAGGTTTC
CAACAAAGCCNTCCAGCCCCNTCGAAAAAACCATTTCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
ACACCCTGCCCCCATCCCGGGAGGAAAAGANCAANAACNCGTTGAGCCTTAACCTTGCTTGGTCNAANGCTTTT
TATCCCAACGNACTTCCCCNTGGAANTGGGAAAAACCAATGGGCCAANCCGAAAAACAATTACAANAACCC

16518.2.edit

TCGAGCGGCCGCCCCGGGCAGGTGTCGGAGTCCAGCACGGGAGGCGTGGTCTTGTAGTTGTTCTCCGGCTGCCCA
TTGCTCTCCCACTCCACGGCGATGTCGCTGGGATAGAAGCCTTTGACCAGGCAGGTGAGGCTGACCTGGTTCTT
GGTCATCTCCTCCCGGGATGGGGGCAGGGTGAACACCTGGGGTTCTCGGGGCTTGCCCTTTGGTTTTGAANATG
GTTTTCTCGATGGGGGCTGGAAGGGCTTTGTTGNAAACCTTGCACTTGACTCCTTGCCATTACCCAGNCCTGG
NGCAGGACGGNGAGGACNCTNACCACACGGAACCGGGCTGGTGGACTGCTCC

Fig. 15XX

85/101

16519.1.edit

AGCGTGGTCGCGGACGANGTCCTGTCAGAGTGGNACTGGTAGAAGTTCANGAACCCCTGAACTGTAAGGGTTCT
TCATCAGTGCCAACAGGATGACATGAAATGATGTACTCAGAAGNGNCCTGGAATGGGGCCCATGANATGGTTGC
C

16519.2.edit

TCGAGCGGCCGCCGGGCAGGTCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGAT
TACCGGCTACATCATCAAGTATGAGAAGCTGGGTCTCCTCCAGAGAAGTGGTCCCTCGGCCCGCCCTGGTG
TCACAGAGGCTACTATTACTGGCCTGGAACCGGAACCGAATATACAATTTATGTCATTGCCCTGAAGAATAAT
CAGAAGAGCGAGCCCTGATTGGAAGGAAAAGACAGACGAGCTTCCCCAACTGGTAACCCCTCCACACCCCAA
TCTTCATGGACCAGAGATCTTGGATGTTCCCTTCCACAGTTCAAAAGACCCCTTCGGCACCCCCCTGGGTATG
AACCTGGGAAAANGNANTTAANCTTTCCTGGCA

16520.1.edit

AGCGTGGTCGCGGCCGAGGTCTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAAC
AGGAGGAAATAGCCCTGTCCAGGAGTTCAGTGTGCTGGGAGCAAGTCTACAGCTACCATCAGCGGCCTTAAAC
CTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGAAGCAGCAAGCCAATT
TCCATTAATTACCGAACAGAAATTGACAAACCATCCAGATGCAAGTGACCGATGTTTACGACAACAGCATTAG
TGTCAGTGGCTGCCTTCAAGGTNCCCTGGTACTGGGTACAGANTAACCACCACTCCAAAAATGGACCAGGA
ACCACAAAACTTAACTGCAGGGTCCAGATCAAAACAGAAATGACTATTGAANGCTTGCAGCCACAGTGGGA
GTATGNGGGTAGTGNCATGCTTCAAGATCCAAGCGGAAAAANGTCAAGCCTTNTGGGTCAA

16520.2.edit

TCGAGCGGCCGCCGGGCAGGTCTTGAGCTCTGCAGTGTCTTCTTACCATCAGGTGCAGGGAATAGTCAT
GGATTCCATCCTCAGGGCTCGAGTAGGTACCCCTGTACCTGGAACTTGCCCTGTGGGCTTTCCAAGCAATT
TTGATGGAATCGACATCCACATCAGTGAATGCCAGTCCCTTAGGGCGATCAATGTTGGTTACTGCAGNCTGAAC
CAGAGGCTGACTCTCTCGCTTGGATTCTGAGCATAGACACTAACACATACTCCACTGTGGGCTGCAANCCTT
CAATAANNCATTTCTGTTGATCTGGACC

16521.2.edit

TCGAGCGGCCGCCGGGCAGGTCTGGTGGGGTCTGGCACACGCACATGGGGNGTTGNTCTNATCCAGCTGCC
CAGCCCCATTGGCGAGTTTGAAGGTGTGCAGCAATGACAACAANACCTTCGACTCTTCTGCCACTTCTTT
GCCACAAAGTGACCCCTGGAGGGCACCAAGAAGGGCCACAAGCTCCACCTGGACTACATCGGGCCTTGCAAATA
CATCCCCCTTGCCCTGGACTCTGAGCTGACCGAATCCCCCTTGCGCATGCGGGACTGGCTCAAGAACCGTCTCT
GGCACCTTGTATGANAGGGATGAAGACACNACCC

Fig. 15YY

86/101

16522.1.edit

AGCGTGGTCGCGGCCGAGGTCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCT
CCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGAGA
GTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGTC
AGTCTTCCTCTTCCCCCGCATCCCCCTTCCAAACCTGCCCGGGCGGCCGCTCGAAAGCCGAATTCAGCACACT
GGCGGCCGGTACTAGTGGANCCNAACCTTGGNANCCAACTGGNGGAANTAATGGGCATAANCTGTTTCTGGGGG
GAAATTGGTATCCNGTTTACAATTCCNCACAACATACGAGCCGGAAGCATAAAAGNGTAAAAGCCTGGGGGNG
GCCTANTGAAGTGAAGCTAACTCACATTAATTNGCGTTGCCGCTCACTGGCCCGCTTTTCCAGC

16522.2.edit

TCGAGCGGCCGCCCGGGCAGGTTTGGAAGGGGGATGCGGGGGAAGAGGAAGACTGACGGTCCCCCAGGAGTTC
AGGTGCTGGGCACGGTGGGCATGTGTGAGTTTTGTACAAGATTTGGGCTCAACTCTCTTGTCCACCTTGGTGT
TGCTGGGCTTGTGATCTACGTTGCAGGTGTAGGTCTGGGNGCCGAAGTTGCTGGAGGGCACGGTCACCACGCTG
CTGAGGGAGTAGAGTCCTGAGGACTGTANGACAGACCTCGGCCGNGACCACGCTAAGCCGAATTCGAGATAT
CCATCACACTGGCGGCCGCTCCGAGCATGCATTTTAGAGG

16523.1.edit

AGCGTGGNCGCGGACGANGACAACAACCCC

16523.2.edit

TCGAGCGGCCGCCCGGGCAGGNCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATC
GGTCATGCTCTTGCCGAACCAGACATGCCTCTTGTCCTTGGGGTTCTTGCTGATGNACCAGTTCTTCTGGGCCA
CACTGGGCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGGTTG
CAGCCTTGGTTGGGGTCAATCCAGTACTCTCCACTCTCCAGTCAGAGTGGCACATCTTGAGGTCACGGCAGGT
GCGGGCGGGGTTCTTGACCT

16524.1.edit

AGCGTGGTCGCGGCCGAGGTCCAGCCTGGAGATAANGGTGAAGGTGGTGCCCCGGACTTCCAGGTATAGCTGG
ACCTCGTGGTAGCCCTGGTGAGAGAGGTGAACTGGCCCTCCAGGACCTGCTGGTTTCCCTGGTGCTCCTGGAC
AGAATGGTGAACCTGGNGGTAAAGGAGAAAGAGGGGCTCCGGNTGANAAAGGTGAAGGAGGCCCTCCTGNATTG
GCAGGGGCCCCANGACTTAGAGGTGGAGCTGGCCCCCTGGCCCCGAAGGAGGAAAGGGTGTCTGCTGGTCTCC
TGGGCCACCTGG

Fig. 15ZZ

87/101

16524.2.edit

TCGAGCGGCCGCCCGGGCAGGTCTGGGCCAGGAGGACCAATAGGACCAGTAGGACCCCTTGGGCCATCTTTCCC
TGGGACACCATCAGCACCTGGACCGCCTGGTTACCCCTTGTACCCCTTTGGACCAGGACTTCCAAGACCTCCTC
TTTCTCCAGGCATTCTTGCAGACCAGGAGTACCANCAGCACCGGTGGCCAGGAGGACCAGCAGCACCCCTTT
CCTCCTTCGGGACCAGGGGGACCAGCTCCACCTCTAAGTCCTGGGGCCCTGCCAATCCAGGAGGGCCTCCTTC
ACCTTTCTCACCCGGAGCCCCTCTTTCT

16526.1.edit

TCGAGCGGCCGCCCGGGCAGGTCCACCGGGATATTCGGGGGTCTGGCAGGAATGGGAGGCATCCAGAACGAGAA
GGAGACCATGCAAAGCCTGAACGACCGCCTGGCCTCTTACCTGGACAGAGTGAGGAGCCTGGAGACCGACAACC
GGAGGCTGGAGAGCAAAATCCGGGAGCACTTGAGAAGAAGGGACCCAGGTCAGAGACTGGAGCCATTACTTC
AAGATCATCGAGGACCTGAGGGCTCANATCTTCGAAATACTGCNGACAATGCCCC

16526.2.edit

ATGCGNGGTCGCGGCCGANGACCANCTCTGGCTCATACTTGACTCTAAAGNCNTCACCAGNANTTACGGNCATT
GCCAATCTGCAGAACGATGCGGGCATTGTCCGCANTATTTGCGAAGATCTGAGCCCTCAGGNCCTCGATGATCT
TGAAGTAANGGCTCCAGTCTCTGACCTGGGGTCCCTTCTTCTCCAAGTGCTCCCGGATTTGCTCTCCAGCCTC
CGGTTCTCGGTCTCCAAGNCTTCTCACTCTGTCCAGGAAAAGAGGCCAGGCGGNCGATCAGGGCTTTTGCATGG
ACT

16527.1.edit

AGCGTGGTCGCGGCCGAGGTTGTACAAGCTTT
TT

16527.2.edit

TCGAGCGGCCGCCCGGGCAGGTCTGCCAACACCAAGATTGGCCCCCGCCGCATCCACACAGTTNGTGTGCGGGG
AGGTAACAAGAAATACCGTGCCCTGAGGNTGGACGNGGGGAATTTCTCCTGGGGCTCAGAGTGTTGTACTCGTA
AAACAAGGATCATCGATGTTGTCTACAATGCATCTAATAACGAGCTGGTTCGTACCAAGACCCTGGTGAAGAAT
TGCATCGTGCTCATNGACAGCACACCGTACCGACAGTGGGTACCGAAGTCCCACTATGCNCCT

Fig. 15AAA

88/101

16528.1.edit

TCGAGCGGCCGCCCGGGCAGGTCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGAT
TACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCTCCAGAGAAGTGGTCCCTCGGCCCGCCCTGGTG
TCACAGAGGCTACTATTACTGGCCTGGAACCGGAACCGAATATACAATTTATGTCATTGCCCTGAAG

16528.2.edit

AGCGTGNTCNCGGCCGAGGATGGGGAAGCTCGNCTGTCTTTTTCTTCCAATCAGGGGCTNNNTCTTCTGATTA
TTCTTCAGGGCAANGACATAAATTGTATATTCGGNTCCCGGTTCCAGNCCAGTAATAGTAGCCTCTGTGACACC
AGGGCGGGGCCGAGGGACCACTTCTCTGGGAGGAGACCCAGGCTTCTCATACTTGATGATGAAGCCGGTAATCC
TGGCAGGTGGCGGGTGGCATGATACCAACAANGAATTGGGTGTGGTGGACCTGCCCGGGCGGGCCGCTCGAAA
ANCCGAATTCNTGCAAGAATATCCATCACACTTGGGCGGGCCGNTCGAACCATGCATCNTAAAAGGGCCCAAT
TTCCCCCTATTAGGNGAAGCCNCATTTAACAATTCACCTGG

16529.1.edit

TCGAGCGGCCGCCCGGGCAGGTCTCGCGGTGCACTGGTGATGCTGGTCTGTTGGTCCCCCGGCCCTCCTGG
ACCTCCTGGTCCCCCTGGTCTCCAGCGTGGTTTCGACTTCAGTTCTCTGCCAGCCACCTCAAGAGAAGG
CTCAGATGGTGGCCGCTACTACCGGGTGATGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACC
ACCCTCAAGAGCCTTGAGCCAGCAGAATCGAAAACATTCGGAACCCAAGAAGGGCAAGCCCGCAAAGAAACCC
GCCCGCACCTGGCCGNGAACCTCCAAGAANGTGCCACNTCTTGACTGGGAAAAAAGGGAAAANTACTTGGAA
TTGGAC

16529.2.edit

AGCGTGGTGGCGGCCGAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATCGG
TCATGCTCTGCGGAACCAGACATGCCTCTTGCTCTGGGGTTCTTGCTGATGTACCAGTTCTTCTGGGCCACA
CTGGGCTGAGTGGGGTACACGAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGGTTGCA
GCCTTGGTTGGGTCAATCCAGTACTCTCCACTCTTCCAGTCAGAAGTGGCACATCTTGAGGTACGGCAGGGT
GCGGGCGGGTTCTTGCGGGTGCCTTCTGGGCTCCCGAATGTTCTNNGAACTTGCTGG

Fig. 15BBB

89/101

16530.1.edit

AGCGTGGTCGCGGCCGAGGTCCACTAGAGGTCTGTGTGCCATTGCCAGGCAGAGTCTCTGCGTTACAACTCC
TAGGAGGGCTTGCTGTGCGGAGGGCTGCTATGGTGTGCTGCGGTTTCATCATGGAGAGTGGGGCCAAAGGCTGC
GAGGTTGTGGTGTCTGGGAACTCCGAGGACAGAGGGCTAAATCCATGAAGTTTGTGGATGGCCTGATGATCCA
CAGCGGAGACCCTGTAACTACTACGTTGACACTTGCTTGTGCGCCACGTGTTGCTCANACANGGGTGGGCTGG
GCATCAAGGNG

16530.2.edit

TCGAGCGGCCGCCCCGGGCAGGTCTGCCAAGGAGACCCTGTTATGCTGTGGGACTGGCTGGGGCATGGCAGGCG
GCTCTGGCTTCCACCCCTTCTGTTCTGAGATGGGGTGGTGGGCAGTATCTCATCTTTGGGTTCCACAATGCTC
ACGTGGTCAGGCAGGGGCTTCTTAGGGCCAATCTTACCAGTTGGGTCCAGGGCAGCATGATCTTACCTTGAT
GCCCAGCACACCCTGTCTGAGCAACAGTGGCGCACAGCAAGTGTCAACGTAAGTAAGTTAACAGGGTCTCCGG
TGTGGATCATCAGGCCATCCACAACTTCATGGATTAACCCTCTGTCCTCGGAG

16531.1.edit

TCGAGCGGCCGCCCCGGGCAGGTGTTTCAGAGGTTCCAAGGTCCACTGTGGAGGTCCAGGAGTGTGGTGGTGG
GCACAGAGGTCCGATGGGTGAAACCATTGACATAGAGACTGTTCTGTCCAGGGTGTAGGGGCCAGCTCTTTG
ATGCCATTGGCCAGTTGGCTCAGCTCCAGTACAGCCGCTCTCTGTTGAGTCCAGGGCTTTTGGGGTCAAGATG
ATGGATGCAGATGGCATCCACTCCAGTGGCTGCTCCATCCTTCTCGGACCTGAGAGAGGTGAGTCTGCAGCCAG
AGTACAGAGGGCCAACACTGGTGTCTTTGAATA

16531.2.edit

AGCGTGGTCGCGGCCGAGGTCTGTACTGGGAGCTAAGCAAACCTGACCAATGACATTGAAGAGCTGGGCCCCCTAC
ACCCTGGACAGGAACAGTCTCTATGTCAATGGTTTACCCATCAGAGCTCTGTGNCACCACCAGCACTCCTGG
GACCTCCACAGTGGATTTAGAACCTCAGGGACTCCATCCTCCCTCTCCAGCCCCACAATTATGGCTGCTGGCC
CTCTCCTGGTACCATTACCCTCAACTTCACCATCACCAACCTGCAGTATGGGGAGGACATGGGTCAACCCTGNC
TCCAGGAAGTTCAACACCACA

16532.1.edit

TCGAGCGGCCGCCCCGGACAGGTCTGGGCGGATAGCACCGGGCATATTTTGGAAATGGATGAGGTCTGGCACCCTG
AGCAGTCCAGCGAGGACTTGGTCTTAGTTGAGCAATTTGGCTAGGAGGATAGTATGCAGCACGGNTCTGAGNCT
GTGGGATAGCTGCCATGAAGTAACCTGAAGGAGGTGCTGGCTGGTANGGGTTGATTACAGGGTTGGGAACAGCT
CGTACACTTGCCATTCTCTGCATATACTGGTTAGTGAGGTGAGCCTGGCCCTCTCTTTTG

Fig. 15CCC

90/101

01_16558.3.edit

AGCGTGGTCGCGGCCGAGGTGAGCCACAGGTGACCGGGGCTGAAGCTGGGGCTGCTGGNCCTGCTGGTCCTG

02_16558.4.edit

CAGCNGCTCCNACGGGGCCTGNGGGACCAACAACACCGTTTTACCCCTTAGGCCCTTTGGCTCCTCTTTCTCCT
TTAGCACCAGGTTGACCAGCAGCNCCANCAGGACCAGCAAATCCATTGGGGCCAGCAGGACCGACCTCACCACG
TTCACCAGGGCTTCCCCGAGGACCAGCAGGACCAGCAGGACCAGCAGCCCAGCTTCGCCCCGGTCACCTGTGG
CTCACCTCGGCCGCGACCACGCT

03_16535.1.edit

TCGAGCGGTGCCCCGGGCAGGTCCACCGGGATAGCCGGGGTCTGGCAGGAATGGGAGGCATCCAGAACGAGAA
GGAGACCATGCAAAGCCTGAACGACCGCCTGGCCTCTTACCTGGACAGAGTGAGGAGCCTGGAGACCGANAACC
GGAGGCTGGANAGCAAAATCCGGGAGCACTTGGAGAAGAAGGGACCCAGGTCAAGAGACTGGAGCCATTACTT
CAAGATCATCGAGGGACCTGGAGG

04_16535.2.edit

AGCGNGGTGCGGGCCGAGGTCCAGCTCTGTCTCATACTTGA CTCTAAAGTCATCAGCAGCAAGACGGGCATTGT
CAATCTGCAGAACGATGCGGGCATTGTCCGCAGTATTTGCGAAGATCTGAGCCCTCAGGTCTCGATGATCTTG
AAGTAATGGCTCCAGTCTCTGACCTGGGGTCCCTTCTTCTCCAAGTGCTCCCGGATTTTGCTCTCCAGCCTCCG
GTTCTCGGTCTCCAGGCTCCTCACTCTGTCCAGGTAAGAAGGCCAGGCGGTGTTTCAGGCTTTGCATGGTCTC
CTTCTCGTTCTGGATGCCTCCCATTCCTGCCAGACCC

05_16536.1.edit

TCGAGCGGCCGCCCCGGGCAGGTGAGGAAGCACATTGGTCTTAGAGCCACTGCCTCCTGGATTCCA C C TGTGCTG
CGGACATCTCCAGGGAGTGAGAAGGGAAGCAGGTCAA CTGCTCAGATCAGTCAGACTGGCTGTTCTCAGTTC
TCACCTGAGCAAGGTCA GTCTGCAGCCAGAGTACAGAGGGCCAACACTGGTGTCTTGAACAAGGGCTTGAGCA
GACCTGCAGAACCTCTCCGTGGTGTGAACTTCTGGAACCAGGGTGTTGCATGTTTTCTCATAATGC
AAGGTTGGTGATGG

Fig. 15DDD

91/101

07_16537.1.edit

AGCGTGGTCGCGGCCGAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATCGG
TCATGCTCTCGCCGAACCAGACATGCCTCTTGTCCTTGGGGTTCCTTGCTGATGTACCAGTTCTTCTGGGCCACA
CTGGGCTGAGTGGGGTACACCGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGGTTGC
AGCCTTGTTGGGGTCAATCCAGTACTCTCACTCTTCCAGTCAGAAGTGGGCACATCTTGAGGTCACCGGCAG
GTGCCGGGCCGGGGTTCCTGCGGCTTGCCCTCTGGGCTCCGGATGTTCTCGATCTGCTTGGCTCAGGCTCTTG
AGGGTGGGTGTCCACCTCGAGGTCACGGTCACCGAAACCTGCCCGGGCGGCCCGCTCGA

08_16537.2.edit

TCGAGCGGTGCCCCGGGCAGGTTTCGTGACCGTGACCTCGAGGTGGACACCACCCTCAAGAGCCTGAGCCAGCA
GATCGAGAACATCCGGAGCCAGAGGGCAGCCGCAAGAACCCCGCCCGCACCTGCCGTGACCTCAAGATGTGCC
ACTCTGACTGGAAGAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTC
TGCAACATGGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCCAGTGTGGGCCAGAAAGAACTGGTACATC
AGCAAGGAACCCCAAGGACAAGAGGCATTGTCTTGGTTCGGCGAGNAGCATGACCCGATGGATTCCAGTTTCGA
GTATTGGCGGCCAGGGCTTCCCGACCCTTGCCGATGTGGACCTCGGCCGCGACCACCGCT

Fig. 15EEE

92/101

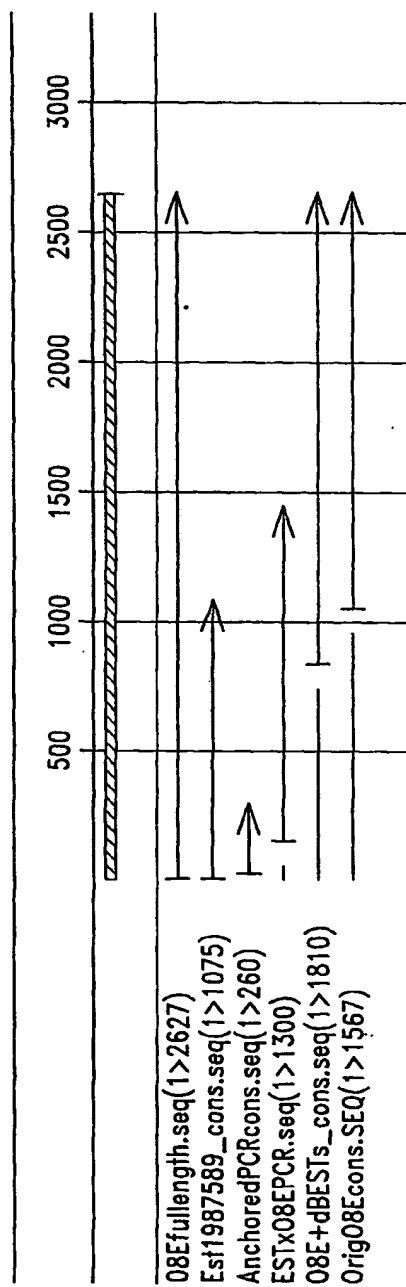


Fig. 16

93/101

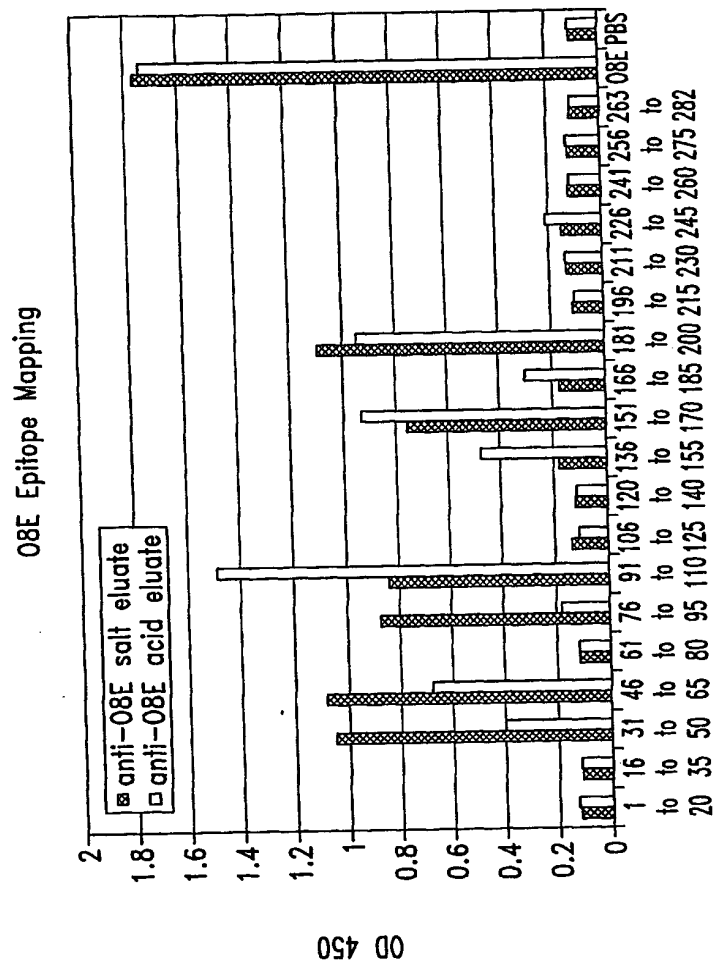
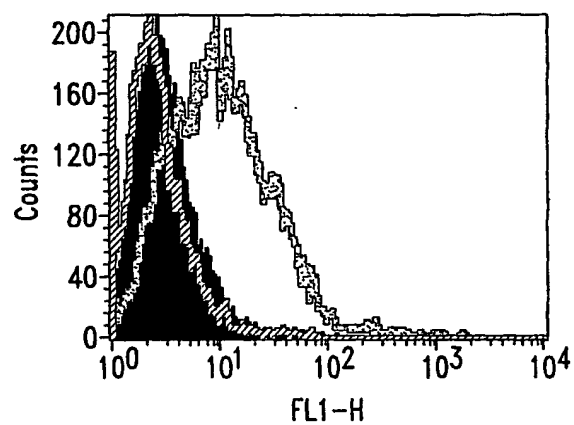


Fig. 17

94/101

O8E Surface Expression



- B305D/HEK stained with anti-O8E antibody
- O8E/HEK stained with anti-O8E antibody
- O8E/HEK stained with an irrelevant antibody

Fig. 18

95/101

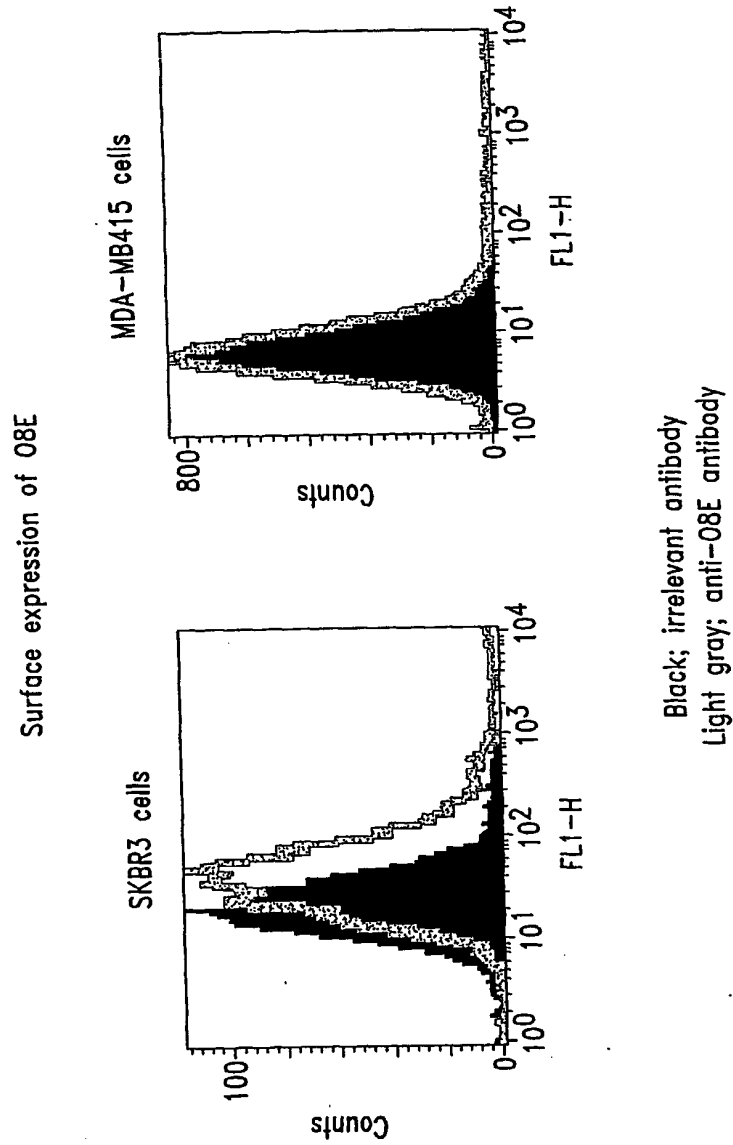
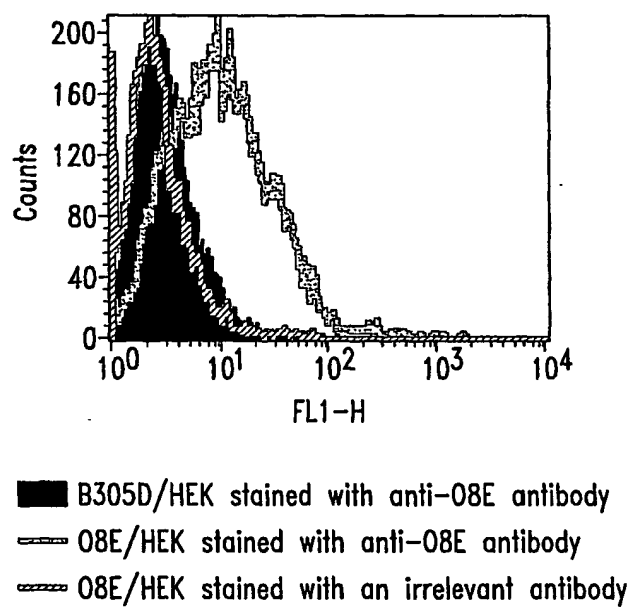


Fig. 19

96/101

O8E Surface Expression

*Fig. 20*

97/101

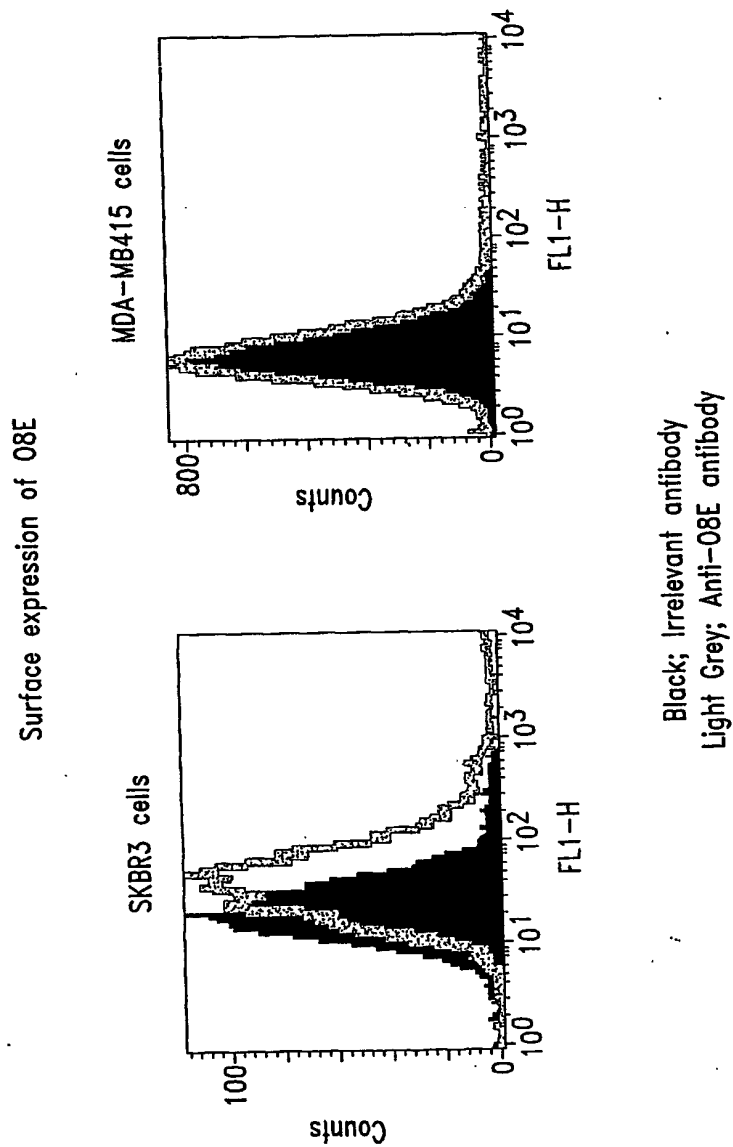
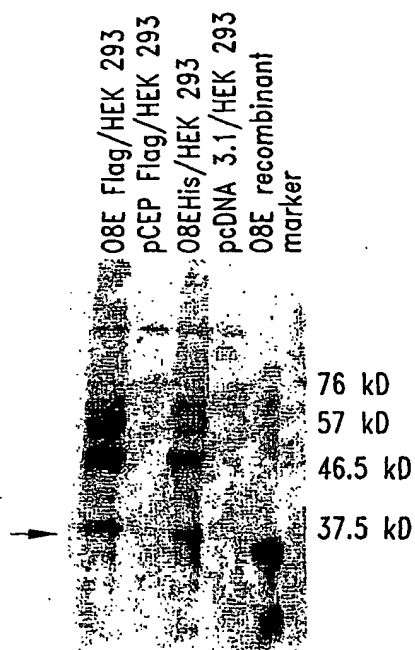


Fig. 21

98/101

O8E expression in HEK293 Cells
(probed with anti-O8E rabbit polyclonal sera #2333L)

*Fig. 22*

99/101

08E Rabbits 01212000

Date: 1/21/99

Antigen on Plate	Sera Sample	Antibody Dilutions											
		1:1000	1:2000	1:4000	1:8000	1:16000	1:32000	1:64000	1:128000	1:256000	1:512000	1:1024000	1:2048000
08E (#632-24)	Preimmune sera (#2576L): 11/10/99	0.13	0.09	0.08	0.07	0.07	0.07	0.07	0.06	0.07	0.07	0.07	0.07
	Average	0.10	0.08	0.07	0.07	0.07	0.07	0.07	0.06	0.06	0.07	0.06	0.07
	α -08E (#2576K): 1/11/2000	2.92	2.81	2.74	2.70	2.58	2.08	1.61	1.01	0.68	0.40	0.24	0.15
	Average	2.93	2.77	2.74	2.69	2.48	2.08	1.57	1.00	0.66	0.40	0.23	0.16
	Preimmune sera (#2333L): 11/10/99	2.93	2.79	2.74	2.69	2.53	2.08	1.59	1.00	0.57	0.40	0.23	0.16
	Average	0.09	0.07	0.06	0.06	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.07
α -08E (#2333L): 1/11/2000	Preimmune sera (#2333L): 11/10/99	0.08	0.07	0.06	0.07	0.10	0.07	0.07	0.07	0.07	0.07	0.07	0.07
	Average	0.08	0.07	0.06	0.06	0.08	0.07	0.07	0.07	0.07	0.07	0.07	0.07
	α -08E (#2333L): 1/11/2000	2.73	2.75	2.64	2.48	2.30	1.78	1.41	0.92	0.58	0.32	0.20	0.14
	Average	2.73	2.76	2.51	2.60	2.37	1.93	1.44	0.88	0.58	0.35	0.20	0.14
Average		2.73	2.76	2.57	2.54	2.33	1.85	1.43	0.90	0.58	0.33	0.20	0.14

Fig. 23

100/101

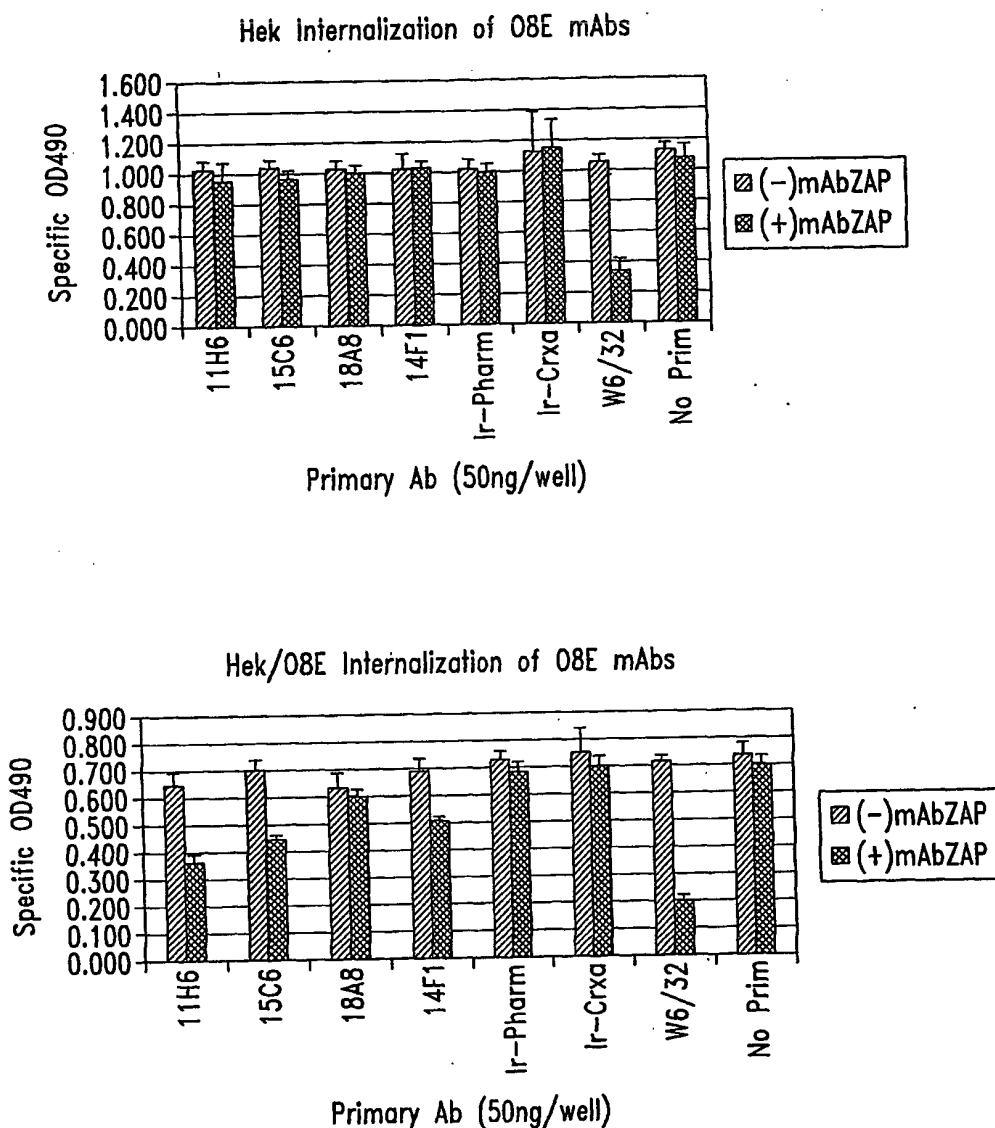
affi-pure 08E #2576L 739.87A&B

Date: 5/2/2000													
Antibody Name Rabbit #, Breed Date Purification Method Buffer Notebook		08E polyclonal 2576L, 1/11/2000 affinity PBS #705, p150											
lot #	739.87A	739.87B											
Antibody Concentration	1.4mg/ml	1.7mg/ml											
Initial Amount	18mg	3mg											
Antigen on Plate	Sera Sample	Antibody Dilutions											
08E #632-24	preimmune sera (2576L)	1:1000	1:2000	1:4000	1:8000	1:16000	1:32000	1:64000	1:128000	1:256000	1:512000	1:1024000	1:2048000
		0.15	0.11	0.09	0.08	0.08	0.07	0.07	0.07	0.07	0.08	0.07	0.08
	Average	0.14	0.10	0.09	0.08	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.07
	α -08E (2576K):2/8/2000	2.74	2.71	2.63	2.49	2.29	1.87	1.39	0.92	0.57	0.33	0.20	0.14
		2.72	2.68	2.64	2.47	2.26	1.93	1.42	0.94	0.57	0.34	0.21	0.14
	Average	2.73	2.70	2.63	2.48	2.27	1.90	1.41	0.93	0.57	0.34	0.21	0.14
	affinity pure α -08E poly	2.69	2.60	2.50	2.21	1.83	1.34	0.99	0.64	0.38	0.22	0.15	0.11
	salt peak 739-87A	2.59	2.48	2.38	2.21	1.82	1.33	1.00	0.62	0.37	0.22	0.14	0.11
	Average	2.64	2.54	2.44	2.21	1.83	1.34	1.00	0.63	0.37	0.22	0.15	0.11
	affinity pure α -08E poly	2.46	2.39	2.40	2.34	2.08	1.73	1.29	0.81	0.49	0.29	0.19	0.13
acid peak 739-67B	2.65	2.66	2.61	2.45	2.14	1.76	1.30	0.82	0.48	0.29	0.19	0.13	
Average	2.56	2.53	2.51	2.39	2.11	1.74	1.30	0.81	0.49	0.29	0.19	0.13	

Fig. 24

101/101

Anti-O8E mAb Binding to O8E Amino Acids
61-80 Induces Ligand Internalization

*Fig. 25*

SEQUENCE LISTING

<110> Corixa Corporation
 Mitcham, Jennifer L.
 King, Gordon E.
 Algate, Paul A.
 Fling, Steven P.
 Retter, Marc W.
 Fanger, Gary Richard
 Reed, Steven G.
 Vedvick, Thomas S.
 Carter, Darrick
 Hill, Paul
 Albone, Earl

<120> COMPOSITIONS AND METHODS FOR THE THERAPY
 AND DIAGNOSIS OF OVARIAN CANCER

<130> 210121.46201PC

<140> PCT

<141> 2001-07-17

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gacatcttgt agtctgcctg agatctgctg atgntttcca ttcactgctt ccagttccag 480
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<213> Homo sapiens

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atcagaaaaag gtgactaata aaggtaccag aagaatatgg ctgcacaaat accagaatct 240
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acaaggcacc gtgatttttg taattctaac ctgaagaaat gtgatgactt ttgtggacat 480
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ccttccttct ggattcacca attgttaaca ttttttcct ctcagctatc cttctaattt 780
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agcttattac tggggtgagg gacagcttac tccatttgac cagattgttt ggctaacaca 960
tcccgaagaa tgattttgtc aggaattatt gttatttaat aaatatttca ggatattttt 1020
cctctacaat aaagtaacaa t                                     1041

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<210> 19

<211> 1043

<212> DNA

<213> Homo sapiens

<400> 19

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ctctgtggaa aactgatgag gaatgaattt accattaccc atgtttctcat ccccaagcaa 60
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cagcagggcc tcatcacact gggctggatt cactatcacc ccacacagac cgcgtttctc 180
tccagtgtcg acctacacac tctactgtct taccagatga tgttgccaga gtcagtagcc 240
attgtttgct cccccaagtt ccaggaaact ggattcttta aactaactga ccatggacta 300
gaggagattt cttcctgtcg ccagaaagga ttctatccac acagcaagga tccacctctg 360
ttctgtagct gcagccacgt gactgttgtg gacagagcag tgaccatcac agaccttoga 420
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agcttattac tggggtgagg gacagcttac tccatttgac cagattgttt ggctaacaca 960
tcccgaagaa tgattttgtc aggaattatt gttatttaat aaatatttca ggatattttt 1020
cctctacaat aaagtaacaa tta                                     1043

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<210> 20

<211> 448

<212> DNA

<213> Homo sapiens

<400> 20

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ggacgacaag gccatggcga tatcggatcc gaattcaagc ctttggaatt aaataaacct 60
ggaacaggga aggtgaaagt tggagtgaga tgtcttccat atctatacct ttgtgcacag 120
ttgaatggga actgtttggg tttagggcat cttagagtgt attgatgaa aaagcagaca 180
ggaactgggt ggaggtcaag tggggaagtt ggtgaatgtg gaataactta cctttgtgct 240
ccacttaaac cagatgtgtt gcagctttcc tgacatgcaa ggatctactt taattccaca 300
ctctcattaa taaattgaat aaaaggggaat gttttggcac ctgatataat ctgccaggct 360
atgtgacagt aggaaggaaat ggtttccctt aacaagccca atgcactgggt ctgactttat 420

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aaattatttta ataaaatgaa ctattatc

448

<210> 21
<211> 411
<212> DNA
<213> Homo sapiens

<400> 21
ggcagtgaca ttcaccatca tgggaaccac cttccctttt cttcaggatt ctctgtagtg 60
gaagagagca cccagtgttg ggctgaaaac atctgaaagt agggagaaga acctaaaata 120
atcagtatct cagagggctc taagggtgcca agaagtctca ctggacattt aagtgccaac 180
aaaggcatac tttcggaatc gccaaagtcaa aactttctaa cttctgtctc tctcagagac 240
aagtgaagact caagagtcta ctgcttttagt ggcaactaca gaaaactggg gttaccacaga 300
aaaacaggag caattagaaa tgggtccaat atttcaaagc tccgcaaaca ggatgtgctt 360
tcctttgccc atttaggggt tcttctcttt cctttctctt tattaaccac t 411

<210> 22
<211> 896
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 230, 320
<223> n = A,T,C or G

<400> 22
tgcgctgaaa acaacggcct cctttactgt taaaatgcag ccacagggtc ttagccgtgg 60
gcatctcaac caccagcctc tgtggggggc aggtggggcg cctgtgggc ctctggggcc 120
acgtccagcc tctgtcctct gccttcctgt cttcgacagt gttcccgcca tccctgggtca 180
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ggccagctcg gccttggcct gccgcgtctc ctccctcarag gctgccagcc ggtcctcgaa 420
ctcctggcgg atcacctggg ccaggttgct gcgctcgcta gaaagctgct cgttcaccgc 480
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gccctcggcc tccccaaagt ggccttcag ctccgagcac cgctcctgaa gcttcgctc 600
cgactgctcc agctcgga gctcggcctc gtacttgtcc cgtaagcgt tgatgcggct 660
ctcggcagcc ttctcactct cctccttggc cagcgccatg tcggcctcca gccggtgaat 720
gaccagctca atctccttgt cccggccttt ccggatttct tccctcagct cctgttccc 780
gttcagcagc cagcctcct ccttctgtgt ggggccggcc tcccacgcct gcctctccag 840
ctccagctgc tgcttcaggg tattcagctc catctggcgg gcctgcagcg tggcca 896

<210> 23
<211> 111
<212> DNA
<213> Homo sapiens

<400> 23
caacttatta cttgaaatta taatatagcc tgtccgtttg ctgtttccag gctgtgatat 60
attttcctag tggtttgact ttaaaaataa ataaggttta attttctccc c 111

<210> 24
<211> 531
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> 472, 494
<223> n = A,T,C or G

<400> 24
tgcaagtcac gggagtttat ttatttaatt tttttcccca gatggagact ctgtcgccca 60
ggctggagtg caatgggtgtg atcttggctc actgcaacct ccacctcctg ggttcaagcg 120
attctcctgc cacagcctcc cgagtagctg ggattacagg tgcccgccac cacaccagc 180
taatttttat atttttagta aagacagggg ttcccatgtg tggccaggct ggtcttgaac 240
ttctgacctc aggtgatcca cctgcctcgg cctcccaaag tggtgggatt acaggcgtga 300
gctaccctgt cctggccagc cactggagtt taaaggacag tcatgttggc tccagcctaa 360
ggcggcattt tcccccatca gaaagcccg ggcctctgta cctcaaaata gggcacctgt 420
aaagtcagtc agtgaagtc ctgctctaac tggccaccg gggccattgg cntctgacac 480
agccttgcca ggangcctgc atctgcaaaa gaaaagttca cttcctttcc g 531

<210> 25
<211> 471
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 377
<223> n = A,T,C or G

<400> 25
cagagaatct kagaaagatg tcgcgttttc ttttaatgaa tgagagaagc ccattttgtat 60
ccctgaatca ttgagaaaag gcggcgggtg cgacagcggc gacctaggga tcgatctgga 120
gggacttggg gagcgtgcag agacctctag ctcgagcgcg agggacctcc cgccgggatg 180
cctggggagc agatggaccc tactggaagt cagttggatt cagatttctc tcagcaagat 240
actccttgcc tgataattga agattctcag cctgaaagcc aggttctaga ggatgattct 300
ggttctcact tcagtatgct atctcgacac ctctctaate tccagacgca caaagaaaat 360
cctgtgttgg atgttngtc caatccttga acaaacagct ggagaagaac gaggagaccg 420
gtaatagtgg gttcaatgaa catttgaaag aaaaccaggt tgcagaccct g 471

<210> 26
<211> 541
<212> DNA
<213> Homo sapiens

<400> 26
gactgtcctg aacaagggac ctctgaccag agagctgcag gagatgcaga gtggtggcag 60
gagtggaaag caaagaacac ccaccttcct cccttgaagg agtagagcaa ccatcagaag 120
atactgtttt attgctctg tcaaacaagt ctctctgagt tgacaaaacc tcaggctctg 180
gtgacttctg aatctgcagt ccactttcca taagttcttg tgcagacaac tgttcttttg 240
cttccatagc agcaacagat gctttggggc taaaaggcat gtcctctgac cttgcagggtg 300
gtggattttg ctcttttaca acatgtacat ccttactggg ctgtgctgtc acagggatgt 360
ccttgctgga ctgttctgct atggggatat ctctgttgga ctgttcttca tgcttaattg 420
cagtattagc atccacatca gacagcctgg tataaccaga gttggtggtt actgattgta 480
gctgctcttt gtcacattca tatggcacia gtattttcct caacatcctg gctctgggaa 540
g 541

<210> 27
<211> 461
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> 367
<223> n = A,T,C or G

<400> 27
gaaatgtata tttaatcatt ctcttgaacg atcagaactc traaatcagt tttctataac 60
arcatgtaat acagtcaccg tggctccaag gtccaggaag gcagtggta acacatgaag 120
agtgtgggaa gggggctgga aacaaagtat tcttttcctt caaagcttca ttcctcaagg 180
cctcaattca agcagtcatt gtccttgctt tcaaaagtct gtgtgtgctt catggaagg 240
atatgtttgt tgccttaatt tgaattgtgg ccaggaaggg tctggagatc taaattcaga 300
gtaagaaaac ctgagctaga actcaggcat ttctcttaca gaacttggct tgcagggtag 360
aatgaangga aagaaactta gaagctcaac aagctgaaga taatcccatc aggcatttcc 420
cataggcctt gcaactctgt tcactgagag atgttatcct g 461

<210> 28
<211> 541
<212> DNA
<213> Homo sapiens

<400> 28
agtctggagt gagcaaacaa gagcaagaaa caarragaag ccaaaagcag aaggctccaa 60
tatgaacaag ataaatctat cttcaaagac atattagaag ttgggaaaat aattcatgtg 120
aactagacaa gtgtgttaag agtgataagt aaaatgcacg tggagacaag tgcattccca 180
gatctcaggg acctccccct gcctgtcacc tggggagtga gaggacagga tagtgcattg 240
tctttgtctc tgaattttta gttatatgtg ctgtaattgtt gctctgagga agccccctgga 300
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aagacgctgc taattgactg ccacttcgca actcaggggc ggctgcattt tagtaatggg 420
tcaaattgatt cactttttat gatgcttccc aagggtgcctt ggcttctctt cccaactgac 480
aaatgcccaa gttgagaaaa atgatcataa ttttagcata aaccgagcaa tcggcgaccc 540
c 541

<210> 29
<211> 411
<212> DNA
<213> Homo sapiens

<400> 29
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agtgtatttc ttacactctg tatctatcac cagaagctga ggtgatagcc cgcttgtcat 120
tgtcatccat attctgggac tcaggcggga actttctgga atattgccag ggagcatggc 180
agaggggcac agtgcattct gggggaatgc acattggctc agcctgggta atgagtata 240
tacattacct ctgttcacaa ctcatgccc agcaccagtc acaaggcccc accaaatacc 300
agagcccaag aaatgtagtc ctgttgatat ggttttgctg tgtcccaacc caaatctcat 360
cttgaattgt aagctcccat aattcccatg tgttgtggga gggacctggt g 411

<210> 30
<211> 511
<212> DNA
<213> Homo sapiens

<400> 30
atcatgagga tgttaccaaa gggatggtac taaaccattt gtattcgtct gttttcacac 60
tgctttgaag atactacctg agactgggta atttataaac aaaagagatt taattgactc 120
acagttctgc atggctgaag aggcctcagg aaacttacag tcatggtgga aggcaaagga 180
ggagcaaggc atgtcttaca tgtcagtagg agagagagcg agagcaggag aacctgccac 240
ttataaacca ttcagatctc ataactccct atcatgagaa aaacatggag gaaaccaccc 300
tcattgatcca atcacctccc gccagggtccc tccctcgaca cgtggggatt ataattcagg 360
attagaggga cacagagaca aaccatatca tcattcatga gaaatccacc ctcatagtcc 420

aatcagctcc taccaggccc cacctccaac actggggatt gcaattcaac atgagatttg 480
 gatggggaca cagattcaaa ccatatcata c 511

<210> 31
 <211> 827
 <212> DNA
 <213> Homo sapiens

<400> 31
 catggccttt ctcccttagag gccagaggtg ctgccctggc tgggagtga gctccaggca 60
 ctaccagctt tcctgatttt cccgtttggt ccattgtgaag agctaccacg agccccagcc 120
 tcacagtgtc cactcaaggg cagcttggtc ctcttgctct gcagaggcag gctggtgtga 180
 ccctgggaac ttgacccggg aacaacaggt ggcccagagt gagtgtggcc tggccctca 240
 acctagtgtc cgtcctctc tctcctggag ccagtcttga gtttaaaggc attaagtgtt 300
 agatacaagc tccttggtgc tggaaaaaca cccctctgct gataaagctc agggggcact 360
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 tccctctggt gctcccacgt ctgttcctca cctccatct ctgggagcag ctgcacctga 480
 ctggccacgc gggggcagtg gaggcacagg ctccagggtg cccgggtacc tggcacccta 540
 tggctttaca agtagagttg gccagtttc cttccacctg aggggagcac tctgactcct 600
 aacagtcttc cttgccctgc catcatctgg ggtggctggc tgtcaagaaa ggccgggcat 660
 gctttctaaa cacagccaca ggaggcttg agggcatctt ccagggtggg aaacagtctt 720
 agataagtaa ggtgacttgc ctaaggcctc ccagcaccct tgatcttgga gtctcacagc 780
 agactgcatg tsaacaactg gaaccgaaaa catgcctcag tataaaa 827

<210> 32
 <211> 291
 <212> DNA
 <213> Homo sapiens

<400> 32
 ccagaacctc cttctctttg gagaatgggg aggcctcttg gagacacaga gggtttcacc 60
 ttgatgacc tctagagaaa ttgcccaaga agccacctt ctggtcccaa cctgcagacc 120
 ccacagcagt cagtttgtca ggccctgctg tagaaggtca cttggctcca ttgcctgctt 180
 ccaaccaatg ggcaggagag aaggccttta tttctcgccc acccattctc ctgtaccagc 240
 acctcgttt tcagtcagyg ttgtccagca acggtaccgt ttacacagtc a 291

<210> 33
 <211> 491
 <212> DNA
 <213> Homo sapiens

<400> 33
 tgcagttagt tttatttatg tgttttsgtc tggaaaacca agtgtccag cagcatgact 60
 gaacatcact cacttcccct acttgatcta caaggccaac gccgagagcc cagaccagga 120
 ttccaaacac actgcacgag aatattgttg atccgctgtc aggttaagtgt ccgtcactga 180
 cccaracgct gttacgtggc acatgactgt acagtgccac gtaacagcac tgtacttttc 240
 tcccatgaac agttacctgc catgtatcta catgattcag aacattttga acagttaatt 300
 ctgacacttg aataatccca tcaaaaaccg taaaatcact ttgatgtttg taacgacaac 360
 atagcatcac tttacgacag aatcatcttg aaaaacagaa caacgaatac atacatctta 420
 aaaaatgctg ggggtgggcca ggcacagctt cagcctgta atcccagcac tttggggaggc 480
 ttaagcgggt g 491

<210> 34
 <211> 521
 <212> DNA
 <213> Homo sapiens

<220>

<221> misc_feature
<222> 453, 476, 487
<223> n = A,T,C or G

<400> 34
tggggcggaag agaagccaag gccaaaggagc tgggtgcggca gctgcagctg gaggccgagg 60
agcagaggaa gcagaagaag cggcagagtg tgtcgggcct gcacagatac cttcacttgc 120
tggatggaaa tgaaaattac ccgtgtcttg tggatgcaga cgggtgatgtg atttccttcc 180
caccaataac caacagtgaag aagacaaagg ttaagaaaac gacttctgat ttgtttttgg 240
aagtaacaag tgccaccagt ctgcagattt gcaaggatgt catggatgcc ctcattctga 300
aatggcaag aatgaaaaa gtacacttta gaaaataaag aggaaggatc actctcagat 360
actgaagccg atgcagtctc tggacaactt ccagatccca caacgaatcc cagtgtgga 420
aaggacgggc ccttccttct ggtgggtgga cangtcccgg tgggtgatct tggaanggaa 480
cctgaangtg gtgtaccccg tccaaggccg accttggcc a c 521

<210> 35
<211> 161
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 18
<223> n = A,T,C or G

<400> 35
tcccgcgctc gcagggcncg tgccacctgc cygtccgccc gctcgctcgc tgcgccgccc 60
cgccgcgctg ccgaccgyca gcatgctgcc gagagtgggc tgccccgcgc tgccgctgcc 120
gcgcgcgccc ctgctgccgc tgctgccgct gctgctgctg c 161

<210> 36
<211> 341
<212> DNA
<213> Homo sapiens

<400> 36
ggcgggtagg catggaactg agaagaacga agaagctttc agactacgtg gggaagaatg 60
aaaaaaccaa aattatcgcc aagattcagc aaaggggaca gggagctcca gcccgagagc 120
ctattattag cagtgaggag cagaagcagc tgatgctgta ctatcacaga agacaagagg 180
agctcaagag attggaagaa aatgatgatg atgcctattt aaactcacca tgggcgggata 240
aactgctttt gaaaagacat tttcatggag tgaaagacat aaagtggaga ccaagatgaa 300
gttcaccagc tgatgacact tccaaagaga ttagctcacc t 341

<210> 37
<211> 521
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 516
<223> n = A,T,C or G

<400> 37
tctgaagggtt aaatgtttca tctaaatagg gataatgrta aacacctata gcatagagtt 60
gtttgagatt aaatgagata atacatgtaa aattatgtgc ctggcataca gcaagattgt 120
tgttgttgtt gatgatgatg atgatgatga taatattttt ctatccccag tgcacaactg 180
cttgaacctt ttagataatc aatacatgtt tcttgaactg agatcaattt ccccatgttg 240

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tctgactgat gaagccctac attttcttct agaggagatg acatttgagc aagatcttaa 300
agaaaatcag atgccttcac ctgaccactg cttggtgatc ccatggcact ttgtacatct 360
ctccattagc tctcatctca ccagcccatc attattgtat gtgctgcctt ctgaagcttg 420
cagctggcta ccatcmggta gaataaaaat catcctttca taaaatagtg accctccttt 480
tttatttgca tttcccaaag ccaagcaccg tgggaggta g 521

```

<210> 38
 <211> 461
 <212> DNA
 <213> Homo sapiens

```

<400> 38
tatgaagaag ggaaaagaag ataatttgtg aaagaaatgg gtccagttac tagtctttga 60
aaagggtcag tctgtagctc ttcttaatga gaataggcag ctttcagttg ctccagggtca 120
gatttcctta gtggtgtatc taatcacagg aaacatctgt ggttccctcc agtctctttc 180
tgggggactt gggcccaactt ctcatctcat ttaattagag gaaatagaac tcaaagtaca 240
atttactgtt gtttaacaat gccacaaaga catggttggg agctatttct tgatttgtgt 300
aaaatgctgt ttttgtgtgc tcataatggt tccaaaaatt ggggtgctggc caaagagaga 360
tactgttaca gaagccagca agaagacctc tgttcattca caccctcggt gatatcagga 420
attgactcca gtgtgtgcaa atccagtttg gcctatcttc t 461

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<210> 39
 <211> 769
 <212> DNA
 <213> Homo sapiens

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<400> 39
tgagggactg attggtttgc tctctgctat tcaattcccc aagcccaactt gttcctgcag 60
cgtcctcctt ctcatccctt ttagttgtac cctctctttc atctgagacc tttccttctt 120
gatgtcgctt tttcttcttc ttgctttttc tgatgttctg ctccagcatgt tctgggtgct 180
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tctttttctt ttttttgggg ggcttgcctc ctgactgcag ttgaggggac ccagggtcct 300
ggcctttgag acgagccagg aaggcctgct cctgggcctc taggcgagca agcttggcct 360
tcatttgtat cccaagacgg gcagccttgt gtgctgttcg cccctcacag gcttggagca 420
gcattctatc agtcagaatc tttggggact tggacccttg gttgtcgtca tcaactgcagc 480
tctccaagtc tttgtttggc ttctctccac ctgaagtcaa tgtagccatc ttcacaaact 540
tctgatacag caagttgggc ttgggatgat tataacgggt ggtctcctta gaaaggctcc 600
ttatctgtac tccatcctgc ccagtttcca ctaccaagtt ggccgcagtc ttgttgaaga 660
gctcattcca ccagtgtttt gtgaactcct tggcagggtc atgtcctacc ccatgagtgt 720
cttgcttcag ygtcaccctg agagcctgag tgataccatt ctcttccg 769

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<210> 40
 <211> 292
 <212> DNA
 <213> Homo sapiens

```

<400> 40
gacaacatga aataaatcct agaggacaaa attaaactca atagagtgtg gtctagttaa 60
aaactcgaaa aatgagcaag tctggtggga gtggaggaag ggctatacta taaatccaag 120
tgggcctcct gatcttaaca agccatgctc attatacaca tctctgaact ggacatacca 180
cctttacgca ggaaacaggg cttggaactt ctaagggaaa ttaacatgca ccaccacat 240
ctaactacc tgccgggtag gtaccatccc tgcttogctg aatcagtgct tc 292

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<210> 41
 <211> 406
 <212> DNA
 <213> Homo sapiens

<400> 41

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ttggaattaa ataaacctgg aacagggaag gtgaaagttg gagtgagatg tcttccatat 60
ctataaccttt gtgcacagtt gaatgggaac tgtttgggtt tagggcatct tagagttgat 120
tgatggaaaa agcagacagg aactgggtggg aggtcaagtg gggaagttgg tgaatgtgga 180
ataacttacc tttgtgctcc acttaaacca gatgtgttgc agctttcctg acatgcaagg 240
atctacttta attccacact ctcatataa aattgaataa aagggaatgt tttggcacct 300
gatataatct gccaggctat gtgacagtag gaaggaatgg tttcccctaa caagcccaat 360
gcactggtct gactttataa attatttaat aaaatgaact attatc 406
```

<210> 42

<211> 381

<212> DNA

<213> Homo sapiens

<400> 42

```
aaactggacc tgcaacaggg acatgaattt actgcarggt ctgagcaagc tcagcccctc 60
tacctcaggg cccacagcc atgactacct ccccaggag cgggagggtg aagggggcct 120
gtctctgcaa gtggagccag agtggaggaa tgagctctga agacacagca cccagccttc 180
tcgcaccagc caagccttaa ctgcctgcct gaccctgaac cagaaccag ctgaactgcc 240
cctccaaggg acaggaaggc tgggggaggg agtttacaac ccaagccatt ccaccccctc 300
ccctgctggg gagaatgaca catcaagctg ctaacaattg gggaagggg aaggaagaaa 360
actctgaaaa caaatcttg t 381
```

<210> 43

<211> 451

<212> DNA

<213> Homo sapiens

<400> 43

```
catgcgtttc accactgttg gccaggctgg tctcgaaact ctggcctcaa gcaatccacc 60
cgccctcagc tccaaaagtg ctgggattac agatgtgagc catggcacca tgccaaaagg 120
ctatatcctt ggctctgtgt ttccgagact gcttttaate ccaacttctc tacatttaga 180
ttaaaaaata ttttattcat ggtcaatctg gaacataatt actgcattct aagtttccac 240
tgatgtatat agaaggctaa aggcacaatt tttatcaaat ctagtagagt aaccaaacat 300
aaaatcatta attactttca acttaataac taattgacat tcctcaaaag agctgttttc 360
aatcctgata ggttctttat tttttcaaaa tatatttgcc atgggatgct aatttgcaat 420
aaggcgcata atgagaatac cccaaactgg a 451
```

<210> 44

<211> 521

<212> DNA

<213> Homo sapiens

<400> 44

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gttggacccc cagggactgg aaagacactt cttgcccgag ctgtggcggg agaagctgat 60
gttccttttt attatgcttc tggatccgaa tttgatgaga tgtttgtggg tggggagcc 120
agccgtatca gaaatctttt tagggaagca aaggcgaatg ctccctgtgt tatatttatt 180
gatgaattag attctgttgg tgggaagaga attgaatctc caatgcattc atattcaagg 240
cagaccataa atcaacttct tgctgaaatg gatggtttta aacccaatga aggagttatc 300
ataataggag ccacaaactt cccagaggca ttagataatg ccttaatacc gtccctggctg 360
ttttgacatg caagttacag ttccaaggcc agatgtaaaa ggtcgaacag aaattttgaa 420
atgggtatctc aataaaataa agtttgatca atcccggtga tccagaaatt atagcctcga 480
ggtactggtg gcttttccgg aagcagagtt gggagaatct t 521
```

<210> 45

<211> 585

<212> DNA

<213> Homo sapiens

<400> 45

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gcctacaaca tccagaaga gtctaccctg cacctggtgc tscgtctcag aggtgggatg 60
cagatcttcg tgaagaccct gactggtaag accatcactc tcgaagtgga gccgagtgc 120
accatygaga acgtcaaagc aaagatccar gacaaggaag gcrtycctcc tgaccagcag 180
aggttgatct ttgccggaaa gcagctggaa gatggdcgca ccctgtctga ctacaacatc 240
cagaaagagt cyaccctgca cctggtgctc cgtctcagag gtgggatgca ratcttcgtg 300
aagaccctga ctggttaagac catcacctc gaggtggagc ccagtgcacac catcgagaat 360
gtcaaggcaa agatccaaga taaggaaagg atccctcctg atcagcagag gttgatcttt 420
gctgggaaac agctggaaga tggacgcacc ctgtctgact acaacatcca gaaagagtcc 480
actctgcact tggctctgcg cttgaggggg ggtgtctaag tttccccttt taaggtttcm 540
acaaatttca ttgcactttc ctttcaataa agttgttgca ttccc 585
```

<210> 46

<211> 481

<212> DNA

<213> Homo sapiens

<400> 46

```
gaactgggcc ctgagcccaa gtcatgcctt gtgtccgcat ctgccgtgtc acctctgtkc 60
ctgcccctca cccctccctc ctggtcttct gagccagcac catctccaaa tagcctattc 120
cttcttgcaa atcacacaca catgcgggcc acacatacct gctgccctgg agatggggaa 180
gtaggagaga tgaatagagg cccatacatt gtacagaagg aggggcaggt gcagataaaa 240
gcagcagacc cagcggcagc tgaggtgcat ggagcacggg tggggccggc attgggctga 300
gcacctgatg ggcctcatct cgtgaatcct cgaggcagcg ccacagcaga ggagtttaagt 360
ggcacctggg ccgagcagag caggagactg agggtcagag tggaggctaa gctgccctgg 420
aactcctcaa tcttgectgc cccctagtat gaagccccct tcctgccctt acaattcctg 480
a 481
```

<210> 47

<211> 461

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 128

<223> n = A,T,C or G

<400> 47

```
atggatctta ctttgccacc caggttggag tgcagtgtg caatcttggc tcaactgcagc 60
cttaacctcc caggctcaag ctatcctcct gccaaagcct tccacatagc tgggactaca 120
ggtagacngc caccacaccc agctaaaatt tttgtatctt ttgtagagac gggatctcgc 180
cacgttgccc aggtggtcc catcctgacc tcaagcagat ctgccacact cagcccccca 240
acgtgctagg attacaggcg tgagccaccg caccagcct ttgttttgct tttaatggaa 300
tcaccagttc ccctccgtgt ctgagcagca gctgtgagaa atgctttgca tctgtgacct 360
ttatgaaggg gaacttccat gctgaatgag ggtaggatta catgctcctg tttcccgggg 420
gtcaagaaag cctcagactc cagcatgata agcagggtga g 461
```

<210> 48

<211> 571

<212> DNA

<213> Homo sapiens

<400> 48

```
ataggggctt taaggaggga attcaggttc aatgaggtcg taaggccagg gctcttatcc 60
agtaagactg gggctcctag atgagaaaga gacccccgag gtcccttctc ctgccgtgtg 120
aggatgcac cagaaggcgg ccgtctgcaa gcgaaggaga ggccgcacca gaaaccgaca 180
```

ccttcacatt ggacttgcag cctctagaac tgagaaaata actgtctgtt ggtaagcca 240
cccagtttgt agtattctct tatggcttcc taagcagact aacaaacaaa caccacaaat 300
taactgatgg cttcgctgtc ttctgtaaaa attgctatga gagaactttt cactcactgt 360
tttgagttt ctcctcagc ccctggttct ttcttctcac ataatcccaa tttcaattta 420
tagttcatgg ccaggcaga gtcattcatc acggcatctc ctgagctaaa ccagcacctg 480
ctctgctcac ttcttgactg gctgctcatc atcagccctc ttgcagagat ttcatttcct 540
cccgtagcag gtacttcacg caccaagctc a 571

<210> 49

<211> 511

<212> DNA

<213> Homo sapiens

<400> 49

ggataatgaa gttgttttat ttagcttggc caaaaaggca tattcctcta tttctttata 60
caacaaatat ccccaaaata aagcaagcat atatatcttg aatgtgtaat aatccagtga 120
taaacagag cagtacttta aaagaaaaaa aaatatgtat ttctgtcagg ttaaaatgag 180
aatcaaaacc atttactctg ctaactcatt attttttgct ttcttttttg ttaagagagg 240
caatgcaata cactgaaaaa ggtttttatc ttatctggca ttggaattag acatatcaat 300
acccagccc ccatttccaa actttaagac cacaacaaag taatttactt ttctgaacat 360
tggttttttc tggaaaatgg gaattataaa atagactttg cagactctta tgagattaaa 420
taagataatg tatgaaattc tttcttcttt tttacttctt tttccttttt gagatggagt 480
ctcaccccg caccagcgt ggagtacagt g 511

<210> 50

<211> 561

<212> DNA

<213> Homo sapiens

<400> 50

ccactgcact ccagcctggg tgacggagtg agactctgtc tcaaaaaaac aaacaaacaa 60
acaaacaaa aactgaaaag gaaatagagt tcctctttcc tcatatatga atatattatt 120
tcaacagatt gttgatcacc taccatatgc ttggtattgt tctaattgct ggggatacag 180
caagaggttc tgagaaact catggagcat gaaagtaaat aaacaaagtt aatttcaagg 240
ccaggcatgg ttgctcacac cttagtccc agcactttgg gaggtgagg cagggtggatc 300
acttggtccc aggagttcaa ggctgcagt agccaagatt gtgccactac tctccaggct 360
gggcaacaga gcaagacct gtctcagggg gaacaaaaag ttaatttcag attttgtaa 420
gtgctgtaaa ggaagtaaat aggttgatat tcaagagagc acctgaaggc caggcgtggg 480
ggctcacgcc tgtggtctaa cgctttggga agcccgagcg ggcggatcac aaggctcagga 540
gaattttggc caggcatggt g 561

<210> 51

<211> 451

<212> DNA

<213> Homo sapiens

<400> 51

agaatccatt tattgggttt taaactagtt acacaactga aatcagtttg gcactacttt 60
atacagggat tacgctgtg tatgccgaca cttaaatact gtaccaggac cactgctgtg 120
cttaggtctg tattcagtc ttcagcatgt agatactaaa aatatactgt agtgttcctt 180
taagggaagac tgtacagggt gtgttgcaag atgacattca ccaatttggt aattatttca 240
accagaaga tacctttcac tctataaact tgtcataggc aaacatgtgg tgttagcatt 300
gagagatgca cacaataatg ttacataaaa gtacagacat tctaataata agtgactga 360
aaaaaaaaa aaccccatat ctcaattttt gtaacaagat aaagaaaata atttaaaaac 420
acaaaaaatg gcattcagtg ggtacaaagc c 451

<210> 52

<211> 682

<212> DNA

<213> Homo sapiens

<400> 52

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caaatatttta atataaatctt ttgaacaag ttcagakgaa ataaaaatca aagtttgcaa 60
aaacgtgaag attaaacttaa ttgtcaaata ttcctcattg ccccaaata gtattttttt 120
tatttctatg caaaagtatg ccttcaaact gcttaaatga tatatgatat gatacacaaa 180
ccagttttca aatagtaaag ccagtcattt tgcaattgta agaaataggt aaaagattat 240
aagacacctt acacacacac acacacacac acacacacgt gtgcaccgcc aatgacaaaa 300
aacaatttgg cctctcctaa aataagaaca tgaagaccct taattgctgc caggagggaa 360
cactgtgtca cccctcccta caatccaggt agtttccttt aatccaatag caaatctggg 420
catatttgag aggagtgatt ctgacagcca csgettgaat cctgtgggga accattcatg 480
tccaccactt ggtgccctga aaaaatgcc aataattttt gctcccactt ctgctgctgt 540
ctcttcacata tcctcacata gacccacag ccgctggccc ctggctgggc atcgcatgtg 600
tggtagagca agtcataggt ctctctttg acgtcacaga agcgatacac caaattgcct 660
ggtcgtcat tgtcataacc ag 682
```

<210> 53

<211> 311

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 208

<223> n = A,T,C or G

<400> 53

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tttgacttta gtaggggtct gaactattta ttttactttg ccmgtaatat ttaraccyta 60
tatatctttc attatgccat cttatcttct aatgbcaagg gaacagwtgc taamctggct 120
tctgcattwa tcacattaaa aatggctttc ttggaaaatc ttcttgatat gaataaagg 180
tcttttavag ccatcattta aagcmggnnt ctctccaaca cgagtctgct sasgggggk 240
gagctgtgaa ctctggctga aggctttccc atacacactg caatgacmtg gtttctgacc 300
agbgtgagtt a 311
```

<210> 54

<211> 561

<212> DNA

<213> Homo sapiens

<400> 54

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agagaagccc cataaatgca atcagtgtgg gaaggccttc agtcagagct caagcctttt 60
ctccatcat cgggttcata ctggagagaa accctatgta tgtaatgaat gcggcagagc 120
cttttggttt aactctcatc ttactgaaca cgtaaggatt cacacaggag aaaaacccta 180
tgtttgtaat gagtgcggca aagcctttcg tcggagttcc actcttgctc agcatcgaag 240
agttcacact ggggagaagc cctaccagtg cgttgaatgt gggaaagctt tcagccagag 300
ctcccagctc accctacatc agccgagttc aactggaga gaagccctat gactgtggtg 360
actgtgggaa ggccttcagc cggaggtcaa ccctcattca gcatcagaaa gttcacagcg 420
gagagactcg taagtgcaga aaacatggtc cagcctttgt tcatggctcc agcctcacag 480
cagatggaca gattccact ggagagaagc acggcagaac cttaaccat ggtgcaaatc 540
tcattctgcy ctggacagtt c 561
```

<210> 55

<211> 811

<212> DNA

<213> Homo sapiens

<400> 55

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gagacaggggt ctcactttgt caccagggct ggaatgcagt ggtgcgatct tacgtagctc 60
actgcagccc tgacctcctg gactcaaaca attctcctgc ctcagccctg caagtagctg 120
ggactgtggg tgcattgccac catgcctggc taacttttgt agtttttcta aagatggggg 180
tttgccatgt tgcacatgct ggtcctgaac tcctgagctc aaacgatctg cccacctcgg 240
cctcccagaa tgttgggatt acaggggtaa accaccacgc ctggcccat tagggattc 300
ttagcatcca ctgtctcact gagattaatc ataagagatg ataagcactg gaagaaaaaa 360
atttttacta ggctttggat atttttttcc tttttcagct ttatacagag gattggatct 420
ttagttttcc tttaactgat aataaaacat tgaaaggaaa taagtttacc tgagattcac 480
agagataacc ggcatcactc ccttgctcaa ttccagtctt taccacatca attattttca 540
gaggtgcagg ataaaggcct ttagtctgct ttgcgacttt ttcttccact tttttgtaaa 600
cctgttgctt gacaaatgga attgacagcg tatgccatga ctattccatt tgtcaggcat 660
acgctgtcaa tttttccacc aatcccttgt ctctctttgg agagatcttc ttatcagcta 720
gtcctttggc aaaagtaatt gcaacttctt ctaggatttc tattgtccgt tccactgggt 780
gaacccctgg gaccaggact aaaacctcca g 811
```

<210> 56

<211> 591

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> 45, 477, 490, 561

<223> n = A,T,C or G

<400> 56

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atctcatata tatatttctt cctgacttta tttgcttgct tctgncacgc atttaaaata 60
tcacagagac caaaatagag cggctttctg gtggaacgca tggcagtcac aggacaaaat 120
acaaaactag ggggtctctgt cttctcatat atcatacaat tttcaagtat tttttttatg 180
tacaaaagagc tactctatct gaaaaaaaat taaaaaataa atgagacaag atagtattatg 240
catcctagga agaaagaatg ggaagaaaga acggggcagc tgggtacaga ttctgtctcc 300
ctgttccccc ggaccactac cttcctgcca ctgagttccc ccacagcctc acccatcatg 360
tcacagggca agtgccaggg taggtgggga ccagtggaga caggaaccag caacatactt 420
tggcctggaa gataaggaga aagtctcaga aacacactgg tgggaagcaa tcccacnggc 480
cgtgccccan gagcttccca cctgctgctg gctccctggg tggttttggg aacagcttgg 540
gcaggccctt ttgggtgggg nccaactggg cctttgggcc cgtgtggaaa g 591
```

<210> 57

<211> 481

<212> DNA

<213> Homo sapiens

<400> 57

```
aaacattgag atggaatgat agggtttccc agaatcaggt ccatatttta actaaatgaa 60
aattatgatt tatagccttc tcaaatacct gccatacttg atatctcaac cagagctaata 120
tttacctctt tacaaattaa ataagcaagt aactggatcc acaatttata atacctgtca 180
attttttctg tattaacact ctatcatagt ttaagcctat tagggacttt aatccttaca 240
aataaacagg tttaaaaatca cctcaatagg caactgccct tctggttttc ttctttgact 300
aaacaatctg aatgcttaag attttccact ttgggtgcta gcagtacaca gtgttacact 360
ctgtattcca gacttcttaa attatagaaa aaggaatgta cactttttgt attctttctg 420
agcagggccg ggaggcaaca tcatctacca tggtagggac ttgtatgcat ggactacttt 480
a 481
```

<210> 58

<211> 141

<212> DNA

<213> Homo sapiens

<400> 58
actctgtcgc ccaggctgga gcccabtgmm gcgatctcga ctccctgcaa gctmcgcctc 60
acaggwtcat gccattctcc tgcctcagca tctggagtag ctgggactac aggcgccagc 120
caccatgccc agctaatttt t 141

<210> 59
<211> 191
<212> DNA
<213> Homo sapiens

<400> 59
accttaaaga cataggagaa tttatactgg gagagaaagc ttacaaatgt aagggttctg 60
acaagacttg ggagtgattc acacctggaa caacatactg gacttcacac tggabagaaa 120
ccttacaagt gtaatgagtg tggcaaagcc tttggcaagc agtcaacact tattcaccat 180
caggcaattc a 191

<210> 60
<211> 480
<212> DNA
<213> Homo sapiens

<400> 60
agtcaggatc atgatggctc agtttccac agcgatgaat ggagggccaa atatgtgggc 60
tattacatct gaagaacgta ctaagcatga taaacagttt gataacctca aaccttcagg 120
aggttacata acagggtgac aagcccgtag ttttttccca cagtcaggtc tgcggccccc 180
ggtttttagct gaaatatggg ccttatcaga tctgaacaag gatgggaaga tggaccagca 240
agagttctct atagctatga aactcatcaa gttaaagttg cagggccaac agctgcctgt 300
agtcctccct cctatcatga aacaaccccc tatgttctct ccaactaatct ctgctcgttt 360
tgggatggga agcatgccca atctgtccat tcatcagcca ttgcctccag ttgcacctat 420
agcaacaccc ttgtcttctg ctacttcagg gaccagtatt cctccctaata gatgcctgct 480

<210> 61
<211> 381
<212> DNA
<213> Homo sapiens

<400> 61
ctttcgattt ccttcaattt gtcacgtttg attttatgaa gttgttcaag ggctaactgc 60
tgtgtattat agctttctct gagttccttc agctgattgt taaatgaatc catttctgag 120
agcttagatg cagtttcttt ttcaagagca tctaattgtt cttaaagtct ttggcataat 180
tcttcctttt ctgatgactt tctatgaagt aaactgatcc ctgaatcagg tgtgttactg 240
agctgcatgt ttttaattct ttcgtttaat agctgcttct cagggaccag atagataagc 300
ttattttgat attccttaag ctcttggtga agttgttcga tttccataat ttccagggtca 360
cactggttat cccaaacttc t 381

<210> 62
<211> 906
<212> DNA
<213> Homo sapiens

<400> 62
gtggagggtga aacggaggca agaaaggggg ctacctcagg agcgaggggac aaagggggcg 60
tgaggcacct aggcgcgggc accccggcga caggaagccg tctgaaccg ggctaccggg 120
taggggaagg gccgcgtag tcctcgagg gccccagagc tggagtcggc tccacagccc 180
cgggcccgtcg gcttctcact tcctggacct ccccggcgcc cgggcctgag gactggctcg 240
gcggaggggag aagaggaaac agacttgagc agctccccgt tgtctcgcaa ctccactgcc 300
gaggaactct catttcttcc ctgcctcctt cacccccac ctcatgtaga aagggtgctga 360

agcgtccgga gggaagaaga acctgggcta ccgtccctggc cttcccmccc ccttcccggg 420
gcgcttttggg gggcgtggag ttgggggttg gggggtgggt gggggttctt ttttgagtg 480
ctggggaact tttttccctt cttcagggtca ggggaaaggg aatgcccaat tcagagagac 540
atgggggcaa gaaggacggg agtggaggag cttctggaac tttgcagccg tcatcgggag 600
gcggcagctc taacagcaga gagcgtcacc gcttgggtatc gaagcacaag cggcataagt 660
ccaaacactc caaagacatg gggttgggtga ccccggaagc agcatccctg ggcacagtta 720
tcaaaccctt ggtggagtat gatgatata gctctgattc cgacaccttc tccgatgaca 780
tggccttcaa actagaccga agggagaacg acgaacgtcg tggatcagat cggagcgacc 840
gcctgcacaa acatcgtcac caccagcaca ggcgttcccg ggacttacta aaagctaaac 900
agaccg 906

<210> 63
<211> 491
<212> DNA
<213> Homo sapiens

<400> 63
gacatgtttg cctgcagggg accagagaca atgggattag ccagtgtctc ctgttcttta 60
tgcttccaga gaggatggg acagctctca ggtcagaatc caggctgaga aggccatgct 120
ggttgggggc ccccggaagc acgggtccgga tcctccctgg catcagcgta gaccgcgtgc 180
tcaggcttgg ggtaccaaac tcatgtctctg tactgttttg gccccatgcg gtgagaggaa 240
aacctagaaa aagattggtc gtgctaagga atcagctgcc ccctcatcct ccgcatccaa 300
tgctggtgac aacatattcc ctctcccagg acacagactc ggtgactcca cactgggctg 360
agtggcctct ggaggctcgt ggcctaaggc agggctccgt aaggctgac ggctgaactg 420
ggtaggggtga gggtttctga cccttcgctt cccatcccat aaccgctgtc aatgagctca 480
cactgtggtc a 491

<210> 64
<211> 511
<212> DNA
<213> Homo sapiens

<400> 64
gatggcatgg tcgttgctaa tgtgcctgct gggatggagc acttcctcct gtgagcccag 60
gggaccgcgc tgcccttga gcttggggca aggagggag agtgatacca ggaagggtgg 120
gctgcagcca ggggccagag tcagttcagg gagtggctct cggccctcaa agctcctccg 180
gggactgctc aggagtgat gtgccctgga gtttcccca acttccttg ccacctgga 240
agggtgcttg ctgctccagg cctctaggct gggctgatgg gtttctccag gacacaagta 300
tcattaaagc caccctctcc tcagcttgct aggccgcaca tgtgggacag gctgtgtctc 360
caacccctc gcctgccctg ccctccatca ggaggagcca gtggaacctt cggaaagctc 420
ccagcatctc agcagccctc aaaagtcgtc ctggggcaag ctctggttct cctgactgga 480
ggtcatctgg gcttggcctg ctctctctcg c 511

<210> 65
<211> 394
<212> DNA
<213> Homo sapiens

<400> 65
taaaaaagt taacaaagg ttatttagac tttcttcatg cccccagatc caggatgtct 60
atgtaaaccg ttatcttaca aagaaagcac aatatttgg ataaactaag tcagtgaactt 120
gcttaactga aatagcgtcc atccaaaagt gggtttaagg taaaactacc tgacgatatt 180
ggcggggatc ctgcagtttg gactgcttgc cgggtttgtc cagggttccg ggtctgttct 240
tggcactcat ggggacaggc atcctgctcg tctgtggggc cccgctggag cccttaactg 300
aagctgaagg tatcgaccst agggggctct agggcagtgg gaccttcac cggaaactaac 360
aagggtcggg gagaggcctc ttgggctatg tggg 394

<210> 66

<211> 359
<212> DNA
<213> Homo sapiens

<400> 66
caagcggttcc tttatggatg taaattcaaa cagtcatgct gagccatccc gggctgacag 60
tcacgttwaa gacactaggt cgggcgccac agtgccaccc aaggagaaga agaatttgga 120
atttttccat gaagatgtac ggaaatctga tgttgaatat gaaaatggcc cccaaatgga 180
attccaaaag gttaccacag gggctgtaag acctagtac cctcctaagt gggaaagagg 240
aatggagaat agtatttctg atgcatcaag aacatcagaa tataaaactg agatcataat 300
gaaggaaaat tccatatcca atatgagttt actcagagac agtagaaact attcccagg 359

<210> 67
<211> 450
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 425
<223> n = A, T, C or G

<400> 67
taggaataac aaatgtttat tcagaaatgg ataagtaata cataatcacc cttcatctct 60
taatgccctt tcctctcctt ctgcacagga gacacagatg ggtaacatag aggcattggga 120
agtggaggag gacacaggac tagcccacca ccttctcttc ccggtctccc aagatgactg 180
cttatagagt ggaggaggca aacagggtccc ctcaatgtac cagatgggtca cctatagcac 240
cagctccaga tggccacgtg gttgcagctg gactcaatga aactctgtga caaccagaag 300
atacctgctt tgggatgaga gggaggataa agccatgcag ggaggatatt taccatccct 360
accctaagca cagtgcgaagc agtgagcccc cggtccccag tacctgaaaa accaaggcct 420
actgnctttt ggatgctctc ttgggccacg 450

<210> 68
<211> 511
<212> DNA
<213> Homo sapiens

<400> 68
aagcctcctg ccctggaaat ctggagcccc ttggagctga gctggacggg gcaggaggagg 60
gctgagaggc aagaccgtct ccctcctgct gcagctgctt cccagcagc cactgctggg 120
cacagcagaa acgccagcag agaaaatggg agccgagagt ccttagccct ggagctgagg 180
ctgectctgg gctgacccgc tggctgtacg tggccagaac tggggttggc atctggcatc 240
catttgaggc caggggtggg gaaagggagg ccaacagagg aaaacctatt cctgctgtga 300
caacacagcc cttgtccac gcagcctaag tgcagggagc gtgatgaagt caggcagcca 360
gtcggggagg acgaggtaac tcagcagcaa tgtcaccttg tagcctatgc gctcaatggc 420
ccggaggggc agcaaccccc cgcacacgtc agccaacagc agtgcctctg caggcaccaa 480
gagagcgatg atggacttga gcgcctgtgt c 511

<210> 69
<211> 511
<212> DNA
<213> Homo sapiens

<400> 69
gtttggcaga agacatgttt aataacattt tcatatttaa aaaatacagc aacaattctc 60
tatctgtcca ccattctgcc ttgcccttcc tggggctgag gcagacaaag gaaaggtaat 120
gaggttaggc cccccaggcg ggctaagtgc tattggcctg ctctgctca aagagagcca 180
tagccagctg ggcacggccc cctagccctt ccaggttgct gagcgggcag cggtggtaga 240

```

gttcttctact gagccgtggg ctgcagtctc gcaggagaa cttctgcacc agccctggct 300
ctacggcccg aaagaggtgg agccctgaga accggaggaa aacatccatc acctccagcc 360
cctccagggc ttcctcctct tcctggcctg ccagttcacc tgccagccgg gctcggggcg 420
ccaggtagtc agcgtttag aagcagccct ccgcagaagc ctgccggtca aatctccccg 480
ctataggagc cccccgggag gggtcagcac c 511

```

```

<210> 70
<211> 511
<212> DNA
<213> Homo sapiens

```

```

<400> 70
caagttgaac gtcaggcttg gcagaggtgg agttagatg aaaacaaagg tgtgattatg 60
aagaggatgt gagtcctttg ggtgtaggag agaaaggctg ttgagcttct atttcaagat 120
acttttacct gtgcaaaaag cacattttcc acctccttct catggcattt gtgtaagggtg 180
agtatgattc ctattccatc tgcattttag aggtgaagaa taacgtacaa gggattcagt 240
gattagcaag ggaccctca ctaagtgttg atggagttag gacagagctc agctgtttga 300
atctcagagc ccaggcagct ggagctgggt aggtaccttg agctggcact aatgtgaggt 360
gcattccctc caaccaggc tcagatccgg aacctgaccg tgctgacccc cgaaggggag 420
gcagggtgta gctggcccg tgggctccct gctcctttca caccacactc tcgctttgag 480
gtgctgggct gggactactt cacagagcag c 511

```

```

<210> 71
<211> 511
<212> DNA
<213> Homo sapiens

```

```

<400> 71
tggcctgggc aggattgga gagaggtagc taccggatg cagtcctttg ggatgaagac 60
tatagggtat gaccccatca tttcccaga ggtctcgcc tcctttggtg ttcagcagct 120
gcccctggag gagatctggc ctctctgtga tttcatcact gtgcacactc ctctctgcc 180
ctccacgaca ggcttgctga atgacaacac ctttgcccag tgcaagaagg ggggtgcgtg 240
ggtgaactgt gcccggtgag ggatcgtgga cgaaggcgcc ctgctccggg ccctgcagtc 300
tggccagtgt gccggggctg cactggacgt gtttacggaa gagccgccac gggaccgggc 360
cttggtggac catgagaatg tcacagctg tccccacctg ggtgccagca ccaaggaggc 420
tcagagccgc tgtggggag aaattgctgt tcagtctgt gacatggtga aggggaaatc 480
tctcacgggg gttgtgaatg ccagggccct t 511

```

```

<210> 72
<211> 2017
<212> DNA
<213> Homo sapiens

```

```

<400> 72
agccagatgg ctgagagctg caagaagaag tcaggatcat gatggctcag tttcccacag 60
cgatgaatgg agggccaaat atgtgggcta ttacatctga agaacgtact aagcatgata 120
aacagtttga taacctcaaa ccttcaggag gttacataac aggtgatcaa gcccgtaatt 180
tttctctaca gtcaggctcg ccggccccg ttttagctga aatatgggce ttatcagatc 240
tgaacaagga tgggaagatg gaccagcaag agttctctat agctatgaaa ctcatcaagt 300
taaagttgca gggccaacag ctgcctgtag tcctccctcc tatcatgaaa caaccctcta 360
tgttctctcc actaatctct gctcgttttg ggatgggaag catgccaat ctgtccattc 420
atcagccatt gcctccagtt gcacctatag caacaccctt gtcttctgct acttcaggga 480
ccagtattcc tcccctaatt atgcctgctc ccctagtgcc ttctgttagt acatcctcat 540
taccaaatgg aactgccagt ctcatcagc ctttatccat tccttattct tcttcaacat 600
tgctcatgc atcatcttac agcctgatga tgggaggatt tgggtgtgct agtatccaga 660
aggcccagtc tctgattgat ttaggatcta gtagctcaac ttctcaact gcttccctct 720
cagggaaact acctaagaca gggacctcag agtgggcagt tcctcagcct tcaagattaa 780
agtatcggca aaaatttaat agtctagaca aaggcatgag cggatacctc tcaggttttc 840

```

```

aagctagaaa tgccttctt cagtcaaate tctctcaaac tcagctagct actatttggg 900
ctctggctga catcgatggt gacggacagt tgaaagctga agaattttatt ctggcgatgc 960
acctcactga catggccaaa gctggacagc cactaccact gacgttgccct cccgagcttg 1020
tccctccatc tttcagaggg ggaaagcaag ttgattctgt taatggaact ctgccttcat 1080
atcagaaaaa acaagaagaa gagcctcaga agaaactgcc agttactttt gaggacaaa 1140
ggaaagccaa ctatgaacga ggaaacatgg agctggagaa gcgacgccaa gtgttgatgg 1200
agcagcagca gaggggaggct gaacgcaaag cccagaaaga gaaggaagag tgggagcgga 1260
aacagagaga actgcaagag caagaatgga agaagcagct ggagttggag aaacgcttg 1320
agaaacagag agagctggag agacagcggg aggaagagag gagaaaggag atagaaagac 1380
gagaggcagc aaaacaggag cttgagagac aacgccgttt agaatgggaa agactccgtc 1440
ggcaggagct gctcagtcag aagaccaggg aacaagaaga cattgtcagj ctgagctcca 1500
gaaagaaaaa tctccacctg gaactggaag cagtgaatgg aaaacatcag cagatctcag 1560
gcagactaca agatgtccaa atcagaaagc aaacacaaaa gactgagcta gaagttttgg 1620
ataaacagtg tgacctggaa attatggaaa tcaaacaaact tcaacaagag cttaaggaat 1680
atcaaaataa gcttatctat ctggtccctg agaagcagct attaaacgaa agaattaaaa 1740
acatgcagct cagtaacaca cctgattcag ggatcagttt acttcataaa aagtcacag 1800
aaaaggaaga attatgccaa agacttaag aacaattaga tgctcttgaa aaagaaactg 1860
catctaagct ctcagaaatg gattcattta acaatcagct gaaggaactc agagaaagct 1920
ataatacaca gcagttagcc cttgaacaac ttcataaaat caaacgtgac aaattgaagg 1980
aaatcgaaag aaaaagatta gagcaaaaaa aaaaaaa 2017

```

<210> 73

<211> 414

<212> DNA

<213> Homo sapiens

<400> 73

```

atggcagtg cattcaccat catgggaacc accttccctt ttcttcagga ttctctgtag 60
tggaagagag caccagtggt tgggtgaaa acatctgaaa gtagggagaa gaacctaaaa 120
taatcagtat ctcagagggc tctaaggtgc caagaagtct cactggacat ttaagtcca 180
acaaaggcat actttcggaa tcgccaaagtc aaaactttct aacttctgtc tctctcagag 240
acaagtgaga ctcaagagtc tactgcttta gtggcaacta cagaaaactg gtgttaccca 300
gaaaaacagg agcaattaga aatggttcca atatttcaaa gctccgcaaa caggatgtgc 360
tttcccttgc ccatttaggg tttcttctct ttcctttctc tttattaacc acta 414

```

<210> 74

<211> 1567

<212> DNA

<213> Homo sapiens

<400> 74

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atatctagaa gtctggagtg agcaacaag agcaagaac aaaaagaagc caaaagcaga 60
aggctccaat atgaacaaga taaatctatc ttcaaagaca tattagaagt tgggaaaata 120
attcatgtga actagacaag tgtgttaaga gtgataagta aaatgcacgt ggagacaagt 180
gcatccccag atctcaggga cctccccctg cctgtcacct ggggagtgag aggacaggat 240
agtgcagtggt ctttgtctct gaatttttag ttatatgtgc tgtaatgttg ctctgaggaa 300
gcccctggaa agtctatccc aacatatcca catcttatat tccacaaatt aagctgtagt 360
atgtacccta agacgtgct aattgactgc cacttcgcaa ctcaggggag gctgcatttt 420
agtaatgggt caaatgattc actttttatg atgcttccaa aggtgccttg gcttctcttc 480
ccaactgaca aatgccaaag ttgagaaaaa tgatcataat tttagcataa acagagcagt 540
cggcgacacc gattttataa ataaactgag caccttcttt ttaaacaac aaatgcgggt 600
ttattttctc gatgatgttc atccgtgaat ggtccaggga aggaccttct accttgacta 660
tatggcatta tgtcatcaca agctctgagg cttctccttt ccatcctgag tggacagcta 720
agacctcagt tttcaatagc atctagagca gtgggactca gctggggtga tttcgcccc 780
catctccggg ggaatgtctg aagacaattt tgttacctca atgagggagt ggagaggat 840
acagtgtctac taccaactag tggataaagg ccagggatgc tgctcaacct cctaccatgt 900
acaggacgtc tccccattac aactacccaa tccgaagtgt caactgtgtc aggactaaga 960
aaccctggtt ttgagtagaa aagggccttg aaagagggga gccacaacaa ctgtctgtct 1020

```

```

cctcacatta gtcattggca aataagcatt ctgtctcttt ggctgctgcc tcagcacaga 1080
gagccagaac tctatcgggc accaggataa catctctcag tgaacagagt tgacaaggcc 1140
tatgggaaat gcctgatggg attatcttca gcttggtgag cttctaagtt tctttccctt 1200
cattctaccc tgcaagccaa gttctgtaag agaaatgcct gagttctagc tcagggttttc 1260
ttactctgaa tttagatctc cagacccttc ctggccacaa ttcaaattaa ggcaacaaac 1320
atataccttc catgaagcac acacagactt ttgaaagcaa ggacaatgac tgcttgaatt 1380
gaggccttga ggaatgaagc tttgaaggaa aagaataactt tgtttccagc ccccttccca 1440
cactcttcat gtgttaacca ctgccttctt ggaccttgga gccacgggtga ctgtattaca 1500
tgttgttata gaaaactgat tttagagttc tgatcgttca agagaatgat taaatataca 1560
tttctta                                     1567

```

<210> 75
 <211> 240
 <212> DNA
 <213> Homo sapiens

```

<400> 75
tcgagcggcc gcccgggcag gtccttcaga cttggactgt gtcacactgc caggcttcca 60
gggctccaac ttgcagacgg cctgttgtgg gacagtctct gtaatcgcg aagcaaccat 120
ggaagacctg ggggaaaaca ccatggtttt atccaccctg agatctttga acaacttcat 180
ctctcagcgt gcggaggagg gctctggact ggatatttct acctcggccg cgaccacgct 240

```

<210> 76
 <211> 330
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 288
 <223> n = A,T,C or G

```

<400> 76
tagcgyggtc gcgcccgagg yctgcttytc tgtccagccc agggcctgtg gggtcagggc 60
ggtgggtgca gatggcatcc actccgggtg cttcccatc tttctctggc ctgagcaagg 120
tcagcctgca gccagagtac agagggccaa cactgggtgt cttgaacaag ggccttagca 180
ggcctgaag grcctctct gtagtgttga acttcctgga gccaggccac atgttctcct 240
cataccgcag gytagygatg gtgaagttga gggtgaaata gtattmangr agatggctgg 300
caracctgcc cgggcggccg ctcsaatcc                                     330

```

<210> 77
 <211> 361
 <212> DNA
 <213> Homo sapiens

```

<400> 77
agcgtggtcg cggccgaggt gtccttcagg gtctgtttat gcccttggtc aagaacacca 60
gtgtcagctc tctgtactct gggtgcagac tgaccttgct caggcctgag aaggatgggg 120
cagccaccag agtggatgct gtctgcaccc atcgtctctga ccccaaaagc cctggactgg 180
acagagagcg gctgtactgg aagctgagcc agctgaccca cggcactact gagctggggc 240
cctacaccct ggacagggac agtctctatg tcaatggttt caccatcgag agctctgtac 300
ccaccaccag caccgggggtg gtcagcgagg agccattcaa cctgcccggg cggccgctcg 360
a                                     361

```

<210> 78
 <211> 356
 <212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 7, 346, 350, 353

<223> n = A,T,C or G

<400> 78

```

ttggggnnttt mgagcggccg cccgggcagg taccggggtg gtcagcgagg agccattcac 60
actgaacttc accatcaaca acctgcggta tgaggagaac atgcagcacc ctgggtccag 120
gaagttcaac accacggaga gggtccttca gggcctgctc aggtccctgt tcaagagcac 180
cagtgttggc cctctgtact ctggctgcag actgactttg ctcagacttg agaaacatgg 240
ggcagccact ggagtggacg ccatctgcac cctccgcctt gatcccaactg gtcctggact 300
ggacagagag cggctatact gggagctgag ccagtcctct ggcggngacn ccnctt 356

```

<210> 79

<211> 226

<212> DNA

<213> Homo sapiens

<400> 79

```

agcgtggctcg cggccgaggt ccagtcgcag catgctcttt ctctgcccc ctggcacagt 60
gaggaagatc tctgctgtca gtgagaaggc tgtcatccac tgagatggca gtcaaaagtg 120
catttaatac acctaacgta tcgaacatca tagcttggcc caggttatct catatgtgct 180
cagaacactt acaatagcct gcagacctgc ccgggcggcc gctcga 226

```

<210> 80

<211> 444

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 23

<223> n = A,T,C or G

<400> 80

```

tgtggtgttg aacttctctg agncagggtg acccatgtcc tccccatact gcaggtttgt 60
gatggtgaag ttgagggtga atggtaccag gagagggcca gcagccataa ttgtsgrgck 120
gsmgmssgag gmwggwgtty cwgaggttcy rarrtccact gtggaggtcc caggagtgtc 180
ggtggtgggc acagagstcy gatgggtgaa accattgaca tagagactgt tcctgtccag 240
ggtgtagggg cccagctctt yratgycatt ggycagttkg ctyagctccc agtacagccr 300
ctctckgyyg mgwccagsgc ttttggggc aagatgatgg atgcagatgg catccactcc 360
agtggctgct ccatccttct cggacctgag agaggtcagt ctgcagccag agtacagagg 420
gccaacactg gtgttctttg aata 444

```

<210> 81

<211> 310

<212> DNA

<213> Homo sapiens

<400> 81

```

tcgagcggcc gcccgggcag gtcaggaagc acattggtct tagagccact gcctcctgga 60
ttccacctgt gctgcggaca tctccaggga gtgcagaagg gaagcaggtc aaactgctca 120
gatcagtcag actggctgtt ctcagttctc acctgagcaa ggtcagctctg cagccagagt 180
acagagggcc aacactggtg ttcttgaaca agggcttgag cagacctgc agaaccctct 240
tccgtggtgt tgaacttcct ggaaaccagg gtgttgcagt ttttctctca taatgcaagg 300
ttggtgatgg 310

```

<210> 82
<211> 571
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 202
<223> n = A,T,C or G

<400> 82
acgggtttcaa tggacacttt tattgtttac ttaatggatc atcaattttg tctcactacc 60
tacaaatgga atttcatctt gtttccatgc tgagtagtga aacagtgaca aagctaataca 120
taataacctta catcaaaaga gaactaagct aacactgctc actttctttt taacaggcaa 180
aatataaata tatgcaactct anaatgcaca atggtttagt cactaaaaaa ttcaaattggg 240
atcttgaaga atgtatgcaa atccagggtg cagtgaagat gagctgagat gctgtgcaac 300
tgtttaaggg ttcttgccac tgcactctct ggccactagc tgaatcttga catggaaggt 360
tttagctaata gccaaagtga gatgcagaaa atgctaagtt gacttagggg ctgtgcacag 420
gaactaaaag gcaggaaagt actaaatatt gctgagagca tccaccccag gaaggacttt 480
accttccagg agctccaaac tggcaccacc cccagtgtct acatggctga ctttatcctc 540
cgtgttccat ttggcacagc aagtggcagt g 571

<210> 83
<211> 551
<212> DNA
<213> Homo sapiens

<400> 83
aaggctgggt ggtttttgat cctgctggag aacctccgct ttcattgtga ggaagaaggg 60
aagggaagaag atgcttcttg gaacaagggt aaagccgagc cagccaaaat agaagctttc 120
cgagcttcac ttccaagct aggggatgtc tatgtcaatg atgcttttgg cactgctcac 180
agagccacaca gctccatggt agggatcaat ctgccacaga aggctgggtg gtttttgatg 240
aagaaggagc tgaactactt tgcaaaaggc ttggagagcc cagagcgacc cttcctggcc 300
atcctgggcg gagctaaagt tgcaagacaag atccagctca tcaataatat gctggacaaa 360
gtcaatgaga tgattatttg tgggtggaatg gcttttacct tccttaaggt gctcaacaac 420
atggagattg gcacttctct gtttgatgaa gagggagcca agattgtcaa agacctaattg 480
tccaaagctg agaagaatgg tgtgaagatt acctgcctg ttgactttgt cactgctgac 540
aagtttgatg a 551

<210> 84
<211> 571
<212> DNA
<213> Homo sapiens

<400> 84
tttgttctt acatttttct aaagagttac ttaaatacagt caactgggtct ttgagactct 60
taagttctga ttccaactta gctaattcat tctgagaact gtggtatagg tggcgtgtct 120
cttctagctg ggacaaaagt tctttgtttt cccctgtag agtatcacag accttctgct 180
gaagctggac ctctgtctgg gcttggact cccaaatctg cttgtcatgt tcaagcctgg 240
aaatgttaat ctttaattct tccatatgga tggacatctg tctaagttga tccttttagaa 300
cactgcaatt atcttctttg agtctaattt cttcttcttt gctttgaatc gcataactaa 360
acttctctc ccaatttctta gcttcatcta tcacctgtc acgatcatcc tggagggaag 420
acatgctctt agtaaaggct gcaagctggg tcacagtact gtccaagttt tcctgaagtt 480
gctgaacttc cttgtctttc ttgttcaaag taacctgaat ctctccaatt gtctcttcca 540
agtggacttt ttctctgcgc aaagcatcca g 571

<210> 85

<211> 561
 <212> DNA
 <213> Homo sapiens

<400> 85
 tcattgcctg tgatggcatc tggaatgtga tgagcagcca ggaagttgta gatttcattc 60
 aatcaaagga ttcagcatgt ggtggaagct gtgaggcaag agaaacaaga actgtatggc 120
 aagttaagaa gcacagagggc aaacaagaag gagacagaaa agcagttgca ggaagctgag 180
 caagaaatgg aggaatgaa agaaaagatg agaaagtttg ctaaatctaa acagcagaaa 240
 atcctagagc tggaagaaga gaatgaccgg cttagggcag aggtgcaccc tgcaggagat 300
 acagctaaaag agtgtatgga aacacttctt tcttccaatg ccagcatgaa ggaagaactt 360
 gaaaggggtca aaatggagta tgaaaccctt tctaagaagt ttcagtcttt aatgtctgag 420
 aaagactctc taagtgaaga ggttcaagat ttaaagcatc agatagaagg taatgtatct 480
 aaacaagcta acctagaggg caccgagaaa catgataacc aaacgaatgt cactgaagag 540
 ggaacacagt ctataccagg t 561

<210> 86
 <211> 795
 <212> DNA
 <213> Homo sapiens

<400> 86
 aagccaataa tcaccattta ttacttaata tatgccaaacc actgtacttg gcagttcaca 60
 aattctcacc gttacaacaa ccccatgagg tatattattcc cattctatag atagggaaac 120
 cacagctcaa gtaagttagg aaactgagcc aagtatacac agaatacga gtggaacaaac 180
 tagaaggaaa gactgacact gctatctgct ggccctccagt gtccctggctc ttttcacacg 240
 ggttcaatgt ctccagcgct gctgctgctg ctgcattacc atgccctcat tgtttttctt 300
 cctctgggtg tcaactgcat ccttcaaaga atctaactca ttccagagac cacttatttc 360
 tttctctctt tctgaaatta cttttaataa ttcttcatga gggggaaaag aagatgcctg 420
 ttggtagttt tggtgtttaa gctgctcaat ttgggactta aacaatttgt tttcatcttg 480
 tacatcctgt aacagctgtg ttttgctaga aagatcactc tccctctctt ttagcatggc 540
 ttctaacctc ttcaattcat tttccttttc tttcaacaca atctcaagtt cttcaaactg 600
 tgatgcagaa gaggcctctt tcaagttatg ttgtgctact tcctgaacat gtgcttttaa 660
 agattcattt tcttcttgaa gatcctgtaa ccacttccct gtattggcta ggtctttctc 720
 tttctcttcc aaaacagcct tcatgggtatt catctgttcc tcttttctt ttaataagtt 780
 caggagcttc agaac 795

<210> 87
 <211> 594
 <212> DNA
 <213> Homo sapiens

<400> 87
 caagcttttt tttttttttt aaaaagtgtt agcattaatg ttttattgtc acgcagatgg 60
 caactgggtt tatgtcttca tattttatat ttttgtaaatt taaaaaaatt acaagtttta 120
 aatagccaat ggctggttat attttcagaa aacatgatta gactaattca ttaatgggtg 180
 cttcaagctt ttccttattg gctccagaaa attcaccac cttttgtccc ttcttaaaaa 240
 actggaatgt tggcatgcat ttgacttcac actctgaagc aacatcctga cagtcatcca 300
 catctacttc aaggaatata acgttggaat acttttcaga gaggggaatga aagaaaggct 360
 tgatcatttt gcaaggccca caccacgtgg ctgagaagtc aactactaca agtttatcac 420
 ctgcagcgtc caaggcttcc tgaaaagcag tcttgctctc gatctgcttc accatcttgg 480
 ctgctggagt ctgacgagcg gctgtaagga ccgatggaaa tggatccaaa gcaccaaaca 540
 gagcttcaag actcgtgctt tggtttgaat tcggatccga tatcgccatg gcct 594

<210> 88
 <211> 557
 <212> DNA
 <213> Homo sapiens

<400> 88

```

aagtgttagc attaatgttt tattgtcacg cagatggcaa ctgggtttat gtcttcatat 60
tttatatatt tgtaaattaa aaaaattmca agttttaaat agccaatggc tggttatatt 120
ttcagaaaac atgattagac taattcatta atggtggctt caagcttttc cttattggct 180
ccagaaaatt caccacactt ttgtcccttc ttaaaaaact ggaatgttgg catgcatttg 240
acttcacact ctgaagcaac atcctgacag tcatccacat ctacttcaag gaatatcacg 300
ttggaatact tttcagagag ggaatgaaag aaaggcttga tcattttgca aggcccacac 360
cacgtggctg agaagtcaac tactacaagt ttatcacctg cagcgtccaa ggcttcctga 420
aaagcagtct tgctctcgat ctgcttcacc atcttggctg ctggagtctg acgagcggct 480
gtaaggaccg atggaaatgg atccaaagca ccaaacagag cttcaagact cgctgcttgg 540
catgaattcg gatccga
557

```

<210> 89

<211> 561

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 544, 551

<223> n = A,T,C or G

<400> 89

```

tacaaccttt attgaaacgc acacgcgcac acacacaaac acccctgttg atagggaana 60
gcacctggcc acaggggtcca ctgaaacggg gaggggatgg cagcttgtaa tgtggctttt 120
gccacaaccc ccttctgaca gggaaggcct tagattgagg cccacactcc catggtgatg 180
gggagctcag aatgggggtcc agggagaatt tggttagggg gaggtgctag ggagggcatga 240
gcagagggga ccctccgagt ggggtcccga gggctgcaga gtcttcagta ctgtccctca 300
cagcagctgt ctcaaggctg ggtccctcaa aggggcgtcc cagcgcgggg cctccctgcg 360
caaacaactg gtacccttgg ctgcgacgag gaagccagca ggacagcagt ggcgcccagc 420
agcacaacag acgcccctgg ggtagggaca gcaggcccag ccctgtcggg tgtctcgga 480
gcaggtcttg ttatcatggc agaagtgtcc tcccacact tcacgtcctt cacaccacg 540
tganggetac nggccaggaa g
561

```

<210> 90

<211> 561

<212> DNA

<213> Homo sapiens

<400> 90

```

cccgtgggtg ccatccacgg agttgttacc tgatcttttg aagcaggatc gcccgctctg 60
actgcagtg aagccccgtg ggcagcagtg atggccatcc ccgcatgcca cggcctctgg 120
gaaggggcag caactggaag tccctgagac ggtaaagatg caggagtggc cggcagagca 180
gtgggcatca acctggcagg ggccaccag atgcctgctc agtgttggg gccatttgtc 240
cagaagggga cggcagcagc tgtagctggc tcctccgggg tccaggcagc aggccacagg 300
gcagaactga ccatctgggc accgcgttcc agccaccagc cctgctgtta aggccaccca 360
gtcaccagg gtccacatgg tctgctgctg tccgactccg cgttccttgg gccctgatgg 420
ttctacctgc tgtgagctgc ccagtgggaa gtatggctgc tgccaatgcc caacgccacc 480
tgctgctccg atcacctgca ctgctgccc aagacactgt gtgtgacctg atccagagta 540
agtgcctctc caaggagaac g
561

```

<210> 91

<211> 541

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature
 <222> 480, 491
 <223> n = A,T,C or G

<400> 91
 gaatcacctt tctggtttag ctagtacttt gtacagaaca atgaggtttc ccacagcgga 60
 gtctccctgg gctctgtttg gctctcggtt aggcaggcct acaccttttc ctctcctcta 120
 tggagagggg aatatgcatt aaggtgaaaa gtcaccttcc aaaagtgaga aagggttcg 180
 attgctgctt caggactgtg gaattatattg gaattgtttta caaatggttg ctacaaaaca 240
 acaaaaaagg taattacaaa atgtgtacat cacaacatgc tttttaaaga cattatgcat 300
 tgtgtcaca ttcccttaaa tgtgtttcc aaaggtgctc agcctctagc ccagctggat 360
 tctccgggaa gaggcagaga cagtttggcg aaaaagacac agggaaggag ggggtggtga 420
 aaggagaaag cagccttcca gttaaagatc agccctcagt taaaggtcag cttcccgcan 480
 gctggcctca ngcggagtct gggtcagagg gaggagcagc agcagggtgg gactggggcg 540
 t 541

<210> 92
 <211> 551
 <212> DNA
 <213> Homo sapiens

<400> 92
 aaccggagcg cgagcagtag ctgggtgggc accatggctg ggatcaccac catcgaggcg 60
 gtgaagcgca agatccagggt tctgcagcag caggcagatg atgcagagga gcgagctgag 120
 cgctccagc gagaagtga gggagaaagg cgggcccggg aacaggctga ggctgaggtg 180
 gcctccttga accgtaggat ccagctggtt gaagaagagc tggaccgtgc tcaggagcgc 240
 ctggccactg ccctgcaaaa gctggaagaa gctgaaaaag ctgctgatga gagtgagaga 300
 ggtatgaagg ttattgaaaa ccgggcctta aaagatgaag aaaagatgga actccaggaa 360
 atccaactca aagaagctaa gcacattgca gaagaggcag ataggaagta tgaagaggtg 420
 gctcgtaagt tgggtatcat tgaaggagac ttggaacgca cagaggaacg agctgagctg 480
 gcagagtcct gttgccgaga gatggatgag cagattagac tgatggacca gaacctgaag 540
 tgtctgagtg c 551

<210> 93
 <211> 531
 <212> DNA
 <213> Homo sapiens

<400> 93
 gagaacttgg cctttattgt gggcccagga gggcaciaag gtcaggaggc ccaagggagg 60
 gatctggttt tctggatagc caggatcatg catgggtatc agtaggaatc cgctgtagct 120
 gcacaggcct cacttgctgc agttccgggg agaacacctg cactgcatgg cgttgatgac 180
 ctogtggtac acgacagagc cattggtgca gtgcaagggc acgcgcatgg gctccgtcct 240
 cgagggcagg cagcaggagc attgctcctg cacatcctcg atgtcaatgg agtacacagc 300
 tttgctggca cactttccct ggcagtaatg aatgtccact tcctcttggg acttacaatc 360
 tcccactttg atgtactgca ccttggtgtg gatgtctttg caatcaggct cctcacatgt 420
 gtcacagcag gtgcctggaa ttttcacgat tttgcctcct tcagccagac acttgtgttc 480
 atcaaatggt gggcagcccg tgaccctcct ctcccagatg tactctctc t 531

<210> 94
 <211> 531
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 517
 <223> n = A,T,C or G

<400> 94

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gacctggacct tgcgggatca gtgccacaca gtgacttgct tggcaaatgg ccagaccttg 60
ctgcagagtc atcgtgtcaa ttgtgacct ggaccccgcc ctcatgtgc caacagccag 120
tctcctgttc ggggtggagga gacgtgtggc tgccgctgga cctgcccttg tgtgtgcacg 180
ggcagttcca ctcggcacat cgtcaccttc gatgggcaga atttcaagct tactggtagc 240
tgctcctatg tcatctttca aaacaaggag caggacctgg aagtgtcct ccacaatggg 300
gcctgcagcc ccggggcaaa acaagcctgc atgaagtcca ttgagattaa gcatgctggc 360
gtctctgctg agctgcacag taacatggag atggcagtg atgggagact ggtccttgcc 420
ccgtacgttg gtgaaaacat ggaagtcagc atctacggcg ctatcatgta tgaagtcagg 480
tttaccatc ttggccacat cctcacatac accgccncaa aacaacgagt t 531

```

<210> 95

<211> 605

<212> DNA

<213> Homo sapiens

<400> 95

```

agatcaacct ctgctggatca ggaggaatgc cttccttgct ttggatcttt gctttgacgt 60
tctcgatagt rwcaactkk r ytsramskma agkgyratgr wmttksyw gw rasyktmwwm 120
rsgraraytt agacayccm cctcwagagc gsagkaccar gtgcagaggt ggactctttc 180
tggatgttgt agtcagacag ggtgctcca tctccagct gtttcccagc aaagatcaac 240
ctctgctgat caggagggat gccttctta tcttgatct ttgccttgac attctcgatg 300
gtgtcaactg gctccacctc gagggtgatg gtcttaccag tcagggtctt cacgaagaty 360
tgcatccac ctctgagacg gagcaccagg tgcagggtg actctttctg gatgtttag 420
tcagacaggg tgcgyccatc ttccagctgc tttccsagca aagatcaacc tctgctggc 480
aggaggratg ccttcttgt cytgatctt tgcyytgacr ttctcratgg tgtcactcgg 540
ctccacttcg agagtgatgg tcttaccagt cagggtcttc acgaagatct gcatccacc 600
tctaa 605

```

<210> 96

<211> 531

<212> DNA

<213> Homo sapiens

<400> 96

```

aagtcacaaa cagacaaaga ttattaccag ctgcaagcta tattagaagc tgaacgaaga 60
gacagaggtc atgattctga gatgattgga gaccttcaag ctgcaattac atctttacaa 120
gaggaggtga agcatctcaa acataatctc gaaaaagtgg aaggagaaag aaaagaggct 180
caagacatgc ttaatcactc agaaaaggaa aagaataatt tagagataga tttaaactac 240
aaacttaaat cattacaaca acggttagaa caagaggtaa atgaacacaa agtaacacaa 300
gctcgtttta ctgacaaaca tcaatctatt gaagaggcaa agtctgtggc aatgtgtgag 360
atggaaaaaa agctgaaaaga agaaagagaa gctcgagaga aggtgaaaa tcgggttgtt 420
cagattgaga aacagtgttc catgctagac gttgatctga agcaatctca gcagaaacta 480
gaacatttga ctggaaataa agaaaggatg gaggatgaag ttaagaatct a 531

```

<210> 97

<211> 1017

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 963, 995, 1001, 1008, 1010

<223> n = A, T, C or G

<400> 97

```

cgctccacc atgtccatca gggtgaccca gaagtcctac aagggtgtcca cctctggccc 60

```

```

ccgggccttc agcagccgct cctacacgag tgggcccggt tcccgcata gtcctcag 120
cttctcccga gtgggcagca gcaactttcg cgtggcctg ggccggcggt atggtggggc 180
cagcggcatg ggaggcatca ccgcagttac ggtcaaccag agcctgctga gcccccttgt 240
cctggaggtg gacccaaca tccaggccgt gcgcaccag gagaaggagc agatcaagac 300
cctcaacaac aagtttgcct ccttcataga caaggtacgg ttcctggagc agcagaaca 360
gatgctggag accaagtga gctcctgca gcagcagaag acggctcgaa gcaacatgga 420
caacatgttc gagagctaca tcaacarcct taggcggcag ctggagactc tgggccagga 480
gaagctgaag ctggaggcgg agcttgcaa catgcagggg ctggtggagg acttcaagaa 540
caagtatgag gatgagatca ataagcgtac agagatggag aacgaatttg tcctcatcaa 600
gaaggatgtg gatgaagctt acatgaacaa ggtagagctg gagtctcgcc tggagggt 660
gaccgacgag atcaacttcc tcaggcagct gtatgaagag gagatccggg agctgcagtc 720
ccagatctcg gacacatctg tgggtgctgc catggacaac agccgctccc tggacatgga 780
cagcatcatt gctgaggtca aggcacagta cgaggatatt gccaacgca gccgggctga 840
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ggatgacctg cggcgacaaa agactgagat ctctgagatg aaccgggaac atcagcccg 960
ctncaggctg agattgaggg cctcaaaggc caganggctt nctggangn ccgccat 1017

```

<210> 98
 <211> 561
 <212> DNA
 <213> Homo sapiens

```

<400> 98
cccggagcca gccaacgagc ggaaatggc agacaatttt tcgctccatg atgcgttatc 60
tgggtctgga aacccaaacc ctcaaggatg gcctggcgca tgggggaacc agcctgctgg 120
ggcagggggc taccagggg cttcctatcc tggggcctac cccgggcagg ccccccagg 180
ggcttatcct ggacaggcac ctccaggcgc ctaccctgga gcacctggag cttatcccgg 240
agcacctgca cctggagtct acccagggcc acccagcggc cctggggcct acccatcttc 300
tggacagcca agtgccaccg gagcctaccg tgccactggc ccctatggcg cccctgctgg 360
gccactgatt gtgccttata acctgccttt gcctggggga gtggtgcctc gcatgctgat 420
aacaattctg ggcacgggtg agcccaatgc aaacagaatt gctttagatt tccaaagagg 480
gaatgatgtt gccttccact ttaaccacg cttcaatgag aacaacagga gagtcattgg 540
ttgaataca aagctggata a

```

<210> 99
 <211> 636
 <212> DNA
 <213> Homo sapiens

```

<400> 99
gggaatgcaa caactttatt gaaaggaaag tgcaatgaaa tttgttgaaa ccttaaaagg 60
ggaaacttag acaccccccc tcragcgmag kaccargtgc aragggtggac tctttctgga 120
tgttgtagtc agacagggtt cgcwccatctt ccagctgttt yccrgcaaag atcaacctct 180
gctgatcagg aggratgcct tocttatctt ggatctttgc cttgacattc tcgatgggtg 240
cactgggctc cacctcgagg gtgatggtct taccagtcag ggtcttcacg aagatytgca 300
tcccacctct gagacggagc accaggtgca gggtrgactc tttctggatg ttgtagtcag 360
acaggggtgc yccatcttcc agctgcttcc csagcaaaga tcaacctctg ctgggtcagga 420
ggratgcctt ccttgctcytg gatctttgcy ttgacrttct caatgggtgtc actcggctcc 480
acttcgagag tgatggtctt accagtcagg gtcttcacga agatctgcat cccacctcta 540
agacggagca ccaggtgcag ggtggactct ttctggatgg ttgtagtcag acaggggtgcg 600
tccatcttcc agctgtttcc cagcaaagat caacct

```

<210> 100
 <211> 697
 <212> DNA
 <213> Homo sapiens

<400> 100

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aggttgatct ttgctgggaa acagctggaa gatggacgca ccctgtctga ctacaacccat 60
ccagaaagag tccaccctgc acctgggtgct ccgtcttaga ggtgggatgc agatcttcgt 120
gaagaccctg actggttaaga ccatcactct cgaagtggag ccgagtgaca ccattgagaa 180
ygtcaargca aagatccarg acaaggaagg catycctcct gaccagcaga ggttgatctt 240
tgctsggaaa gcagctggaa gatggrogca ccctgtctga ctacaacatc cagaagaggt 300
cyaccctgca cctggtgctc cgtctcagag gtgggatgca ratcttcgtg aagaccctga 360
ctggtaagac catcaccctc gaggtggagc ccagtgcacac catcgagaat gtcaaggcaa 420
agatccaaga taaggaaggc atccctcctg atcagcagag gttgatcttt gctgggaaac 480
agctggaaga tggacgcacc ctgtctgact acaacatcca gaaagagtcc acctytgcac 540
ytggtmctbc gtctyagagg kgggrtgcaa atctwmgtkw agacactcac tkkyaagryy 600
atcamcmwtg akktcgakys castkwact wtcrakaamg tyrwwgcawa gatccmagac 660
aaggaaggca ttcctcctga ccagcagagg ttgatct 697

```

<210> 101

<211> 451

<212> DNA

<213> Homo sapiens

<400> 101

```

atggagtctc actctgtcga ccaggctgga gcgctgtggt gcgatatcgg ctactgcag 60
tctccacttc ctgggttcaa ggcatactcc tgctcagcc tcccgagtag ctgggactac 120
aggcaggcgt caccataatt tttgtatttt tagtagagac atggtttcgc catgttggt 180
gggctgggtct cgaactcctg acctcaagtg atctgtcctg gcctcccaaa gtgttgggat 240
tacaggcgaa agccaacgct cccggccagg gaacaacttt agaatgaagg aaatatgcaa 300
aagaacatca catcaaggat caattaatta ccatctatta attactatat gtgggtaatt 360
atgactatctt cccaagcatt ctacgttgac tgcttgagaa gatgtttgtc ctgcatgggt 420
gagagtggag aagggccagg attcttaggt t 451

```

<210> 102

<211> 571

<212> DNA

<213> Homo sapiens

<400> 102

```

agcgcggtct tccggcgcga gaaagctgaa ggtgatgtgg ccgccctcaa ccgacgcac 60
cagctcggtt agggagggtt ggacagggct caggaaacgac tggccacggc cctgcagaag 120
ctggaggagg cagaaaaagc tgcagatgag agtgagagag gaatgaagg gatagaaaac 180
cgggccatga aggatgagga gaagatggag attcaggaga tgcaactcaa agaggccaa 240
cacattgctg aagaggctga ccgcaaatac gaggaggtag ctcgtaagct ggtcatctg 300
gagggtgagc tggagagggc agaggagcgt gcggagggtg ctgaactaaa atgtggtgac 360
ctggaagaag aactcaagaa tgttactaac aatctgaaat ctctggaggc tgcactgaa 420
aagtattctg aaaaggagga caaatatgaa gaagaaatta aacttctgtc tgacaaactg 480
aaagaggctg agaccctgct tgaatttgca gagagaacgg ttgcaaaact ggaaaagaca 540
attgatgacc tggaaagaaa acttgcccag c 571

```

<210> 103

<211> 451

<212> DNA

<213> Homo sapiens

<400> 103

```

gtgcacaggt cccatttatt gtagaaaata ataataatta cagtgatgaa tagctcttct 60
taaattacaa aacagaaacc acaaagaagg aagaggaaaa accccaggac ttccaagggt 120
gaagctgtcc cctcctccct gccaccctcc caggctcatt agtgtccttg gaaggggag 180
aggactcaga ggggatcagt ctccaggggc cctgggctga agcgggtgag gcagagagtc 240
ctgaggccac agagctgggc aacctgagcc gccctctctg cccctcccc caccactgcc 300
caaactctgt tacagcacct tcgcccctcc cctctaaacc cgtccatcca ctctgcactt 360
cccaggcagg tgggtggggc aggcctcagc catactcctg ggcgcgggtt tcggtgagca 420

```

aggcacagtc ccagagggtga tatcaaggcc t 451

<210> 104
<211> 441
<212> DNA
<213> Homo sapiens

<400> 104
gcaaggaact ggtctgctca cacttgctgg cttgcgcac aggactggct ttatctcctg 60
actcacgggtg caaagggtgca ctctgcgaac gttaagtcct tccccagcgc ttggaatcct 120
acggcccccac cagccggatc ccctcagcct tccaggtcct caactcccgt ggacgctgaa 180
caatggcctc catggggcta caggtaatgg gcatcgcgct ggccgtcctg ggctggctgg 240
ccgtcatgct gtgctgcgcg ctgcccattg ggcgcgtgac ggccttcac ggacgcaaca 300
ttgtcacctc gcagaccatc tgggagggcc tatggatgaa ctgcgtgggtg cagagcaccg 360
gccagatgca gtgcaagggtg tacgactcgc tgctggcact gccgcaggac ctgcaggcgg 420
cccgcgccct cgtcatcatc a 441

<210> 105
<211> 509
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 195
<223> n = A,T,C or G

<400> 105
tgcaaaagggt acacaggggt tcaaaaataa aaattttctt tccccctccc caaacctgta 60
ccccagctcc cgcaccacaa ccccttcct ccccgggga aagcaagaag gagcagggtg 120
ggcatctgca gctgggaaga gagaggcgg ggaggtgcc agctcgggtg tggctctttt 180
ccaaatataa atacntgtgt cagaactgga aaatcctcca gcaaccacca cccaagcaact 240
ctccgttttc tgccgggtgt tggagagggg cggggggcag gggcgccagg caccggctgg 300
ctgcggtcta ctgcatccgc tgggtgtgca ccccgcgagc ctctgctgc tcattgtaga 360
agagatgaca ctcggggtcc ccccggtatg tgggggtcc ctggatcagc ttcccggtgt 420
tgggggttac acaccagcac tccccacgct gcccgttcag agacatcttg cactgtttga 480
ggtgttacag gccatgcttg tcacagttg 509

<210> 106
<211> 571
<212> DNA
<213> Homo sapiens

<400> 106
gggttgagg gactggttct ttatttcaaa aagacacttg tcaatattca gtatcaaaac 60
agttgcacta ttgatttctc tttctcccaa tcggcccaa agagaccaca taaaaggaga 120
gtacatttta agccaataag ctgcaggatg tacacctaac agacctccta gaaaccttac 180
cagaaaatgg ggactgggta ggaaggaaa cttaaaagat caacaaactg ccagcccacg 240
gactgcagag gctgtcacag ccagatgggg tggccagggt gccacaaacc caaagcaaag 300
tttcaaaata atataaaatt taaaaagttt tgtacataag ctattcaaga tttctccagc 360
actgactgat acaaagcaca attgagatgg cacttctaga gacagcagct tcaaaccacg 420
aaaagggtga tgagatgagt ttcacatggc taaatcagtg gcaaaaacac agtcttcttt 480
ctttctttct ttcaaggagg caggaaagca attaagtggt cacctcaaca taagggggac 540
atgatccatt ctgtaagcag ttgtgaaggg g 571

<210> 107
<211> 555
<212> DNA

<213> Homo sapiens

<400> 107

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caggaaccgg agcgcgagca gtagctgggt gggcaccatg gctgggatca ccaccatcga 60
ggcgggtgaag cgcaagatcc aggttctgca gcagcaggca gatgatgcag aggagcgagc 120
tgagcgcctc cagcgagaag ttgagggaga aaggcgggcc cgggaacagg ctgaggctga 180
ggtggcctcc ttgaaccgta ggatccagct ggttgaagaa gagctggacc gtgctcagga 240
gcgcctggcc actgccctgc aaaagctgga agaagctgaa aaagctgctg atgagagtga 300
gagaggtatg aaggttattg aaaaccgggc cttaaaagat gaagaaaaga tggaaactcca 360
ggaaatccaa ctcaagaag ctaagcacat tgcagaagag gcagatagga agtatgaaga 420
ggtggctcgt aagttggtga tcattgaagg agacttgga cgcacagagg aacgagctga 480
gctggcagag tcccgttgcc gagagatgga tgagcagatt agactgatgg accagaacct 540
gaagtgtctg agtgc                                     555

```

<210> 108

<211> 541

<212> DNA

<213> Homo sapiens

<400> 108

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atctacgtca tcaatcaggc tggagacacc atgttcaatc gagctaagct gctcaatatt 60
ggctttcaag aggccttgaa ggactatgat tacaactgct ttgtgttcag tgatgtggac 120
ctcattccga tggacgaccg taatgcctac aggtgttttt cgcagccacg gcacatttct 180
gttgcaatgg acaagttcgg gtttagcctg ccatatgttc agtatttttg aggtgtctct 240
gctctcagta aacaacagtt tcttgccatc aatggattcc ctaataatta ttgggggttg 300
ggaggagaag atgacgacat ttttaacaga ttagttcata aaggcatgtc tatatcacgt 360
ccaaatgctg tagtagggag gtgtcgaatg atccggcatt caagagacaa gaaaaatgag 420
cccaatcctc agaggtttga ccggatcgca catacaaagg aaacgatgcy cttcgatggg 480
ttgaactcac ttacctacaa ggtgttggat gtcagagata cccgttatat acccaaatca 540
c                                     541

```

<210> 109

<211> 411

<212> DNA

<213> Homo sapiens

<400> 109

```

ctagacctct aattaaaagg cacaatcatg ctggagaatg aacagtctga ccccgagggc 60
cacagcgaat tttagggaag gaggcaaaga ggtgagaagg gaaaggaaag aagggaaggaa 120
ggagaacaat aagaactgga gacgttgggt gggtcaggga gtgtggtgga ggctcggaga 180
gatggtaaac aaacctgact gctatgagtt ttcaacccca tagtctaggg ccatgagggc 240
gtcagttctt ggtggctgag ggtccttcca cccagccac ctgggggagt ggagtgggga 300
gttctgccag gtaagcagat gttgtctccc aagttcctga cccagatgtc tggcaggata 360
acgctgacct gttccctcaa caagggaacct gaaagtaatt ttgctcttta c 411

```

<210> 110

<211> 451

<212> DNA

<213> Homo sapiens

<400> 110

```

ccgaattcaa gcgtcaacga tccytccctt accatcaaat caattggcca ccaatggtac 60
tgaacctacg agtacaccga ctacgggcgg actaatcttc aactcctaca tacttcccc 120
attattccta gaaccaggcg acctgcgact ccttgacgtt gacaatcgag tagtactccc 180
gattgaagcc cccattcgta taataattac atcacaagac gtcttgact catgagctgt 240
ccccacatta ggcttaaaaa cagatgcaat tccggacgt ctaagccaaa ccactttcac 300
cgctacacga ccgggggtat actacggtca atgtcttgaa atctgtggag caaaccacag 360
tttcatgccc atcgtcctag aattaattcc cctaaaaatc tttgaaatag ggcccgtatt 420

```


taccctatag caccctctct acccctcta g 451

<210> 111
<211> 541
<212> DNA
<213> Homo sapiens

<400> 111
gctcttcaca cttttattgt taattctctt cacatggcag atacagagct gtcgtcttga 60
agaccaccac tgaccaggaa atgccacttt tacaaaaatca tcccccttt tcatgattgg 120
aacagttttc ctgaccgtct gggagcgttg aagggtgacc agcacatttg cacatgcaaa 180
aaaggagtga cccaaggcc tcaaccacac ttcccagagc tcaccatggg ctgcagggtga 240
cttgccaggt ttgggggtcg tgagctttcc ttgctgctgc ggtggggagg ccctcaagaa 300
ctgagaggcc ggggtatgct tcatgagtgt taacatttac gggacaaaag cgcattatta 360
ggataaggaa cagccacagc acttcatgct tgtgagggtt agctgtagga gcgggtgaaa 420
ggattccagt ttatgaaaat ttaaagcaaa caacggtttt tagctgggtg ggaaacagga 480
aaactgtgat gtcggccaat gaccaccatt tttctgcccc tgtgaaggtc cccatgaaac 540
c 541

<210> 112
<211> 521
<212> DNA
<213> Homo sapiens

<400> 112
caagcgcttg gcgtttggac ccagttcagt gaggttcttg gggtttgtgc ctttggggat 60
tttggtttga cccaggggtc agccttagga aggtcttcag gaggaggccg agttccccct 120
cagtaccacc cctctctccc cactttccct ctcccggcaa catctctggg aatcaacagc 180
atattgacac gttggagccg agcctgaaca tgcccctcgg cccacagaca tggaaaaccc 240
ccttccttgc ctaaggtgtc tgagtttctg gctcttgagg catttccaga cttgaaattc 300
tcatcagtc attgctcttg agtctttgca gagaacctca gatcagggtc acctgggaga 360
aagactttgt cccacttac agatctatct cctcccttgg gaagggcagg gaatggggac 420
ggtgtatgga ggggaaggga tctcctgcgc ccttcattgc cacacttggg gggaccatga 480
acatcttttag tgtctgagct tctcaaatta ctgcaatagg a 521

<210> 113
<211> 568
<212> DNA
<213> Homo sapiens

<400> 113
agcgtcaa at cagaatggaa aagactcaaa accatcatca acaccaagat caaaaggaca 60
agratccttc aagaacacag aaaaaactcc taaaacacca aaaggaccta gttctgtaga 120
agacattaaa gcaaaaatgc aagcaagtat agaaaaaggt gggtctcttc ccaaagtgga 180
agccaaattc atcaattatg tgaagaattg cttccggatg actgaccaag aggcatttca 240
agatctcttg cagtggagga agtctcttta agaaaatagt ttaacaatt tggtaaaaaa 300
ttttccgtct tatttcattt ctgtaacagt tgatatctgg ctgtcctttt tataatgcag 360
agtgagaact ttccctaccg tgtttgataa atgttgtcca ggttctattg ccaagaatgt 420
gttggtccaaa atgocctgtt agtttttaaa gatggaactc caccctttgc ttggttttaa 480
gtatgtatgg aatgttatga taggacatag tagtagcggg ggtcagacat ggaaatgggt 540
ggsmgacaaa aatatacatg tgaaataa 568

<210> 114
<211> 483
<212> DNA
<213> Homo sapiens

<400> 114

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tccgaattcc aagcgaatta tggacaaacg attcctttta gaggattact tttttcaatt 60
tcggtttttag taatctaggc tttgcctgta aagaatacaa cgatggattt taaatactgt 120
ttgtggaatg tgtttaaagg attgattcta gaacctttgt atatttgata gtatttctaa 180
ctttcatttc tttactgttt gcagttaatg ttcattgttct gctatgcaat cgttttatatg 240
cacgtttctt taattttttt agattttcct ggatgtatag tttaaacaac aaaaagtcta 300
tttaaaactg tagcagtagt ttacagttct agcaaagagg aaagttgtgg ggttaaaactt 360
tgtattttct ttcttataga ggcttctaaa aaggtatttt tatatgttct ttttaacaaa 420
tattgtgtac aacctttaaa acatcaatgt ttggatcaaa acaagacca gcttattttc 480
tgc 483

```

<210> 115

<211> 521

<212> DNA

<213> Homo sapiens

<400> 115

```

tgtggtggcg cgggctgagg tggaggccca ggactctgac cctgcccctg ccttcagcaa 60
ggcccccggc agcgccggcc actacgaact gccgtgggtt gaaaaatata ggccagtaaa 120
gctgaatgaa attgtcgga atgaagacac cgtgagcagg ctagaggctt ttgcaaggga 180
aggaaatgtg cccaacatca tcattgcggg cctccagga accggcaaga ccacaagcat 240
tctgtgcttg gcccgggccc tgctgggccc agcactcaaa gatgccatgt tggaaactcaa 300
tgcttcaaat gacaggggca ttgacgttgt gaggaataaa attaaaatgt ttgctcaaca 360
aaaagtcact cttcccaaag gccgacataa gatcatcatt ctggatgaag cagacagcat 420
gaccgacgga gcccgacaag ccttgaggag aaccatggaa atctactcta aaaccactcg 480
ttcgcccttg cttgtaatgc ttcggataag atcatcgagc c 521

```

<210> 116

<211> 501

<212> DNA

<213> Homo sapiens

<400> 116

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ctttgcaaag cttttatttc atgtctgcgg catggaatcc acctgcacat ggcatcttag 60
ctgtgaagga gaaagcagtg cacgagaagg aatgagtggg cggaaccaac ggccctccaca 120
agctgccttc cagcagcctg ccaaggccat ggagagaga gactgcaaac aaacacaagc 180
aaacagagtc tcttcacagc tggagtctga aagctcatag tggcatgtgt gaatctgaca 240
aaattaaaag tgtgcatagt ccattacatg cataaaacac taataataat cctgtttaca 300
cgtgactgca gcaggcaggt ccagctccac cactgccctc ctgccacatc acatcaagtg 360
ccatggttta gaggttttt catatgtaat tcttttattc tgtaaaaggt aacaaaatat 420
acagaacaaa actttccctt tttaaaacta atgttacaaa tctgtattat cacttgata 480
taaatagtat ataagctgat c 501

```

<210> 117

<211> 451

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 320

<223> n = A,T,C or G

<400> 117

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caagggatat atgttgaggg tacrgrgtga cactgaacag atcacaaagc acgagaaaca 60
ttagttctct cctcccccag cgtctccttc gtctccctgg tttccgatg tccacagagt 120
gagattgtcc ctaagtaact gcatgatcag agtgctgkct ttataagact cttcattcag 180
cgtatccaat tcagcaattg cttcatcaaa tgccgttttt gccaggctac aggccttttc 240
aggagagttt agaattctcat agtaaaagac tgagaaattt agtgccagac caagacgaat 300

```

tggtgtgtga ggctgcattn ctttcttact aatttcaaat gcttcctggt aagcctgctg 360
ggagtctgac acaagtgggt tgtttgttgc tccagatgcc acttcagaaa gatacctaaa 420
ataatctcct ttcattttca aagtagaaca c 451

<210> 118

<211> 501

<212> DNA

<213> Homo sapiens

<400> 118

tccggagccg gggtagtcgc cgccgccgcc gccggtgcag ccaactgcagg caccgctgcc 60
gccgcctgag tagtgggctt aggaaggaag aggtcatctc gtcgagagct tcgctcggaa 120
gggtctttgt tccctgcagc cctcccacgg gaatgacaat ggataaaaagt gagctggtag 180
agaaaagccaa actcgcgtgag caggctgagc gatatgatga tatggctgca gccatgagg 240
cagtacaga acaggggcat gaactctcca acgaagagag aaatctgctc tctgttgctt 300
acaagaatgt ggtaaggccg cccgccgctc ttctggcgt gtcactctcca gcattgagca 360
gaaaacagag aggaatgaga agaagcagca gatgggcaaa gaggaccgtg agaagataga 420
ggcagaactg caggacatct gcaatgatgt tctggagctt gttggacaaa tatcttattc 480
caatgtaca caaccagaa a 501

<210> 119

<211> 391

<212> DNA

<213> Homo sapiens

<400> 119

aaaaagcagc argttcaaca caaaatagaa atctcaaagt taggatagaa caaaaccaag 60
tgtgtgaggg gggaaagcaac agcaaaagga agaatgaga tgttgcaaaa aagatggagg 120
agggttcccc tctcctctgg ggactgactc aaacactgat gtggcagtat acaccattcc 180
agagtcaggg gtgttcattc ttttttggga gtaagaaaag gtggggatta agaagacgtt 240
tctggaggct tagggaccaa ggctggctc tttccccct cccaaccccc ttgatccctt 300
tctctgatca ggggaaagga gctcgaatga gggaggtaga gttggaaaagg gaaaggattc 360
cacttgacag aatgggacag actccttccc a 391

<210> 120

<211> 421

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 409

<223> n = A,T,C or G

<400> 120

tggcaatagc acagccatcc aggagctctt cargcgcac tcggagcagt tcaactgcat 60
gttccgccgg aaggccttcc tccactggta cacaggcgag ggcattggag agatggagtt 120
caccgaggct gagagcaaca tgaacgacct cgtctctgag tatcaagcag taccaggatg 180
ccaccgcaga agaggaggag gatttcggtg aggaggccga agaggaggcc taaggcagag 240
ccccatcac ctcaggcttc tcagttccct tagccgtctt actcaactgc ccctttctc 300
tccctcagaa tttgtgtttg ctgcctctat cttgtttttt gttttttctt ctgggggggt 360
ctagaacagt gcctggcaca tagtaggcgc tcaataaata cttggttgnt gaatgtctcc 420
t 421

<210> 121

<211> 206

<212> DNA

<213> Homo sapiens

<400> 121

```
agctggcgct agggctcggt tgtgaaatac agcgtrgtca gcccttgccg tcaagtgtaga 60
aaccacagcc tgtaaggctg gtcttcgtcc atctgctttt ttctgaaata cactaagagc 120
agccacaaaa ctgtaacctc aaggaaacca taaagcttgg agtgccttaa tttttaacca 180
gtttccaata aaacggttta ctacct                                     206
```

<210> 122

<211> 131

<212> DNA

<213> Homo sapiens

<400> 122

```
ggagatgaag atgaggaagc tgagtcagct acgggcargc gggcagctga agatgatgag 60
gatgacgatg tcgataccaa gaagcagaag accgacgagg atgactagac agcaaaaaag 120
gaaaagttaa a                                                    131
```

<210> 123

<211> 231

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 166, 202, 222, 225

<223> n = A,T,C or G

<400> 123

```
gatgaaaatt aaataacttaa attaatcaaa aggcactacg ataccaccta aaacctactg 60
cctcagtggc agtakgctaa kgaagatcaa gctacagsac atyatcta atgaatgtta 120
gcaattacat akcargaagc atgtttgctt tccagaagac tatggnacaa tggtcattwg 180
ggccaagag gatatttgcc cnggaaagga tcaagataga tnaangtaaa g          231
```

<210> 124

<211> 521

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 284, 412, 513

<223> n = A,T,C or G

<400> 124

```
gagtagcaac gcaaagcgct tggatttgag tctgtgggsg acttcgggtc cggctctctgc 60
agcagccgtg atcgcttagt ggagtgttta gggtagttgg ccaggatgcc gaatatcaaa 120
atcttcagca ggcagctccc accaggactt atctcasaaa attgctgacc gcctgggcct 180
ggagctaggc aagtggtgta ctaagaaatt cagcaaccag gagacctgtg tggaaattgg 240
tgaaagtgtg ccgtggagag gatgtctaca ttgttcagag tggntgtggc gaaatcaatg 300
acaatttaat ggagcttttg atcatgatta atgcctgcaa gattgcttca gccagccggg 360
ttactgcagt catcccatgc ttcccttatg ccccggcagg ataagaaaga tnagagccgg 420
gccgccaatc tcagccaagc ttggtgcaaa tatgctatct gtagcagtcg agatcatatt 480
atcaccatgg acctacatgc ttctcaaatt canggctttt t                    521
```

<210> 125

<211> 341

<212> DNA

<213> Homo sapiens

<220>
 <221> misc_feature
 <222> 277
 <223> n = A,T,C or G

<400> 125
 atgcaaaagg ggacacaggg ggttcaaaaa taaaaatttc tcttccccct ccccaaacct 60
 gtaccccagc tccccgacca caaccccctt cctcccccg ggaagcaag aaggagcagg 120
 tgtggcatct gcagctggga agagagaggc cggggagggt ccgagctcgg tgctgggtctc 180
 tttccaaata taaatacgtg tgtcagaact ggaaaatcct ccagcaccca ccaccaagc 240
 actctccgtt ttctgccgtt gtttgagag gggcgnggg caggggcgcc aggcaccggc 300
 tggtgcggt ctactgcac cgctgggtgt gcaccccgcg a 341

<210> 126
 <211> 521
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 353, 399, 455
 <223> n = A,T,C or G

<400> 126
 aggttgga aggtcatgca ggtgcagatt gtccaggskc agccacaggg tcaagcccaa 60
 caggcccaga gtggcactgg acagaccatg caggtgatgc agcagatcat cactaacaca 120
 ggagagatcc agcagatccc ggtgcagctg aatgccggcc agctgcagta tatccgctta 180
 gccagcctg tatcaggcac tcaagttgtg caggggacaga tccagacact tgccaccaat 240
 gctcaacaga ttacacagac agaggtccag caaggacagc agcagttcaa gccagttcac 300
 aagatggaca gcagctctac cagatccagc aagtcaccat gcctgcgggc cangacctcg 360
 ccagcccatg ttcatccagt caagccaacc agcccttcna cgggcaggcc cccaggtga 420
 ccggcgactg aagggcctga gctggcaagg ccaangacac ccaacacaat ttttgccata 480
 cagccccag gcaatgggca cagcctttct tcccagagga c 521

<210> 127
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 127
 tgagatttat tgcatttcat gcagcttgaa gtccatgcaa aggrgactag cacagttttt 60
 aatgcattta aaaaataaaa gggaggtggg cagcaaacac acaaagtcct agtttcctgg 120
 gtccctggga gaaaagagtg tggcaatgaa tccaccact ctccacaggg aataaatctg 180
 tctcttaa at gcaaagaatg tttccatggc ctctggatgc aaatacacag agctctgggg 240
 tcagagcaag ggatggggag aggaccacga gtgaaaaagc agctacacac attcacctaa 300
 ttccatctga gggcaagaac aacgtggcaa gtcttggggg tagcagctgt t 351

<210> 128
 <211> 521
 <212> DNA
 <213> Homo sapiens

<400> 128
 tccagacatg ctctgtcct aggcggggag caggaaccag acctgctatg ggaagcagaa 60
 agagttaag gaaggtttcc ttctattcct gttccttctc ttttgctttt gaacagtttt 120
 taaatatact aatagctaag tcatttgcca gccagggtccc ggtgaacagt agagaacaag 180
 gagcttgcta agaattaatt ttgctgtttt tcacccatt caaacagagc tgccctgttc 240

cctgatggag ttccattcct gccagggcac ggctgagtaa cacgaagcca ttcaagaaag 300
gcgggtgtga aatcactgcc accccatgga cagaccctc actcttcctt cttagccgca 360
gcgctactta ataaatata ttatactttg aaattatgat aaccgatttt tcccatgagg 420
catcctaagg gcacttgcca gctcttatcc ggacagtcaa gcactgttgt tggacaacag 480
ataaaggaaa agaaaaagaa gaaaaacaacc gcaacttctg t 521

<210> 129

<211> 521

<212> DNA

<213> Homo sapiens

<400> 129

tgagacggac cactggcctg gtccccctc atktgctgtc gtaggacctg acatgaaacg 60
cagatctagt ggcagagagg aagatgatga ggaacttctg agacgtcggc agcttcaaga 120
agagcaatta atgaagctta actcaggcct gggacagttg atcttgaaag aagagatgga 180
gaaagagagc cgggaaaggt catctctgtt agccagtcgc tacgattctc ccatcaactc 240
agcttcacat attccatcat ctaaaactgc atctctccct ggctatggaa gaaatgggct 300
tcaccggcct gtttctaccg acttcgctca gtataacagc tatggggatg tcagcggggg 360
agtgcgagat taccagacac ttccagatgg ccacatgcct gcaatgagaa tggaccgagg 420
agtgtctatg cccaacatgt tggaaccaaa gatatttcca tatgaaatgc tcatggtgac 480
caacagaggg ccgaaaccaaa atctcagaga ggtggacaga a 521

<210> 130

<211> 270

<212> DNA

<213> Homo sapiens

<400> 130

tcactttatt tttcttgtat aaaaacccta tgtttagacc acagctggag cctgagtcgg 60
ctgcacggag actctgggtg gggctcttgac gaggtggtca gtgaactcct gatagggaga 120
cttggatgaat acagtctcct tccagaggtc gggggtcagg tagctgtagg tcttagaaat 180
ggcatcaaag gtggccttgg cgaagtggc cagggtggca gtgcagcccc gggctgaggt 240
gtagcagtc tcatgaccag ccatcatgag 270

<210> 131

<211> 341

<212> DNA

<213> Homo sapiens

<400> 131

ctggaatata gaccgtgat cgacaaaact ttgaacgagg ctgactgtgc caccgtcccc 60
ccagccattc gtcctactg atgagacaag atgtggtgat gacagaatca gcttttgtaa 120
ttatgtataa tagctcatgc atgtgtccat gtcataactg tcttcatacg cttctgcact 180
ctggggaaga aggagtacat tgaagggaga ttggcaccta gtggctggga gcttgccagg 240
aaccagtggt ccagggagcg tggcacttac ctttgtccct tgcttcattc ttgtgagatg 300
ataaaactgg gcacagctct taaataaaat ataatgaac a 341

<210> 132

<211> 844

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 37

<223> n = A,T,C or G

<400> 132

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tgaatgggga ggagctgacc caggaaatgg agcttgngga gaccaggcct gcaggggatg 60
gaaccttcca gaagtgggca tctgtggtgg tgcctcttgg gaaggagcag aagtacacat 120
gccatgtgga acatgagggg ctgcctgagc cctcaccct gagatggggc aaggaggagc 180
ctccttcac caccaagact aacacagtaa tcattgctgt tccggttgtc cttggagctg 240
tggatcatcct tggagctgtg atggcttttg tgatgaagag gaggagaaac acaggtggaa 300
aaggagggga ctatgctctg gctccaggct cccagagctc tgatatgtct ctcccagatt 360
gtaaagtgtg aagacagctg cctggtgtgg acttgggtgac agacaatgtc ttcacacatc 420
tcctgtgaca tccagagacc tcagtctctt ttagtcaagt gtctgatgtt ccctgtgagt 480
ctgcgggctc aaagtgaaga actgtggagc ccagtcacc cctgcacacc aggaccctat 540
ccctgcactg ccctgtgttc ccttccacag ccaaccttgc tgctccagcc aaacattggt 600
ggacatctgc agcctgtcag ctccatgcta cctgacctt caactcctca cttccacatc 660
gagaataata atttgaatgt ggggtgctgg agagatggct cagcgctgac tgctcttcca 720
aaggctcctga gttcaaatcc cagcaaccac atgggtggctc acaaccatct gtaatgggat 780
ctaataccct cttctgcagt gtctgaagac asctacagtg tacttacata taataataaa 840
taag 844

```

<210> 133

<211> 601

<212> DNA

<213> Homo sapiens

<400> 133

```

ggcggggcgc ggcgcgcccc gccacacgca cgccgggctt gccagtttat aaaggagag 60
agcaagcagc gactcttgaa gctctgtttg gtgctttgga tccatttcca tcggctccta 120
cagccgctcg tcagactcca gcagccaaga tggatgaagc gatcgagagc aagactgctt 180
ttcaggaagc cttggacgct gcaggtgata aacttgtagt agttgacttc tcagccacgt 240
gggtgtgggccc ttgcaaaatg atcaagcctt tctttcattc cctctctgaa aagtattcca 300
acgtgatatt ccttgaagta gatgtggatg actgtcagga tgttgcttca gagtgtgaag 360
tcaaatgcat gccaacattc cagtttttta agaagggaca aaagggtgggt gaattttctg 420
gagccaataa ggaaaagctt gaagccacca ttaatgaatt agtctaataca tgttttctga 480
aaatataacc agccattggc tattttaaacc ttgtaatttt ttaattttac aaaaataata 540
aatatgaaga cataaacccm gttgccatct gcgtgacaat aaaacattaa tgctaacact 600
t 601

```

<210> 134

<211> 421

<212> DNA

<213> Homo sapiens

<400> 134

```

tcacataaga aatttaagca agttaccta tcttaaaaaa cacaacgaat gcattttaat 60
agagaaaccc ttccctccct ccacctccct cccccacct cctcatgaat taagaatcta 120
agagaagaag taaccataaa accaagtttt gtggaatcca tcatccagag tgcttacatg 180
gtgattaggt taatattgcc ttcttacaaa atttctattt taataaaaaa tataaccttg 240
attgcttatt acaaaaaaat tcagtacaaa agttcaatat attgaaaaat gcttttcccc 300
tcctcacag caccgtttta tatatagcag agaataatga agagattgct agtctagatg 360
gggcaatcct caaattacac caagacgcac agtggtttat ttaccctccc cttctcataa 420
g 421

```

<210> 135

<211> 511

<212> DNA

<213> Homo sapiens

<400> 135

```

ggaaaggatt caagaattag aggacttgct tgctrragaa aaagacaact ctgcgtcgcat 60
gctgacagac aaagagagag agatggcgga aataagggat caaatgcagc aacagctgaa 120
tgactatgaa cagcttcttg atgtaaagtt agccctggac atggaaatca gtgcttacag 180

```

```

gaaactctta gaaggcgaag aagagaggtt gaagctgtct ccaagccctt cttcccgtgt 240
gacagtatcc cgagcatcct caagtcgtag tgtaccgtac aactagagga aagcggaaga 300
gggttgatgt ggaagaatca gaggcgaagt agtagtgta gcatctctca ttccgcctca 360
accactggaa atgtttgcat cgaagaaatt gatgttgatg ggaaatttat ccgcgttgaa 420
gaacacttct gaacaggatc aaccaatggg aaggcttggg agatgatcag aaaaattgga 480
gacacatcag tcagttataa atatacctca a                                     511

```

```

<210> 136
<211> 341
<212> DNA
<213> Homo sapiens

```

```

<400> 136
catgggtttc accaggttgg ccaggtctgt cttgaactsc tgacctcagg tgatccaccc 60
gcctcggcct cccaaagtgc tgggattaca ggcgtgagcc accacgcccg gccccaaag 120
ctgtttcttt tgtctttagc gtaaaagtct cctgccatgc agtatctaca taactgacgt 180
gactgccagc aagctcagtc actccgtggg ctttttctct ttccagttct tctctctctc 240
ttcaagttct gcctcagtga aagctgcagg tccccagtta agtgatcagg tgagggttct 300
ttgaacctgg ttctatcagt cgaattaatc cttcatgatg g                                     341

```

```

<210> 137
<211> 551
<212> DNA
<213> Homo sapiens

```

```

<400> 137
gatgtgttgg accctctgtg tcaaaaaaaaa cctcacaag aatcccctgc tcattacaga 60
agaagatgca tttaaaatat gggttathtt caacttttta tctgaggaca agtatccatt 120
aattattgtg tcagaagaga ttgaatacct gcttaagaag cttacagaag ctatgggagg 180
aggttggcag caagaacaat ttgaacatta taaaaaaca tttgatgaca gtaaaaatgg 240
cctttctgca tgggaactta ttgagcttat tggaaatgga cagtttagca aaggcatgga 300
ccggcagact gtgtctatgg caattaatga agtctttaat gaacttatat tagatgtgtt 360
aaagcagggt tacatgatga aaaagggcca cagacggaaa aactggactg aaagatggtt 420
tgtactaaaa cccaacataa tttcttacta tgtgagttag gatctgaagg ataagaaaag 480
agacattctc ttgatgaaa attgctgtgt agaagtcctt gcctgacaaa agatggaaaag 540
aatgccttt t                                     551

```

```

<210> 138
<211> 531
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 490
<223> n = A,T,C or G

```

```

<400> 138
gactggttct ttatttcaaa aagacacttg tcaatattca gtrtcaaac agttgcacta 60
ttgatttctc tttctcccaa tcggcccaa agagaccaca taaaaggaga gtacatttta 120
agccaataag ctgcaggatg tacacctaac agacctcta gaaaccttac cagaaaatgg 180
ggactgggta gggaaggaaa cttaaaagat caacaaactg ccagcccacg gactgcagag 240
gctgtcacag ccagatgggg tggccagggt gccacaaacc caaagcaaag tttcaaaaata 300
atataaaatt taaaaagttt tgtacataag ctattcaaga tttctccagc actgactgat 360
acaaagcaca attgagatgg cacttctaga gacagcagct tcaaaccag aaaaagggtga 420
tgagatgaag tttcacatgg ctaaatcagt ggcaaaaaca cagtcttctt tctttctttc 480
tttcaaggan gcaggaaaagc aattaagtgg tcaccttaac ataaggggga c                                     531

```


<210> 139
<211> 521
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 517
<223> n = A,T,C or G

<400> 139
tgggtgggca ccatggctgg gatcaccacc atcgaggcgg tgaagcgcaa gatccaggtt 60
ctgcagcagc aggcagatga tgcagaggag cgagctgagc gcctccagcg agaagttgag 120
ggagaaaggc gggcccggga acaggctgag gctgaggtgg cctccttgaa ccgtaggatac 180
cagctgggtg aagaagagct ggaccgtgct caggagcgcc tggccactgc cctgcaaaaag 240
ctggaagaag ctgaaaaaagc tgctgatgag agtgagagag gtatgaaggt tattgaaaac 300
cgggccttaa aagatgaaga aaagatggaa ctccaggaaa tccaactcaa agaagctaag 360
cacattgcag aagaggcaga taggaagtat gaagaggtgg ctcgtaagtt ggtgatcatt 420
gaaggagact tggaaccgca cagaaggaaac gagcttgagc ttggcaaaaag tcccgttgcc 480
cagagatggg atgaaccaga ttagactgat ggaccanaac c 521

<210> 140
<211> 571
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 7
<223> n = A,T,C or G

<400> 140
aggggcnegc ggtgcgtggg ccactgggtg accgacttag cctggccaga ctctcagcac 60
ctggaagcgc cccgagagtg acagcgtgag gctgggaggg aggacttggc ttgagcttgt 120
taaaactctgc tctgagccct cttgtcgccg gcatttagat ggctcccgcg aagaagggtg 180
gcgagaagaa aaaggccgct tctgccatca acgaagtggg aaccgcagaa tacaccatca 240
acattcacaa ggcacatccat ggagtgggct tcaagaagcg tgcacctcgg gcaactcaaa 300
agattcgga aattgccatg aaggagatgg gaactccaga tgtgcgcatt gacaccaggc 360
tcaacaaagc tgtctggggc aaaggaataa ggaatgtgcc ataccgaatc cgggtgtgcg 420
ctgtccagaa aacgtaatga ggatgaagat tcaccaataa agctatatac tttggttacc 480
tatgtacctg ttaccacttt caaaaatcta cagacagtca atgtggatga gaactaatcg 540
ctgatcgtca gatcaaataa agttataaaa t 571

<210> 141
<211> 531
<212> DNA
<213> Homo sapiens

<400> 141
tcgggagcca cacttggccc tcttctctc caaagsgcca gaacctcctt ctctttggag 60
aatggggagg cctcttggag acacagaggg tttcaccttg gatgacctt agagaaattg 120
cccaagaagc ccaccttctg gtcccaacct gcagacccca cagcagtcag ttggtcaggc 180
cctgctgtag aaggtcactt ggctccattg cctgcttcca accaatgggc aggagagaag 240
gcctttatct ctgcccacc cattctctct gtaccagcac ctccgttttc agtcagtggt 300
gtccagcaac ggtaccggtt acacagtcac ctccagacaca ccatttcacc tcccttgcca 360
agctgttagc cttagagtga ttgcagtga cactgtttac acaccgtgaa tccattccca 420
tcagtcatt ccagttggca ccagcctgaa ccatttggtta cctgggtgta actggagtc 480
tgtttacaag gtggagtcgg ggcttgctga cttctcttca tttgagggca c 531

<210> 142
<211> 491
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 410
<223> n = A,T,C or G

<400> 142
acctagacag aaggtgggtg agggaggact ggtaggaggc tgaggcaatt ccttggtagt 60
ttgtcctgaa accctactgg agaagtcagc atgaggcacc tactgagaga agtgcccaga 120
aactgctgac tgcattctgtt aagagttaac agtaaaggag tagaagtgtg tttctgaatc 180
agagtggaag cgtctcaagg gtcccacagt ggaggtccct gagctacctc ctttcctga 240
gtgggaagag tgaagcccat gaagaactga gatgaagcaa ggatgggggtt cctgggctcc 300
aggcaagggc tgtgctctct gcagcaggga gccccacgag tcagaagaaa agaactaatc 360
atgtgttgca agaaaccttg cccggatact agcggaaaac tggaggcggn ggtgggggca 420
caggaaagtg gaagtgattt gatggagagc agagaagcct atgcacagtg gccgagtcca 480
cttgtaaagt g 491

<210> 143
<211> 515
<212> DNA
<213> Homo sapiens

<400> 143
ttcaagcaat tgtaacaagt atatgtagat tagagtgagc aaaatcatat acaattttca 60
tttcagttg ctattttcca aattgttctg taatgtcgtt aaaattactt aaaaattaac 120
aaagccaaaa atttatattta tgacaagaaa gccatcccta cattaatctt acttttccac 180
tcaccggccc atctccttcc tctttttcct aactatgcca ttaaaaactgt tctactgggc 240
cgggcgtgtg gctcatgect gtaateccag cattttggga ggccaaggca ggccgatcat 300
gaggtcaaga gattgagacc atcctggcca acatggtgaa accccgcctc gactaagaat 360
acaaaaatta gctgggcatg gtggcgcatg cctgtagtct cagctactcg ggaggctgag 420
gcagaagaat cgcttgaacc cgggaggcag aggatgcagt gagccccgat cgcgccactg 480
cactctagcc tgggcgacag actgagactc tgctc 515

<210> 144
<211> 340
<212> DNA
<213> Homo sapiens

<400> 144
tgtgccagtc tacaggccta tcagcagcga ctccctcagc aacagatggg gtccccctgtt 60
cagcccaacc ccatgagccc ccagcagcat atgtcccaa atcaggccca gtccccacac 120
ctacaaggcc agcagatccc taattctctc tccaatcaag tgcgctctcc ccagcctgtc 180
ccttctccac ggccacagtc ccagcccccc cactccagtc cttccccaag gatgcagcct 240
cagccttctc cacaccacgt ttccccacag acaagttccc cacatcctgg actggtagtt 300
gcccaggcca accccatgga acaagggcac tttgccagcc 340

<210> 145
<211> 630
<212> DNA
<213> Homo sapiens

<400> 145
tgtaaaaact tgtttttaaat tttgtataaa ataaagggtg tccatgcccc cgggggctgt 60

```

aggaaatcca agcagaccag ctgggggtggg gggatgtagc ctacctcggg ggactgtctg 120
tcctcaaaac gggctgagaa ggcccgtcag gggcccagggt cccacagaga ggcctgggat 180
actcccccaa cccgaggggc agactgggca gtggggagcc cccatcgtgc cccagagggt 240
gccacaggct gaaggagggg cctgaggcac cgcagcctgc aacccccagg gctgcagtcc 300
actaactttt tacagaataa aaggaacatg gggatgggga aaaaagcacc aggtcaggca 360
gggcccagag gccccagatc ccaggagggc caggactcag gatgccagca ccaccctagc 420
agctcccaca gtcctggca caggaggccg ccacggattg gcacaggccg ctgctggcca 480
tcacgccaca tttggagaac ttgtcccagc agaggtcagc tcggaggagc tcctcgtggg 540
cacacactgt acgaacacag atctccttgt taatgacgta cacacggcgg aggctgcggg 600
gacagggcac gggaggtctc agccccactt
630

```

<210> 146

<211> 521

<212> DNA

<213> Homo sapiens

<400> 146

```

atggctgctg gatttaggtg gtaatagggg ctgtgggcca taaatctgaa gccttgagaa 60
ccttgggtct ggagagccat gaagaggga ggaaaagagg gcaagtcctg aacctaacca 120
atgacctgat ggattgctcg accaagacac agaagtgaag tctgtgtctg tgcacttccc 180
acagactgga gtttttggtg ctgaatagag ccagttgcta aaaaattggg ggtttggtga 240
agaaatctga ttgttggtg tattcaatgt gtgattttaa aaataaacag caacaacaat 300
aaaaaccctg actggctgtt tttccctgt attctttaca actatTTTTT gaccctctga 360
aaattattat acttcaccta aatggaagac tgctgtgtt gtggaaattt tgtaattttt 420
taatttattt tattctctct ctttttatt ttgcctgcag aatccgttga gagactaata 480
aggcttaata ttttaattgat ttgtttaata tgtatataaa t
521

```

<210> 147

<211> 562

<212> DNA

<213> Homo sapiens

<400> 147

```

ggcatgcgag cgcactcggc ggacgcaagg gcggcgggga gcacacggag cactgcaggc 60
gccgggttgg gacagcgtct tcgctgctgc tggatagtcg tgttttcggg gatcgaggat 120
actcaccaga aaccgaaaat gccgaaacca atcaatgtcc gagttaccac catggatgca 180
gagctggagt ttgcaatcca gccaaatata actggaaaac agctttttga tcagggtgga 240
aagactatcg gcctccgga agtgtgttac tttggcctcc actatgtgga taataaagg 300
tttccctacct ggctgaagct ggataagaag gtgtctgccc aggaggtcag gaaggagaat 360
ccccctcagt tcaagttccg ggccaaagt ctacctgaa gatgtggctg aggagctcat 420
ccaggacatc acccagaaac ttttcttct tcaagtgaag gaaggaaatcc ttagcgatga 480
gatctactgc ccccttgar actgcctgct tcttggggtc ctacgcttgt gcatgccaa 540
tttggggact accaccaaga ag
562

```

<210> 148

<211> 820

<212> DNA

<213> Homo sapiens

<400> 148

```

gaaggagtcg ggatactcag cattgatgca ccccaatttc aaagcggcat tcttcggcag 60
gtctctggga caatctctag ggtcactacc tggaaactcg ttaggttaca actgaatgct 120
gaaaggaaag aacacctgca gaaccggaca gaaattcacc ccggcgatca gctgattgat 180
ctcggctcgac cagaagtcac ggctaaagat gacgaggacg ttgtcaattc cctgggcttt 240
tcgaagttag tccagcagca gtctgaggtt ttcgggcccgg ttatgcacct ggaccaccag 300
caccagctcc cggggggccc aggtgccagc cttatctaca ttcctcaggg tctgatcaaa 360
gttcagctgg tacaccagg accggtaccg cagcgtcagg ttgtccgctc gggctggggg 420
accgcccggg ccagggaagc cgccgacacg ttggagacc tgcggtatgcc cacagccaca 480

```

```

gaggggtggt cccaccgcg gccgcggca cccgcgcgg gttcggcgtc cagcaacggt 540
ggggcgaggg cctcgttctt cctttgtcgc ccattgctgc tccagaggac gaagccgcag 600
gcggccacca cgagcgtcag gattagcacc ttccgtttgt agatgcggaa cctcatggtc 660
tccagggccg ggagcgcagc tacagctcga gcgtcggcgc cgccgctagg agccgcggct 720
cggcttcgtc tccgtcctct ccattcagca ccacgggtcc cgaaaaaagc tcagccscgg 780
tcccaaccgc accctagctt cgttacctgc gcctcgttg 820

```

<210> 149
 <211> 501
 <212> DNA
 <213> Homo sapiens

```

<400> 149
cagatTTTTA tttgcagtgc tcaactggggc cgtttcttgc tgettatttg tctgctagcc 60
tgctcttcca gctgcatggc caggcgcaag gccttgatga catctcgag ggctgagaaa 120
tgcttggttt gctgggccag agcagattcc gctttgttca caaaggctctc caggtcatag 180
tctggctgct cggctcatctc agagagctca agccagtctg gtccttgctg tatgatctcc 240
ttgagctctt ccatagcctt ctctccagc tccctgatct gagtcatggc ttcgttaaa 300
ctggacatct gggaagacag ttctctctct tccttgata aattgcctgg aatcagcgcc 360
ccgttagagc aggttccat ctcttctgtt tccatttgaa tcaactgctc tccactgggc 420
ccactgtggg ggctcagctc cttgaccctg ctgcatact taagggtgtt taaaggatat 480
tcacaggagc ttatgcctgg t 501

```

<210> 150
 <211> 511
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 457, 479
 <223> n = A, T, C or G

```

<400> 150
ctctcttggg tacatgaacc caagttgaaa gtggacttaa caaagtatct ggagaaccaa 60
gcattctgct ttgactttgc atttgatgaa acagcttcga atgaagttgt ctacagggtc 120
acagcaaggc cactggtaca gacaatcttt gaaggtggaa aagcaacttg tttgcatat 180
ggccagacag gaagtggcaa gacacatact atgggcggag acctctctgg gaaagccag 240
aatgcatcca aagggatcta tgccatggcc ttccgggacg tcttctctg aagaatcaac 300
cctgctaccg gaagttgggc ctggaagtct atgtgacatt cttcgagatc tacaatggga 360
agctgtttga cctgctcaac aagaaggcca agcttgccgc tgctggaaga cggcaagcaa 420
caggtgcaag tgggtggggc ttgcaggaac atctggntaa ctctgcttga tgatggcant 480
caagatgatc gacatgggca gcgcctgcag a 511

```

<210> 151
 <211> 566
 <212> DNA
 <213> Homo sapiens

```

<400> 151
tcccgaattc aagcgacaaa ttggawagt aaatggaaga tgcctatcat gaacatcagg 60
caaatctttt gcgccaagat ctgatgagac gacaggaaga attaagacgc atggaagaac 120
ttcacaatca agaaatgcag aaacgtaaag aaatgcaatt gaggcaagag gaggaacgac 180
gtagaagaga ggaagagatg atgattcgtc aacgtgagat ggaagaacaa atgaggcgcc 240
aaagagagga aagttacagc cgaatgggct acatggatcc acgggaaaga gacatgcgaa 300
tgggtggcgg aggagcaatg aacatgggag atccctatgg ttcaggaggc cagaaatttc 360
cacctctagg aggtggtggt ggcatagggt atgaagctaa tcctggcggt ccaccagcaa 420
ccatgagtgg ttccatgatg ggaagtgaca tgcgtactga gcgctttggg caggagaggtg 480

```

cggggcctgt ggggtggacag ggtcctagag gaatggggcc tggaactcca gcaggatatg 540
gtagagggag agaagagtac gaaggc 566

<210> 152
<211> 518
<212> DNA
<213> Homo sapiens

<400> 152
ttcgtgaaga ccctgactgg taagaccatc actctcgaag tggagcccga gtgacaccat 60
tgagaatgtc aaggcaaaga tccaagacaa ggaaggcatc cctcctgacc agcakagggt 120
gatctttgct gggaaacagc tggaagatgg acgcaccctg tctgactaca acatccagaa 180
agagtcacac ctgcacctgg tgctccgtct cagagggtgg atgcaaactc tcgtgaagac 240
cctgactggg aagaccatca ccctcgaggt ggagcccagt gacaccatcg agaattgtcaa 300
ggcaaagatc caagataagg aaggcatccc tctgtatcag cagagggtga tctttgtctg 360
gaaacagctg gaagatggac gcacctgtc tgactacaac atccagaaag agtccactct 420
gcacttggtc ctgcgcttga gggggggtgt ctaagtttcc ccttttaagg tttcaacaaa 480
tttcattgca ctttcctttc aataaagttg ttgcattc 518

<210> 153
<211> 542
<212> DNA
<213> Homo sapiens

<400> 153
gcgcgggtgc gtgggccact ggggtgaccga cttagcctgg ccagactctc agcacctgga 60
agcgccccga gagtgcacgc gtgaggctgg gagggaggac ttggcttgag cttgttaaac 120
tctgtcttga gcctccttgt cgcctgcatt tagatggctc ccgcaaagaa ggggtggcag 180
aagaaaaagg gccgttctgc catcaacgaa gtggtaaccc gagaatacac catcaacatt 240
cacaagcgca tccatggagt gggcttcaag aagcgtgcac ctcgggcact caaagagatt 300
cggaaatttg ccatgaagga gatgggaact ccagatgtgc gcattgacac cagggtcaac 360
aaagctgtct gggccaaaagg aataaggaat gtgccatacc gaatccgtgt gcggctgtcc 420
agaaaacgta atgaggatga agattcacca aataagctat atactttggt tacctatgta 480
cctgttacca ctttcaaaaa tctacagaca gtcaatgtgg atgagaacta atcgctgac 540
gt 562

<210> 154
<211> 411
<212> DNA
<213> Homo sapiens

<400> 154
aattctttat ttaaatacaac aaactcatct tctcaagcc ccagaccatg gtaggcagcc 60
ctccctctcc atccctcac cccaccctt agccacagtg aagggaatgg aaaatgagaa 120
gccacgaggg cccctgccag ggaaggctgc ccagatgtg tggtagcac agtcagtga 180
gctgtggctg gggcagcagc tgccacagcc tctccctat aaattaagtt cctgcagcca 240
cagctgtggg agaagcatac ttgtagaagc aaggccagtc cagcatcaga aggcagaggg 300
agcatcagt actcccagcc atggaatgaa cggaggacac agagctcaga gacagaacag 360
gccaggggga agaaggagag acagaatagg ccagggcatg gcggtgaggg a 411

<210> 155
<211> 421
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 173

<223> n = A,T,C or G

<400> 155

```
tgatgaatct ggggtgggctg gcagtagccc gagatgatgg gctcttctct ggggatccca 60
actggttccc taagaaatcc aaggagaatc ctcggaactt ctoggataac cagctgcaag 120
agggcaagaa cgtgatcggg ttacagatgg gcaccaaccg cggggcgtct cangcaggca 180
tgactggcta cgggatgcca cgccagatcc tctgatccca cccaggcct tgcccctgcc 240
ctcccacgaa tggttaatat atatgtagat atatatttta gcagtacat tcccagagag 300
ccccagagct ctcaagctcc tttctgtcag ggtggggggt tcaagcctgt cctgtcacct 360
ctgaagtgcc tgctggcatc ctctcccca tgcttactaa tacattccct tcccacatagc 420
c 421
```

<210> 156

<211> 670

<212> DNA

<213> Homo sapiens

<400> 156

```
agcggagctc cctcccctgg tggctacaac ccacacacgc caggctcagg catcgagcag 60
aactccagcg actgggtaac cactgacatt caggtgaagg tgcgggacac ctacctggat 120
acacaggtgg tgggacagac aggtgtcatc cgcagtgtca cggggggcat gtgctctgtg 180
tacctgaagg acagtgagaa ggttgtcagc atttccagtg agcacctgga gcctatcacc 240
bccaccaaga acaacaaggt gaaagtgatc ctgggcgagg atcgggaagc cacgggcgtc 300
ctactgagca ttgatggtga ggatggcatt gtccgtatgg accttgatga gcagctcaag 360
atcctcaacc tccgcttcct ggggaagctc ctggaagcct gaagcaggca gggccggtgg 420
acttcgtcgg atgaagagt atcctccttc cttccctggc ccttggtgtg gacacaagat 480
cctcctgcag ggctaggcgg attgttctgg atttcccttt gtttttctt ttaggtttcc 540
atcttttccc tccctggtgc tcattggaat ctgagtagag tctgggggag ggtccccacc 600
ttcctgtacc tctcctccac agcttgcttt tgttgtaccg tctttcaata aaaagaagct 660
gtttggtcta 670
```

<210> 157

<211> 421

<212> DNA

<213> Homo sapiens

<400> 157

```
ggttcacage actgctgctt gtgtgttgcc ggccaggaat tccaggctca caaggctatc 60
ttagcagctc gttctccggt ttttagtgcc atgtttgaac atgaaatgga ggagagcaaa 120
aagaatcgag ttgaaatcaa tgatgtggag cctgaagttt ttaaggaaat gatgtgcttc 180
atttacacgg ggaaggctcc aaacctcgac aaaatggctg atgatttgct ggcagctgct 240
gacaagtatg ccctggagcg cttaaaggtc atgtgtgagg atgccctctg cagtaacctg 300
tccgtggaga acgctgcaga aattctcatc ctggccgacc tccacagtgc agatcagttg 360
aaaactcagg cagtggattt catcaactat catgcttcgg atgtcttga gacctcttgg 420
g 421
```

<210> 158

<211> 321

<212> DNA

<213> Homo sapiens

<400> 158

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tcgtagccat ttttctgctt ctttggagaa tgacgccaca ctgactgctc attgtcgttg 60
gttccatgcc aattggtgaa atagaacctc atccggtagt ggagccggag ggacatcttg 120
tcatcaacgg tgatggtgag atttggagca taccagagct tgggtgtctc gccatacagg 180
gcaaagaggt tgtgacaaag aggagagata cggcatgcct gtgcagccct gatgcacagt 240
tcctctgctg tgtactctcc actgcccagc cggaggggct ccctgtccga cagatagaag 300
atcacttcca cccctggctt g 321
```

<210> 159
<211> 596
<212> DNA
<213> Homo sapiens

<400> 159
tggcacactg ctcttaagaa actatgawga tctgagattt ttttgtgtat gtttttgact 60
cttttgagtg gtaatcatat gtgtctttat agatgtacat acctccttgc acaaattggag 120
gggaattcat tttcatcact gggagtgtcc ttagtgtata aaaaccatgc tggatatatg 180
cttcaagttg taaaaatgaa agtgacttta aaagaaaata ggggatggtc caggatctcc 240
actgataaga ctgtttttaa gtaacttaag gacctttggg tctacaagta tatgtgaaaa 300
aaatgagact tactgggtga ggaaattcat tgtttaaaga tggtcgtgtg tgtgtgtgtg 360
tgtgtgtgtg ttgtgtgtgt ttttgtttt taaggagggg aatttattat ttaccgttgc 420
ttgaaattac tgkgtaaata tatgtytgat aatgatttgc tytttgvcmataaaaattag 480
gvctgtataa gtwtaratg cmtccctggg kgttgatytt ccmagatatt gatgatamcc 540
cttaaaattg taaccygcct ttttccctt gctytcmtt aaagtctatt cmaaaag 596

<210> 160
<211> 515
<212> DNA
<213> Homo sapiens

<400> 160
gggggtaggc tctttattag acggttattg ctgtactaca gggtcagagt gcagtgtaag 60
cagtgtcaga ggcccgctt cagcccaaga atgtggattt tctctcccta ttgatcacag 120
tgggtgggtt tcttcagaaa agccccagag gcagggacca gtgagctcca aggttagaag 180
tggaaactgga aggccttcagt cacatgctgc ttccacgctt ccaggctggg cagcaaggag 240
gagatgccca tgacgtgcca ggtctcccca tctgacacca gtgaagtctg gtaggacagc 300
agccgcacgc ctgcctctgc caggaggcca atcatggtag gcagcattgc agggtcagag 360
gtctgagtc ggaataggag caggggcagg tccctgcgga gaggcacttc tggcctgaag 420
acagctccat tgagccctg cagtacaggy gtagtgcctt ggaccaagcc cacagcctgg 480
taaggggagc ctgccagggc cacggccagg aggca 515

<210> 161
<211> 936
<212> DNA
<213> Homo sapiens

<400> 161
taatttctta gtcgtttgga atccttaagc atgcaaaagc tttgaacaga aggggttcaca 60
aaggaaccag ggttgtctta tggcatccag ttaagccaga gctgggaatg cctctgggtc 120
atccacatca ggagcagaag cacttgactt gtcggtcctg ctgccacggt ttgggcgcc 180
accacgccca cgtccacctc gtcctccctt gccgccacgt cctgggcggc caaggctcc 240
aaaattgatc tccagctgag acgttatatc atttgctggc ttccggaaat gatgggtccat 300
aaccgaatct tcagcatgag cctcttctact ctttgattta tgaagaacaa atcccttctt 360
ccactgccca tcagcacctt catttggttt tccgatatta aattctactt ttgcccggtc 420
cttattttga atagccttcc actcatccaa agtcatctct tttggacctt cctcttttac 480
ctcttcaact tcattctcct tattttcagt gtctgccact ggatgatgtt cttoaccttc 540
aggtgtttcc tcagtcacat ttgattgac caagtcagtt aattcgtctt tgacagttcc 600
ccagttgtga gatccgctac ctccacgttt gtcctcgtgc ttcaggccag atctatcact 660
tccactatgc ctatcaaatt cacgtttgcc acgagaatca aatccatctc ctccggccat 720
tccacgtcca cgccccctc gacctcttcc aagaccacca cgacctgaa taggtcggtc 780
aataatcggc ctatcaactg aaaattcgcc tccctcaccc ttttcttcaa gtggcttttc 840
gaatcttcgt tcacgaggtg gtcgccttct tggctcttca tcaattattt tcccttcacc 900
ctgaagttgt tgatcaggtc ttcttccaac tctgtgc 936

<210> 162

<211> 950
<212> DNA
<213> Homo sapiens

<400> 162
aagcggatgg acctgagtca gccgaatcct. agcccccttc cttgggcctg ctgtgggtgct 60
cgacatcagt gacagacgga agcagcagac catcaaggct acgggaggcc cggggcgctt 120
gcgaagatga agtttggtg cctctccttc cggcagcctt atgctggctt tgtcttaaat 180
ggaatcaaga ctgtggagac gcgctggcgt cctctgctga gcagccagcg gaactgtacc 240
atcgccgtcc acattgctca cagggactgg gaaggcgatg cctgtcggga gctgctggtg 300
gagagactcg ggatgactcc tgcctcagatt caggccttgc tcaggaaaagg ggaaaagttt 360
ggtcgaggag tgatagcggg actcgttgac attggggaaa ctttgcaatg ccccgaaagc 420
ttaactcccc atgaggttgt ggaactagaa aatcaagctg cactgaccaa cctgaagcag 480
aagtacctga ctgtgatttc aaaccccagg tgggtactgg agcccatacc taggaaagga 540
ggcaaggatg tattccaggt agacatccca gagcacctga tccctttggg gcatgaagtg 600
tgacaagtgt gggctcctga aaggaatgtt ccrgagaaac cagctaaatc atggcacctt 660
caatttgcca tcgtgacgca gacctgtata aattagggtt aagatgaatt tccactgctt 720
tggagagtcc caccactaa gcactgtgca tgtaaacagg ttcctttgct cagatgaagg 780
aagtaggggg tggggctttc cttgtgtgat gcctccttag gcacacaggc aatgtctcaa 840
gtactttgac cttagggtag aaggcaaaagc tgccagtaaa tgtctcagca ttgctgctaa 900
ttttggtcct gctagtttct ggattgtaca aataaatgtg ttgtagatga 950

<210> 163
<211> 475
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 301, 317, 331, 458, 464, 470
<223> n = A,T,C or G

<400> 163
tcgagcggcc gcccgggcag gtgtcggagt ccagcacggg aggcgtggtc ttgtagttgt 60
tctccggctg cccattgctc tcccactcca cggcgatgtc gctgggtag aagcctttga 120
ccaggcaggt caggetgacc tggttcttgg tcctctcctc ccgggatggg ggcagggtgt 180
acacctgtgg ttctcggggc tgccccttgg ctttgagat ggttttctcg atgggggctg 240
ggagggcttt gttggagacc ttgcacttgt actccttgcc attcaaccag tcctgggtgca 300
ngacggtgag gacgctnacc acacggtacg ngctggtgta ctgctcctcc cgcggttttg 360
tcttggcatt atgcacctcc acgccgtcca cgtaccaatt gaacttgacc tcagggtcctt 420
cgtggctcac gtccaccacc acgcatgtaa cctcaaanct cggncgcgan cagcg 475

<210> 164
<211> 476
<212> DNA
<213> Homo sapiens

<400> 164
agcgtggtcg cggccgaggt ctgaggttac atgcgtggtg gtggacgtga gccacgaaga 60
ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa 120
gcgcggggag gagcagtaca acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca 180
ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc 240
ccccatcgag aaaacatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac 300
cctgccccca tcccgggagg agatgaccaa gaaccaggtc agcctgacct gcttgggtcaa 360
aggcttctat cccagcgaca tcgcccgtgg agtgggagag caatgggcag ccggagaaca 420
actacaagac cagcctccc gtgctggact ccgacacctg ccgggcggcc gtcga 476

<210> 165

<211> 256
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 10, 37, 249
<223> n = A,T,C or G

<400> 165
agcgtggttn cggccgaggt cccaaccaag gctgcancct ggatgccatc aaagtcttct 60
gcaacatgga gactggtgag acctgcgtgt accccactca gcccagtgtg gccagaaga 120
actggtacat cagcaagaac cccaaggaca agaggcatgt ctggttcggc gagagcatga 180
ccgatggatt ccagttcgag tatggcggcc agggctccga ccctgccgat gtggacctgc 240
ccgggcggnc gctcga 256

<210> 166
<211> 332
<212> DNA
<213> Homo sapiens

<400> 166
agcgtgggtcg cggccgaggt caagaacccc gccgcacct gccgtgacct caagatgtgc 60
cactctgact ggaagagtgg agagtactgg attgacccca accaaggctg caacctggat 120
gccatcaaag tcttctgcaa catggagact ggtgagacct gcgtgtacct cactcagccc 180
agtgtggccc agaagaactg gtacatcagc aagaacccca aggacaagag gcatgtctgg 240
ttcggcgaga gcatgaccga tggattccag ttcgagtatg gcggccaggg ctccgacct 300
gccgatgtgg acctgcccgg gcggccgctc ga 332

<210> 167
<211> 332
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 77, 109, 136, 184, 198
<223> n = A,T,C or G

<400> 167
tcgagcggtc gcccgggcag gtccacatcg gcagggtcgg agccctggcc gccatactcg 60
aactggaatc catcggnat gctctcgccg aaccagacat gcctcttgnc cttgggggtc 120
ttgctgatgt accagntctt ctgggccaca ctgggctgag tggggtacac gcaggtctca 180
ccantctcca tgttgcanaa gactttgatg gcatccaggt tgcagccttg gttgggggtca 240
atccagtact ctccactctt ccagacagag tggcacatct tgaggtcacg gcaggtgcgg 300
gcggggttct tgacctcggt cgcgaccacg ct 332

<210> 168
<211> 276
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 72, 84
<223> n = A,T,C or G

<400> 168

tcgagcggcc gcccgggcag gtcctcctca gagcggtagc tgttcttatt gccccggcag 60
cctccataga tnaagttatt gcangagttc ctctccacgt caaagtacca gcgtgggaag 120
gatgcacggc aaggcccagt gactgcgttg gcggtgcagt attcttcata gttgaacata 180
tcgctggagt ggacttcaga atcctgcctt ctggggagcac ttggggacaga ggaatccgct 240
gcattcctgc tgggtggacct cggccgcgac cacgct 276

<210> 169
<211> 276
<212> DNA
<213> Homo sapiens

<400> 169
agcgtggtcg cgcccgaggt ccaccagcag gaatgcagcg gattcctctg tcccaagtgc 60
tcccagaagc caggattctg aagaccactc cagcgatatg ttcaactatg aagaatactg 120
caccgccaac gcagtcaactg ggccttgccg tgcctccttc ccacgctggt actttgacgt 180
ggagaggaac tcctgcaata acttcatcta tggaggctgc cggggcaata agaacagcta 240
ccgctctgag gaggacctgc ccgggcggcc gctcga 276

<210> 170
<211> 332
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 294
<223> n = A,T,C or G

<400> 170
tcgagcggcc gcccgggcag gtccacatcg gcagggtcgg agccctggcc gccatactcg 60
aactggaatc catcggtcat gctctcgccg aaccagacat gcctcttgtc cttggggttc 120
ttgctgatgt accagttctt ctgggccaca ctgggctgag tggggtagac gcagggtctca 180
ccagtctcca tgttgagaa gactttgatg gcattccagg tgcagccttg gttgggggtca 240
atccagtact ctccactctt ccagccagaa tggcacatct tgaggtcacg gcangtgcgg 300
gcggggttct tgacctcgcc cgcgaccacg ct 332

<210> 171
<211> 333
<212> DNA
<213> Homo sapiens

<400> 171
agcgtggtcg cgcccgaggt caagaaaccc cgcccgacc tgccgtgacc tcaagatgtg 60
ccactctggc tggaagagtg gagagtactg gattgacccc aaccaaggct gcaacctgga 120
tgccatcaaa gtcttctgca acatggagac tgggtgagacc tgcgtgtacc ccactcagcc 180
cagtgtggcc cagaagaact ggtacatcag caagaacccc aaggacaaga ggcattgtctg 240
gtcggcgag agcatgaccg atggattcca gttcgagtat ggcggccagg gctccgaccc 300
tgccgatgtg gacctgcccg ggcggccgct cga 333

<210> 172
<211> 527
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 46, 125, 140, 148, 220, 229, 291, 388, 456
<223> n = A,T,C or G

<400> 172
agcgtgggtcg cggccgaggt cctgtcagag tggcactggt agaagntcca ggaaccctga 60
actgtaaggg ttcttcatca gtgccaacag gatgacatga aatgatgtac tcagaagtgt 120
cctgnaatgg ggcccatgan atggttgntc gagagagagc ttcttgtcct acattcggcg 180
ggtatggtct tggcctatgc cttatggggg tggccgttgn gggcgggtng gtccgcctaa 240
aaccatgttc ctcaaagatc atttgttgcc caacactggg ttgctgacca naagtgccag 300
gaagctgaat accatttcca gtgtcatacc caggggtgggt gacgaaagg gtcttttgaa 360
ctgtggaagg aacatccaag atctctgntc catgaagatt ggggtgtgga agggttacca 420
gttggggaag ctgctgtct ttttccttc aatcangggc tcgctcttct gaattattct 480
cagggcaatg acataaattg tatattcggg tcccgggttc aggccag 527

<210> 173
<211> 635
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 444, 453, 517, 540, 546, 551, 573, 593
<223> n = A,T,C or G

<400> 173
tcgagcggcc gcccgggcag gtccaccaca cccaattcct tgctgggtatc atggcagccg 60
ccacgtgccca ggattaccgg ctacatcatc aagtatgaga agcctgggtc tcttcccaga 120
gaagtgggtcc ctcgccccg ccctgggtgc acagaggcta ctattactgg cctggaaccg 180
ggaaccgaat atacaattta tgtcattgcc ctgaagaata atcagaagag cgagccccctg 240
attggaagga aaaagacaga cgagcttccc caactggtaa cccttcaca cccaatctt 300
catggaccag agatcttga tgttccttc acagtccaag agacccttt cgtaaccac 360
cctgggtatg aacttgaaa tggatttcag cttcctggca cttctggtca gcaaccag 420
gttgggcaac aaatgatctt tgangaacat gnttttaggc ggaccacacc ggccacaacg 480
ggcacccttc taaggcatag gccagaaca taccgncga atgtaggaca agaagctctn 540
tctcanacaa ncatctcatg ggccccatc cangacact ctgagtacat canttcatg 600
catcctggtg gcactgataa aaacccttac agtta 635

<210> 174
<211> 572
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 457, 511, 520, 552, 568
<223> n = A,T,C or G

<400> 174
agcgtgggtcg cggcgaggt cctgtcagag tggcactggt agaagttcca ggaaccctga 60
actgtaaggg ttcttcatca gtgccaacag gatgacatga aatgatgtac tcagaagtgt 120
cctggaatgg ggcccatgag atggttgtct gagagagagc ttcttgtcct acattcggcg 180
ggtatggtct tggcctatgc cttatggggg tggccgttgt gggcgggtgt gtccgcctaa 240
aaccatgttc ctcaaagatc atttgttgcc caacactggg ttgctgacca gaagtgccag 300
gaagctgaat accatttcca gtgtcatacc caggggtgggt gacgaaagg gtcttttgaa 360
ctgtggaagg aacatccaag atctctggtc catgaagatt ggggtgtgga agggttacca 420
gttggggaag ctgctgtgtc ttttccttc caatcanggg ctgctcttc tgattattct 480
tcagggcaat gacataaatt gtatattcgg ntcccggtgn cagccaataa taataacct 540
ctgtgacacc anggcggggc cgaagganct ct 572

<210> 175

<211> 372
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 247
<223> n = A,T,C or G

<400> 175
agcgtggtcg cggccgaggt cctcaccaga ggtaccacct acaacatcat agtggaggca 60
ctgaaagacc agcagaggca taagggtcgg gaagagggtg ttaccgtggg caactctgtc 120
aacgaaggct tgaaccaacc tacggatgac tcgtgctttg acccctacac agtttcccat 180
tatgccgttg gagatgagtg ggaacgaatg tctgaatcag gctttaaact gttgtgccag 240
tgcttangct ttggaagtgg tcatttcaga tgtgattcat ctagatgggtg ccatgacaat 300
ggtgtgaact acaagattgg agagaagtgg gaccgtcagg gagaaaatgg acctgcccgg 360
gcggccgctc ga 372

<210> 176
<211> 372
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 251
<223> n = A,T,C or G

<400> 176
tcgagcggcc gcccgggcag gtccattttc tccctgacgg tcccacttct ctccaatctt 60
gtagtccaca ccattgtcat ggcaccatct agatgaatca catctgaaat gaccacttcc 120
aaagcctaag cactggcaca acagtttaaa gcctgattca gacattcgtt cccactcatc 180
tccaacggca taatgggaaa ctgtgtaggg gtcaaagcac gagtcatecg taggttggtt 240
caagccttcg ntgacagagt tgcccacggt aacaacctct tcccgaacct tatgcctctg 300
ctggtctttc agtgcctcca ctatgatgtt gtaggtggta cctctggtga ggacctcggc 360
cgcgaccacg ct 372

<210> 177
<211> 269
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 94, 225
<223> n = A,T,C or G

<400> 177
agcgtggccg cggccgaggt ccattggctg gaacggcatc aacttggag ccagtgatcg 60
tctcagcctt ggttctccag ctaatggatga tggnggtctc agtagcatct gtcacacgag 120
cccttcttgg tgggctgaca ttctccagag tggtgacaac accctgagct ggtctgcttg 180
tcaaagtgtc cttaagagca tagacactca cttcatattt ggcgnccacc ataagtctctg 240
atacaaccac ggaatgacct gtcaggaac 269

<210> 178
<211> 529
<212> DNA
<213> Homo sapiens

<400> 178

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tcgagcggcc gcccgggcag gtcctcagac cgggttctga gtacacagtc agtgtggttg 60
ccttgacaga tgatatggag agccagcccc tgattggaac ccagtccaca gctattcctg 120
caccaactga cctgaagttc actcaggtca caccacaag cctgagcgcc cagtggacac 180
cacccaatgt tcagctcact ggatatcgag tgcggtgac cccaaggag aagaccggac 240
caatgaaaga aatcaacctt gctcctgaca gctcatccgt ggttgatca ggacttatgg 300
cggccaccaa atatgaagtg agtgtctatg ctcttaagga cactttgaca agcagaccag 360
ctcaggtgtg tgtcaccact ctggagaatg tcagcccacc aagaagggtc cgtgtgacag 420
atgctactga gaccaccatc accattagct ggagaaccaa gactgagacg atcactggct 480
tccaagttga tgccgttcca gccaatggac ctcggccgag accacgctt 529
```

<210> 179

<211> 454

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 64

<223> n = A,T,C or G

<400> 179

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agcgtggtcg cggccgaggt ctggccgaac tgccagtga cagggaagat gtacatgtta 60
tagntcttct cgaagtcccg ggccagcagc tcacggggt ggtctcctgc ctccaggcgc 120
ttctcattct ctggatcctt cttcaccgcg agcttctgct tctcagtcag aaggttgttg 180
tcctcatccc tctcatacag ggtgaccagg acgttcttga gccagtcccg catgcgcagg 240
gggaattcgg tcagctcaga gtccaggcaa ggggggatgt atttgcaagg cccgatgtag 300
tccaagtgga gcttgtggcc cttcttggtg cctccaagg tgcactttgt ggcaaagaag 360
tggcaggaag agtcgaaggt cttgttgtca ttgctgcaca ctttctcaa ctcgccaatg 420
ggggctgggc agacctgccg gggcgccgcg tcga 454
```

<210> 180

<211> 454

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 55, 299, 317, 332, 342, 348

<223> n = A,T,C or G

<400> 180

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tcgagcggcc gcccgggcag gtctgccag ccccatcttg cgagtttgag aaggngtgca 60
gcaatgacaa caagaccttc gactcttctt gccacttctt tgccacaaag tgcaccttg 120
agggcaccaa gaaggccac aagctccacc tggtactacat cgggccttgc aaatacatcc 180
ccccttgctt ggactctgag ctgaccgaat tccccctgcg catgcgggac tggctcaaga 240
acgtcctggt caccctgtat gagagggatg aggacaacaa ccttctgact gagaagcana 300
agctgcgggt gaagaanac catgagaatg anaagcgctt gnaggcanga gaccaccccg 360
tggagctgct ggcccgggac ttcgagaaga actataacat gtacatcttc cctgtacact 420
ggcagttcgg ccagacctcg gccgcgacca cgct 454
```

<210> 181

<211> 102

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature
<222> 8, 47, 60, 67
<223> n = A,T,C or G

<400> 181
agecgtggntg cggacgacgc ccacaaagcc attgtatgta gttttanttc agctgcaaan 60
aatacncca gcatccacct tactaaccag catatgcaga ca 102

<210> 182
<211> 337
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 169, 195, 253, 314
<223> n = A,T,C or G

<400> 182
tcgagcggtc gcccgggcag gtctgggcgg atagcaccgg gcatattttg gaatggatga 60
ggtctggcac cctgagcagc ccagcgagga cttggtctta gttgagcaat ttggctagga 120
ggatagtatg cagcacggtt ctgagtctgt gggatagctg ccatgaagna acctgaagga 180
ggcgctggct ggtanggggt gattacaggg ctgggaacag ctcgtaact tgccattctc 240
tgcatatact ggntagttag gcgagcctgg cgctcttctt tgcgctgagc taaagctaca 300
tacaatggct ttngggacct cggccgcgac cacgctt 337

<210> 183
<211> 374
<212> DNA
<213> Homo sapiens

<400> 183
tcgagcggcc gcccgggcag gtccattttc tccctgacgg tcccacttct ctccaattct 60
gtagtccaca ccattgtcat gacaccatct agatgaatca catctgaaat gaccacttcc 120
aaagcctaag cactggcaca acagtttaaa gcctgattca gacattcgtt cccactcatc 180
tccaacggca taatgggaaa ctgtgtaggg gtcaaagcac gagtcaccc taggttggtt 240
caagccttcg ttgacagaag ttgccacgg taacaacctc ttcccgaacc ttatgcctct 300
gtcgtgtctt caagtgcctc cactatgatg ttgtaggtag cacctctggt gaggacctcg 360
gccgcgacca cgct 374

<210> 184
<211> 375
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 30, 174, 248, 285, 306, 332, 345, 368
<223> n = A,T,C or G

<400> 184
agecgtggtt gcggccgagg tcctcaccan aggtgccacc tacaacatca tagtggaggc 60
actgaaagac cagcagaggc ataagggttc ggaagagggt gttaccgtgg gcaactctgt 120
caacgaaggc ttgaaccaac ctacggatga ctcgctctt gaccctaca cagnttccca 180
ttatgccgtt ggagatgagt gggaaacgaat gtctgaatca ggctttaaac tggttgacca 240
gtgcttange tttggaagtg gtcatttcag atgtgattca tctanatggt gtcatgacaa 300
tggtgngaac tacaagattg gagagaagtg gnaccgtcag ggganaaaat ggacctgccc 360
gggcggcncg ctca 375

<210> 185
<211> 148
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 28, 36, 86
<223> n = A,T,C or G

<400> 185
agcgtggtcg cgcccgaggt ctggcttinct gctcangtga ttatcctgaa ccatccaggc 60
caaataagcg ccggctatgc ccctgnattg gattgccaca cggtcacat tgcattgcaag 120
tttctgtagc tgaaggaaaa gattgatac 148

<210> 186
<211> 397
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 78
<223> n = A,T,C or G

<400> 186
tcgagcggcc gcccgggcag gtccaattga aacaaacagt tctgagaccg ttcttccacc 60
actgattaag agtggggngg cgggtattag ggataatatt catttagcct tctgagcttt 120
ctgggcagac ttggtgacct tgcdagctcc agcagccttc tgggccactg ctttgatgac 180
acccaccgca actgtctgtc tcatatcacg aacagcaaag cgacccaaag gtggatagtc 240
tgagaagctc tcaacacaca tgggcttgcc aggaaccata tcaacaatgg gcagcatcac 300
cagacttcaa gaatttaagg gccatcttcc agctttttac cagaacggcg atcaatcttt 360
tccttcagct cagcaaactt gcatgcaatg tgagccg 397

<210> 187
<211> 584
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 145, 286, 363, 365, 425, 433, 452, 462, 471, 512, 514, 534,
536, 540, 565, 583
<223> n = A,T,C or G

<400> 187
tcgagcggcc gcccgggcag gtccagaggg ctgtgctgaa gtttgctgct gccactggag 60
ccactccaat tgctggccgc ttcactcctg gaaccttcac taaccagatc caggcagcct 120
tcgggagcc acggcttctt gtggnactg accccagggc tgaccaccag cctctcacgg 180
aggcatctta tgttaacctt cctaccattg cgctgtgtaa cacagattct cctctgcgct 240
atgtggacat tgccatccca tgcaacaaca agggagctca ctcagngggg tttgatgtgg 300
tggtatgctg ctcggaagt tctgcgcatg cgtggcacca tttcccgatg acacccatgg 360
gangncatgc ctgatctgga cttctacaga gatcctgaag agattgaaaa agaagaacag 420
gctgnttgct ganaaagcaa gtgaccaagg angaaatttc angggtgaaa nggactgctc 480
ccgctcctga attcactgct actcaacctg angntgcaga ctggtcttga aggnagnacan 540
gggccctctg ggcctattta agcancttcg gtcgcgaaca cgnt 584

<210> 188
<211> 579
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 7, 136, 486
<223> n = A,T,C or G

<400> 188
agcgtgngtc gcgccgaggg tgctgaatag gcacagaggg cacctgtaca ccttcagacc 60
agtctgcaac ctcaggctga gtagcagtga actcaggagc gggagcagtc cattcaccct 120
gaaattcctc cttggncact gccttctcag cagcagcctg ctcttctttt tcaatctctt 180
caggatctct gtagaagtac agatcaggca tgacctccca tgggtgttca cgggaaatgg 240
tgccacgcat ggcagaaact tcccagacca gcattccacca catcaaacc actgagttag 300
ctcccttggt gttgcatggg atgggcaatg tccacatagc gcagaggaga atctgtgtta 360
cacagcgcaa tggtaggttag gttaacataa gatgcctccg cgagaagctg gtggtcagcc 420
ctgggggtcaa gtaaccacaa gaagcgtgg ctcccgaag gctgcctgga tctggttagt 480
gaaggntcca ggagtgaagc ggccaacaat tggagtggct tcagtggcaa gcagcaaaact 540
tcagcacaag ccctctggac ctgcccggcg gccgctcga 579

<210> 189
<211> 374
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 41, 280, 314, 330, 350, 353
<223> n = A,T,C or G

<400> 189
tcgagcggcc gcccgggcag gtccattttc tccctgacgg ncccacttct ctccaatctt 60
gtagttcaca ccattgtcat ggcaccatct agatgaatca catctgaaat gaccacttcc 120
aaagcctaag cactggcaca acagtttaaa gcctgattca gacattcggt cccactcatc 180
tccaacggca taatgggaaa ctgtgtaggg gtcaaagcac gagtcaccc taggttggtt 240
caagccttcg ttgacagagt tgcccacggg aacaacctcn tcccgaacc ttatgcctct 300
gctgggcttt cagngcctcc actatgatgn tgtagggggg cacctctggn gangacctcg 360
gccgcgacca cgct 374

<210> 190
<211> 373
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 247, 304, 306, 332, 337
<223> n = A,T,C or G

<400> 190
agcgtgggtcg cggccgaggt cctcaccaga ggtgccacct acaacatcat agtggaggca 60
ctgaaagacc agcagaggca taaggctcgg gaagaggttg ttaccgtggg caactctgtc 120
aacgaaggt tgaaccaacc tacggatgac tcgtgctttg acccctacac agtttcccat 180
tatgccgttg gagatgagtg ggaacgaatg tctgaatcag gctttaaact gttgtgccag 240
tgcttangct ttggaagtgg gtcatttcag atgtgattca tctagatggt gccatgacaa 300
tgngngaac tacaagattg gagagaagtg gnaccgncag ggagaaaatg gacctgcccg 360

ggcggccgct cga

373

<210> 191

<211> 354

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 218, 299, 306, 326, 333, 337, 341

<223> n = A,T,C or G

<400> 191

```
agcgtggtcg cggccgaggt ccacatcggc agggtcggag ccctggccgc cataactcgaa 60
ctggaatcca tcggtcatgc tctcgccgaa ccagacatgc ctcttgcct tggggttctt 120
gctgatgtac cagttcttct gggccacact gggctgagtg gggtaacgc aggtctcacc 180
agtctccatg ttgcagaaga ctttgatggc atccaggntg caaccttggg tggggtaaat 240
ccagtactct ccactcttcc agccagagtg gcacatcttg aggtcacggc aggtgcggnc 300
gggggntttt gcggctgccc tctggncttc gngtgnctc natctgctgg ctca 354
```

<210> 192

<211> 587

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 276

<223> n = A,T,C or G

<400> 192

```
tcgagcggcc gcccgggcag gtctcgcggt cgcactgggt atgctgggtc tgttgggtccc 60
cccgccctc ctggacctcc tggccccctt ggtcctccca gcgctgggtt cgacttcage 120
ttctgcccc agccacctca agagaaggct cacgatgggt gccgtacta ccgggctgat 180
gatgccaatg tggttcgtga ccgtgacctc gaggtggaca ccacctcaa gagcctgagc 240
cagcagatcg agaacatccg gagcccagag ggcagncgca agaacccgc ccgcacctgc 300
cgtgacctca agatgtgcca ctctgactgg aagagtggag agtactggat tgaccccaac 360
caagctgcaa cctggatgcc atcaaagtct tctgcaacat ggagactggg gagacctgcg 420
tgtacccac tcagcccagt gtggcccaaa agaactggta catcagcaag aaccccaagg 480
acaagaagca tgtctggttc ggcgagaaca tgaccgatgg attccagttc gagtatggcg 540
ggcagggtc cgacctgcc gatggggacc ttggccgcga acacgct 587
```

<210> 193

<211> 98

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 8, 9, 33, 58, 71, 90

<223> n = A,T,C or G

<400> 193

```
agcgtggng cggccgaggt ataaatatcc agnccatata ctccctccac acgctganag 60
atgaagctgt ncaaagatct cagggtggan aaaacccat 98
```

<210> 194

<211> 240

<212> DNA

<213> Homo sapiens

<400> 194

```
tgcagcggcc gcccgggcag gtccttcaga cttggactgt gtcacactgc caggcttcca 60
gggctccaac ttgcagacgg cctgttgtgg gacagtctct gtaatcgca aagcaaccat 120
ggaagacctg ggggaaaaca ccatggtttt atocaccctg agatcttga acaacttcat 180
ctctcagcgt gcggagggag gctctggact ggatatttct acctcgcccg cgaccacgct 240
```

<210> 195

<211> 400

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 22, 37, 39, 105, 268, 276, 302, 323, 331, 335, 347, 351, 371, 378

<223> n = A,T,C or G

<400> 195

```
cgagcgggcg accgggcag tncagactcc aatccanana accatcaagc cagatgtcag 60
aagctacacc atcacaggtt tacaaccagg cactgactac aaganctacc tgcacacctt 120
gaatgacaat gctcggagct ccctgtgtgt catcgacgcc tccactgcca ttgatgcacc 180
atccaacctg cgtttcctgg ccaccacacc caattccttg ctggtatcat ggcagccgcc 240
acgtgccagg attaccggta catcatcnag tatganaagc ctgggcctcc tcccagagaa 300
gnggtccctc ggccccgcc tgntgtccca naggntacta ttactgngcc ngcaaccggc 360
aaccgatatc nattttgnca ttggccttca acaataatta 400
```

<210> 196

<211> 494

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 19, 83, 168, 252, 271, 292, 430

<223> n = A,T,C or G

<400> 196

```
agcgtgggtc gggcccgang tctgtcaga gtggcactgg tagaagttcc aggaaccctg 60
aactgtaagg gttcttcata agngccaaca ggatgacatg aaatgatgta ctcagaagtg 120
tcttggaatg gggcccatga gatggtgtc tgagagagag cttcttgncc tgtcttttcc 180
cttccaatca ggggtcgtct cttctgatta ttcttcaggg caatgacata aattgtatat 240
tcgggtcccg gntccaggcc agtaatagta ncctctgtga caccagggcg gngccgaggg 300
accacttctc tgggaggaga ccaggcttc tcatacttga tgatgtaacc ggtaatcctg 360
gcacgtggcg gctgccatga taccagcaag gaattggggg gtggtggcca ggaaacgcag 420
gttgatggg gcatcaatgg cagtggaggc cgtcgatgac cacaggggga gctccgacat 480
tgtcattcaa ggtg 494
```

<210> 197

<211> 118

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 8, 71, 96

<223> n = A,T,C or G

<400> 197

agcgtggncg cggccgaggt gcagcgcggg ctgtgccacc ttctgctctc tgcccaacga 60
taaggagggt nccctgcccc aggagaacat taactntccc cagctcggcc tctgcccg 118

<210> 198

<211> 403

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 41, 53, 98, 195, 350

<223> n = A,T,C or G

<400> 198

tcgagcggcc gcccgggcag gttttttttg ctgaaagtgg ntactttatt ggntgggaaa 60
gggagaagct gtggtcagcc caagaggga tacagagncc cgaaaaagg gagggcaggt 120
gggctggaac cagacgcagg gccaggcaga aactttctct cctcactgct cagcctgggt 180
gtggctggag ctcanaaatt gggagtgaca caggacacct tcccacagcc attgcggcgg 240
catttcatct ggccaggaca ctggctgtcc acctggcact ggtcccgaca gaagcccag 300
ctggggaaaag ttaatgttca cctgggggca ggaaccctcc ttatcattgn gcagagagca 360
gaaggtggca cagcccgcgc tgcacctcgg ccgcgaccac gct 403

<210> 199

<211> 167

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 92, 107

<223> n = A,T,C or G

<400> 199

tcgagcggcc gcccgggcag gtccaccata agtcctgata caaccacgga tgagctgtca 60
ggagcaaggt tgatttcttt cattggtccg gncctctcct tgggggncac ccgcactcga 120
tatccagtga gctgaacatt ggggtggcgtc cactgggcgc tcaggct 167

<210> 200

<211> 252

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 210, 226, 227, 230, 236

<223> n = A,T,C or G

<400> 200

tcgagcgggt cggccgggca ggtccaccac acccaattcc ttgctgggtat catggcagcc 60
gccacgtgcc aggattaccg gctacatcat caagtatgag aagcctgggt ctccctcccag 120
agaagcggtc cctcgccccc gccctgggtg cacagagget actattactg gcctggaacc 180
gggaaccgaa tatacaattt atgtcattgn cctgaagaat aatcannan agcgancccc 240
tgattggaag ga 252

<210> 201
<211> 91
<212> DNA
<213> Homo sapiens

<400> 201
agcgtggtcg cggccgaggt tgtacaagct tttttttttt tttttttttt tttttttttt 60
tttttttttt tttttttttt tttttttttt t 91

<210> 202
<211> 368
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 9, 354
<223> n = A,T,C or G

<400> 202
tcgagcggnc gcccgggcag gtctgccaac accaagattg gcccccgccg catccacaca 60
gtccgtgtgc ggggaggtaa caagaaatac cgtgccctga ggttgacgt ggggaatttc 120
tcctggggct cagagtgttg tactcgtaaa acaaggatca tcgatgttgt ctacaatgca 180
tctaataacg agctggttcg taccaagacc ctggtgaaga attgcatcgt gtcacacgac 240
agcacaccgt accgacagt gtacgagtc cactatgcgc tgccccctggg ccgcaagaag 300
ggagccaagc tgactcctga ggaagaagag attttaaaca aaaaacgatc taanaaaaaa 360
aaaacaat 368

<210> 203
<211> 340
<212> DNA
<213> Homo sapiens

<400> 203
agcgtggtcg cggccgaggt gaaatggtat tcagcttctt ggcacttctg gtcagcaacc 60
cagtgttggg caacaaatga tctttgagga acatggtttt aggcggacca caccgcccac 120
aacggccacc ccataaagc ataggccaag accataaccg ccgaatgtag gacaagaagc 180
tctctctcag acaacctct catgggcccc attccaggac acttctgagt acatcatttc 240
atgtcatcct gttggcactg atgaagaacc cttacagttc agggttcctg gaacttctac 300
cagtgccact ctgacaggac ctgccccggc ggccgctcga 340

<210> 204
<211> 341
<212> DNA
<213> Homo sapiens

<400> 204
tcgagcggcc gcccgggcag gtccgtcag agtggcactg gtagaagtgc caggaaccct 60
gaactgtaag ggttcttcat cagtccaac aggatgacat gaaatgatgt actcagaagt 120
gtccctggaat ggggcccacg agatggttgt ctgagagaga gcttcttgct ctacattcgg 180
cgggtatggt cttggcctat gccttatggg ggtggccgtt gtgggcggtg tggtcgcct 240
aaaaccatgt tcctcaaaga tcatttgttg cccaacactg ggttgctgac cagaagtgc 300
aggaagctga ataccatttc acctcgcccg cgaccacgct a 341

<210> 205
<211> 770
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature

<222> 529, 591, 623, 626, 629, 630, 656, 702, 709, 712, 717, 743, 746, 749, 759, 762, 766

<223> n = A,T,C or G

<400> 205

```

tcgagcggcc gcccgggcag gtctcccttc ttgcgggcca ggggcagcgc atagtgggac 60
tcgtaccact gtcggtacgg tgtgctgtcg atgagcacga tgcaattctt caccaggggtc 120
ttggtacgaa ccagctcggt attagatgca ttgtagacaa catcgatgat ccttgtttta 180
cgagtacaac actctgagcc ccaggagaaa ttccccacgt ccaacctcag ggcacgggtat 240
ttcttggtac ctccccgcac acggactgtg tggatgcggc gggggccaag ctgactcctg 300
aggaagaaga gattttaaac aaaaaacgat ctaaaaaaat tcagaagaaa tatgatgaaa 360
ggaaaaagaa tgccaaaatc agcagtctcc tggaggagca gttccagcag ggcaagcttc 420
ttgctgtcat cgcttcaagg ccgggacagt gtgaccgagc agatggctat gtgctagagg 480
gcaaagaagt ggagtcttat ctttaagaaaa tcagggccca gaatggtgng tcttcaacta 540
atccaaaggg gagtttcaga ccagtgcagt cagcaaaaac attgatactg ntggccaaat 600
ttattggtgc agggcttgca cantangann ggctgggtct tggggcttgg attggnacaa 660
gctttggcag ccttttcttt ggttttgcca aaaacctttt gntgaagang anacctnggg 720
cggaccctt aaccgattcc acnccnggng gcgttctang gncccncttg 770

```

<210> 206

<211> 810

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 574, 621, 625, 636, 668, 673, 704, 728, 743, 767, 772, 786, 789, 807, 809, 810

<223> n = A,T,C or G

<400> 206

```

agcgtggtcg cggccgaggt ctgctgcttc agcgaagggt ttctggcata accaatgata 60
aggctgccaa agactgttcc aataccagca ccagaaccag ccactcctac tgttcagca 120
cctgcaccaa taaatttggc agcagtatca atgtctctgc tgattgcaact ggtctgaaac 180
tccctttgga ttagtggaga cacaccattc tgggacctga ttttcctaag atagaactcc 240
aactctttgc cctctagcac atagccatct gctcggtcac actgtcccgg ccttgaagcg 300
atgcacgcaa gaagcttgcc ctgctggaac tgctcctcca ggagactgct gattttggca 360
ttctttttcc tttcatcata tttcttctga atttttttag atcgtttttt gtttaaaatc 420
tcttcttctc caggagtcag cttggccccc gccgcattcca cacagtccgt gtgcggggag 480
gtaacaagaa ataccgtgcc ctgaggttgg acgtggggaa tttctcctgg ggctcagagt 540
ggtgtactcg taaaacaagg atcatcgatg gtgntacaa tgcattctaat aacgagctgg 600
gtcgaccca aagaacctgg ngaanaaatg gatcgntca tcgacaggac accgtaccgg 660
acaggggnac gantcccaact atgcgcttgc ccctgggccc caanaaagga aaactgcccg 720
ggcgccntc gaaagcccaa ttntggaaaa aatccatcac actggngggc cngtcgagca 780
tgcantana ggggcccatt cccctnann 810

```

<210> 207

<211> 257

<212> DNA

<213> Homo sapiens

<400> 207

```

tcgagcggcc gcccgggcag gtccccaacc aaggctgcaa cctggatgcc atcaaagtct 60
tctgaacat ggagactggt gagacctgcg tgtacccac tcagccaggt gtggcccaga 120
agaactggta catcagcaag aacccaagg acaagaggca tgtctggttc ggcgagagca 180

```

tgaccgatgg attccagttc gagtatggcg gccagggctc cgaccctgcc gatgtggacc 240
tcggccgcga ccacgct 257

<210> 208

<211> 257

<212> DNA

<213> Homo sapiens

<400> 208

agcgtgggtcg cggccgaggt ccacatcggc agggtcggag ccctggccgc catactcgaa 60
ctggaatcca tcggtcatgc tctcgccgaa ccagacatgc ctcttgctct tggggttctt 120
gctgatgtac cagttcttct gggccacact gggctgagtg gggtaacgc aggtctcacc 180
agtctccatg ttgcagaaga ctttgatggc atccaggttg cagccttggg tggggacctg 240
cccgggcggc cgctcga 257

<210> 209

<211> 747

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 453, 538, 540, 542, 546, 554, 556, 598, 659, 670, 679, 689,
693, 711, 723, 724, 731, 747

<223> n = A,T,C or G

<400> 209

tcgagcggcc gcccgggcag gtccaccaca cccaattcct tgctgggtatc atggcagccg 60
ccacgtgcca ggattaccgg ctacatcatc aagtatgaga agcctgggtc tcctcccaga 120
gaagtgggtcc ctcgcccccg ccctgggtgc acagaggcta ctattactgg cctggaaccg 180
ggaaccgaat atacaattta tgtcattgcc ctgaagaata atcagaagag cgagccccctg 240
attggaagga aaaagacaga cgagcttccc caactggtaa cccttccaca cccaatctt 300
catggaccag agatcttgga tgttccttcc acagtcaaaa agaccctttt cgtaaccac 360
cctgggtatg aacttgaaa tggattcag ctctcctggca cttctggta gcaaccctg 420
gttgggcaac aaatgatctt tgaggaacat ggnnttaggc ggaccacacc gccacaacg 480
gccaccccca taaggcatag gccaaagacca taccgcgcga atgtaggaca agaagctntn 540
tntcanacac catntnatgg gcccattcc aggacacttc tgagtacatc atttatgnca 600
tctgtggcac ttgatgaaaa cccttacagt tcagggttct ggaactttta ccagccctnt 660
tacaggactn ggccggacnc cttaagcna ttncaccctg gggcggttcta nggtcccact 720
cgnnactgg ngaaaatggc tactgtn 747

<210> 210

<211> 872

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 165, 174, 181, 256, 260, 269, 271, 277, 286, 289, 294, 298,
300, 301, 303, 308, 311, 321, 325, 328, 329, 333, 338, 342,
346, 349, 351, 357, 359, 364, 366, 379, 385, 395, 396, 397,
407, 408, 410, 414, 415, 429, 431, 434, 435, 440, 443

<223> n = A,T,C or G

<221> misc_feature

<222> 444, 446, 447, 448, 449, 450, 451, 464, 470, 472, 475, 479,
483, 484, 485, 488, 494, 496, 497, 504, 508, 509, 511, 513,
517, 522, 524, 526, 532, 533, 542, 543, 553, 559, 566, 567,

571, 572, 578, 582, 588, 591, 594, 595, 596, 600, 606

<223> n = A,T,C or G

<221> misc_feature

<222> 612, 614, 617, 618, 629, 630, 631, 652, 654, 655, 661, 663,
664, 666, 671, 673, 678, 679, 681, 688, 690, 691, 698, 706,
707, 708, 714, 719, 721, 723, 726, 741, 751, 761, 762, 769,
770, 778, 779, 781, 782, 785, 791, 802, 807, 808, 812

<223> n = A,T,C or G

<221> misc_feature

<222> 815, 820, 827, 828, 838, 841, 844, 851, 857, 864, 866, 869,
872

<223> n = A,T,C or G

<400> 210

```
agcgtggtcg cggccgaggt ccactagagg tctgtgtgcc attgccagc cagagtctct 60
gcgttacaaa ctccataggag ggcttgcgtg gcggagggcc tgctatggtg tgctgcggtt 120
catcatggag agtggggcca aaggctgcga ggtgtgtgtg tctgngaaac tccnaggaca 180
ngagggctaa attccatgaa gtttgtggat ggcctgatga tccacaatcg gagaccctgt 240
taactactac cgtctnaccn cctgctgtnc nccccnttt ctgctnaana catngggntn 300
ntncttgnc ntccttgggt ngaanatnna atngcctncc cnttctanc nctactngnt 360
ccananttgg cctttaaana atccnccttg ccttinnncac tggttcanntn tttnttcgta 420
aacccatna nttnnattan atnntnnnnn nctcaccccc ctcttcattn anccnatang 480
ctnnnaantc cttannncct ccncccnnt ncncctctac tnantcttc tnnccatta 540
cnnagctctt tcntttaana taatgnngcc nngctctnca tntctacnat ntgnnaatn 600
ccccncccc cnancgnntt tttgacctnn naacctcctt tctcttccc tncnaaatt 660
ncnnanttcc ncnttcnnc ntttcggntn ntccatnct tccannnct tcantctanc 720
ncnctncaac ttattttcct ntcacccctt nttctttaca nccccctnn tctactcnc 780
nnttncatta natttgaaac tncacnncnt anttncctcn ctctacnntt ttattttncg 840
ntcnctctac ntaatanttt aatnanttnt cn 872
```

<210> 211

<211> 517

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 462, 464, 506

<223> n = A,T,C or G

<400> 211

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tcgagcggcc gcccgggcag gtctgccaag gagaccctgt tatgctgtgg ggactggctg 60
gggcatggca ggcggctctg gcttcccaacc cttctgttct gagatggggg tgggtgggcag 120
tatctcatct ttgggttcca caatgctcac gtggtcaggc aggggcttct tagggccaat 180
cttaccagtt ggggtcccagg gcagcatgat cttcaccttg atgccagca caccctgtct 240
gagcaacacg tggcgcacaa gcagtgtcaa cgtagtaagt taacagggtc tccgctgtgg 300
atcatcaggc catccacaaa cttcatggat tttagccctct gtccctcggag tttcccagac 360
accacaacct cgcagccttt ggccccactc tccatgatga accgcagcac accatagcag 420
gcccctcgca caagcaagcc ctccaaagaa tttgtaacgc ananactctg ctggcaatgg 480
cacacaaacc tctagtggac ctcggnccgc accacgc 517
```

<210> 212

<211> 695

<212> DNA

<213> Homo sapiens

<220>
<221> misc_feature
<222> 432, 476, 522, 547, 621, 624, 647, 679
<223> n = A,T,C or G

<400> 212
tcgagcggcc gcccgggcag gtctggtcca ggatagcctg cgagtcctcc tactgctact 60
ccagacttga catcatatga atcatactgg ggagaatagt tctgaggacc agtagggcat 120
gattcacaga ttccaggggg gccaggagaa ccaggggacc ctggttgtcc tggaatacca 180
gggtcaccat ttctcccagg aataccagga gggcctggat ctcccttggg gccttgaggt 240
ccttgaccat taggagggcg agtaggagca gttgagggt gtgggcaaac tgcacaacat 300
tctccaaatg gaatttcttg gttggggcag tctaattctt gatccgtcac atattatgtc 360
atcgcagaga acggatcctg agtcacagac acatatttgg catggttctg gcttccagac 420
atctctatcc gncataggac tgaccaagat gggaacatcc tccttcaaca agcttnctgt 480
tgtgccaaaa ataatagtgg gatgaagcag accgagaagt anccagctcc cctttttgca 540
caaagcntca tcatgtctaa atatcagaca tgagacttct ttgggcaaaa aaggagaaaa 600
agaaaaagca gttcaaagta nccnccatca agttggttcc ttgcccnttc agcaccgggg 660
ccccgttata aaacacctng ggccggacc ccctt 695

<210> 213
<211> 804
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 552, 555, 592, 624, 629, 633, 658, 695, 697, 698, 700, 702,
745, 753, 755, 762, 773, 786, 788, 793, 795
<223> n = A,T,C or G

<400> 213
agcgtggtcg cgcccgaggt gttttatgac gggcccggtg ctgaaggga ggaacaact 60
tgatggtgct actttgaact gcttttctt tctcctttt gcacaaagag tctcatgtct 120
gatatttaga catgatgagc tttgtgcaa aggggagctg gctacttctc gctctgcttc 180
atccactat tattttgga caacaggaag ctgttgaagg aggatgttcc catcttggtc 240
agtcctatgc ggatagagat gtctggaagc cagaaccatg ccaaataatgt gtctgtgact 300
caggatccgt tctctgcgat gacataatat gtgacgatca agaattagac tgccccaacc 360
cagaaattcc atttgagaa tgttgtgcag tttgccaca gcctccaact gctcctactc 420
gccctcctaa tgggtcaagga cctcaaggcc ccaagggaga tccagccct cctggtattc 480
ctgggagaaa tgggtaccct ggtattccag gacaaccagg gtcccctggt tctcctggcc 540
cccctggaat cngngaatc atgccctact ggtcctcaa ctattctccc anatgattca 600
tatgatgtca agtctgggat agcnagtang ganggactcg caggctattc tggaccanac 660
ctgccggggg ggcgttcgaa agcccgaatc tgcananntn cnttcacact ggcggccgtc 720
gagctgcttt aaaaggcca ttccncttt agngnggggg antacaatta ctnggcggcg 780
ttttanancg cngnctggg aaat 804

<210> 214
<211> 594
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 452, 509, 585
<223> n = A,T,C or G

<400> 214
agcgtggtcg cgcccgaggt ccacatcggc aggtcgagg cctggccgc catactcgaa 60


```

ctggaatcca tcggtcatgc tctcgccgaa ccagacatgc ctcttgtcct tggggttctt 120
gctgatgtac cagttcttct gggccacact gggctgagtg gggtagacgc aggtctcacc 180
agtctccatg ttgcagaaga ctttgatggc atccaggttg cagccttggg tggggccaat 240
ccagtactct ccactcttcc agtcagagtg gcacatcttg aggtcacggc aggtgcgggc 300
gggggttctt cggtgcacct ctgggctccg gatgttctcg atctgctggc tcaggctctt 360
gaggggtggtg tccacctcga gggtcacggc acgaaccaca ttggcatcat cagcccggta 420
gtagcggcca ccatcgtgag ccttctcttg angtggctgg ggcaggaact gaagtcgaaa 480
ccagcgctgg gaggaccagg gggaccaana ggtccaggaa gggcccgggg gggaccaaca 540
ggaccagcat caccaagtgc gacccgcgag aacctgcccg gccgnccgct cgaa 594

```

```

<210> 215
<211> 590
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 8, 9
<223> n = A,T,C or G

```

```

<400> 215
tcgagcgnnc gcccgggcag gtctcgcggt cgcactgggt atgctgggtcc tgttgggtccc 60
cccggccctc ctggacctcc tgggtcccct ggtcctccca gcgctggttt cgacttcagc 120
ttcttgcccc agccacctca agagaaggct cagcatgggt gccgtacta ccgggtgat 180
gatgccaatg tggttcgtga ccgtgacctc gaggtggaca ccacctcaa gagcctgagc 240
cagcagatcg agaaccatccg gagcccgag ggcagccgca agaaccgcc ccgcacctgc 300
cgtgacctca agatgtgcc a tctgactgg aagagtggag agtactggat tgaccccaac 360
caaggctgca acctggatgc catcaaagtc ttctgcaaca tggagactgg tgagacctgc 420
gtgtacccca ctacgcccag tgtggcccag aagaactggt acatcagcaa gaaccccaag 480
gacaagaggc atgtctggtt cggcgagagc atgaccgatg gattccagtt cgagtatggc 540
ggccagggct cccaccctgc cgatgtggac ctccggccgc gaccaccctt 590

```

```

<210> 216
<211> 801
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 2, 22, 25, 26, 328, 373, 385, 440, 473, 534, 571, 572, 573,
582, 587, 589, 593, 600, 605, 617, 633, 642, 653, 672, 681,
685, 696, 699, 709, 715, 717, 726, 731, 739, 742, 745, 758,
769, 772, 778, 780, 788, 789, 791, 793, 796
<223> n = A,T,C or G

```

```

<400> 216
tngagcggcc gcccgggcag gntgnnaacg ctggctcctgc tgggtcctcct ggcaaggctg 60
gtgaagatgg tcaccctgga aaacccggac gacctggtga gagaggagtt gttggaccac 120
agggtgctcg tggtttccct ggaactcctg gacttctctg cttcaaaggc attaggggac 180
acaatggctc ggtggtgatt aagggacagc ccggtgctcc tgggtggaag ggtgaacctg 240
gtgcccttgg tgaaaatgga actccaggtc aaacaggagc ccgtgggctt cctggtgaga 300
gaggaccgtg ttggtgcccc tggccanac ctccggccgc accacgctaa gccccaattt 360
ccagcacact gngggccgtt actantggat ccgagctcgg taccaagctt ggcgtaatca 420
tggcatagc tgtttcctgn gtgaaattgt tatccgctca caatttcaca cancatacga 480
agccggaaag cataaagtgt aaagccttgg ggtgctaatt agtgagctaa ctncatttaa 540
attgcttgc gctcactgcc cgcttttcca nnngggaaac cntggcntng cngcttttcc 600
ttaantgaaa tccgcnacc ccgggggaaa agncggtttg cngtattggg gcncttttcc 660
ccttctctcg gnttacttga nttantgggc tttggncgnt tcgggttgng gcgancnggt 720

```

tcaacntcac nccaaaggng gnaanacggt ttccccanaa tccgggggnt ancccaangn 780
 aaaacatnng ncnnaanggc t 801

<210> 217
 <211> 349
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 10, 157, 170
 <223> n = A,T,C or G

<400> 217
 agcgtgggtn ggggccgagg tctgggccag gggcaccaac acgtcctctc tcaccaggaa 60
 gccacgggc tctgtttga cctggagttc cattttcacc aggggcacca gggtcacctt 120
 tcacaccagg agcaccgggc tgtcccttca atccatncag accattgtgn cccctaatac 180
 ctttgaagcc aggaagtcca ggagttccag ggaaccacc gagcacctg tggccaaca 240
 actcctctc caccaggtag tccgggtttt ccagggtgac catcttcacc agccttgcca 300
 ggaggaccag caggaccagc gttaccaacc tgcccgggcg gccgctcga 349

<210> 218
 <211> 372
 <212> DNA
 <213> Homo sapiens

<400> 218
 tcgagcggcc gcccgggcag gtccattttc tccctgacgg tcccacttct ctccaatctt 60
 gtagttcaca ccattgtcat ggcaccatct agatgaatca catctgaaat gaccacttcc 120
 aaagcctaag cactggcaca acagtttaaa gcctgattca gacattcgtt cccactcatc 180
 tccaacggca taatgggaaa ctgtgtaggg gtcaaagcac gagtcacccg taggttggtt 240
 caagccttcg ttgacagagt tgccacgggt aacaacctct tccgaacct tatgcctctg 300
 ctggtctttc agtgcctcca ctatgatgtt gtaggtggca cctctggtga ggacctcgcc 360
 cgcgaccagc ct 372

<210> 219
 <211> 374
 <212> DNA
 <213> Homo sapiens

<400> 219
 agcgtgggtag cgcccgagggt cctcaccaga ggtgccacct acaacatcat agtggaggca 60
 ctgaaagacc agcagaggca taagggtcgg gaagaggttg ttaccgtggg caactctgtc 120
 aacgaaggct tgaaccaacc tacggatgac tcgtgctttg accctacac agtttcccat 180
 tatgccgttg gagatgagtg ggaacgaatg tctgaatcag gctttaaact gttgtgccag 240
 tgcttaggct ttggaagtgg tcatttcaag atgtgattca tctagatggt gccatgacaa 300
 tgggtgtgaac tacaagattg gagagaagtg ggaccgtcag ggagaaaatg gacctgcccg 360
 ggccggccgc tcga 374

<210> 220
 <211> 828
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 8, 9, 557, 571, 587, 588, 601, 642, 643, 647, 654, 664, 681,
 688, 698, 719, 720, 725, 734, 738, 743, 744, 757, 765, 773,

778, 780, 782, 783, 793, 798, 805, 809, 822, 827

<223> n = A,T,C or G

<400> 220

```

tcgagcggnnc gcccgggcag gtccagtagt gccttcggga ctgggttcac ccccgaggtct 60
gcggcaggttg tcacagcgcc agccccgctg gcctccaaag catgtgcagg agcaaatggc 120
accgagatat tccttctgcc actgttctcc tacgtgggtat gtcttcccat catcgtaaca 180
cggttgctca tgagggtcac acttgaattc tccttttccg ttcccaagac atgtgcagct 240
catttggttg gctctatagt ttggggaaag tttgttgaaa ctgtgccact gacctttact 300
tcctccttct ctactggagc tttcgtacct tccacttctg ctgttggttaaatgtgtgat 360
cttctatcaa ttctattgac agtaccact tctcccaaac atccaggga atagtattt 420
cagagcgatt aggagaacca aattatggg cagaaataag gggcttttcc acaggtttt 480
ctttggagga agatttcagt ggtgacttta aaagaatact caacagtgtc ttcacccca 540
tagcaaaaga agaaacngta aatgatggaa ngcttctgga gatgccnca tttaaggga 600
nccagaaact tcaccatcta caggacctac ttcagtttac annaagncac atantctgac 660
tcanaaaagga cccaagtagc nccatggna gcacttttag cctttcccct ggggaaaann 720
ttacnttctt aaancctngg ccnngacccc cttaagncca aattntggaa aanttcctn 780
cnnctggggg gcngttcnac atgcntttta agggcccaat tncccent 828

```

<210> 221

<211> 476

<212> DNA

<213> Homo sapiens

<400> 221

```

tcgagcgggc gcccgggcag gtgtcggagt ccagcacggg aggcgtggtc ttgtagtgt 60
tctcgggtg cccattgctc tcccactcca cggcgatgtc gctgggatag aagcctttga 120
ccaggcaggt caggctgacc tgggtcttgg tcatctctc cgggatggg ggcagggtgt 180
acacctgtgg ttctcggggc tgccctttgg ctttgagat ggttttctcg atgggggtg 240
ggagggtttt gttggagacc ttgcacttgt actccttgcc attcagccag tctgtgtgca 300
ggacggtgag gacgctgacc acacggtacg tgcgtgtgta ctgctcctcc cgcgggtttg 360
tcttggtcatt atgcacctcc acgccgtcca cgtaccagt gaacttgacc tcagggtctt 420
cgtggtcac gtccaccacc acgcatgtaa cctcagacct cggccgcgac cacgct 476

```

<210> 222

<211> 477

<212> DNA

<213> Homo sapiens

<400> 222

```

agcgtggtcg cggccgaggt ctgaggttac atgcgtggtg gtggacgtga gccacgaaga 60
ccctgaggtc aagttcaact ggtacgtgga cggcggtggag gtgcataatg ccaagacaaa 120
gccgcgggag gagcagtaca acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca 180
ccaggactgg ctgaatggca aggagtacaa gtgcaaggct tocaacaaag ccctcccagc 240
ccccatcgag aaaaccatct ccaaagccaa agggcaagcc ccgagaacca caggtgtaca 300
ccctgcccc atcccgggag gagatgacca agaaccaggt cagcctgacc tgctgtgtca 360
aaggcttcta tcccagcgac atcgccgtgg agtgggagag caatgggag ccggagaaca 420
actacaagac cagcctccc gtgctggact ccgacacctg cccgggcggc cgctcga 477

```

<210> 223

<211> 361

<212> DNA

<213> Homo sapiens

<400> 223

```

tcgagcgggc gcccgggcag gttgaatggc tctcgtctga ccaccccggt gctggtggtg 60
ggtacagagc tccgatgggt gaaaccattg acatagagac tgtccctgtc cagggtgtag 120
gggcccagct cagtgatgcc gtgggtcagc tggtcagct tccagtacag ccgctctctg 180

```

tccagtccag ggcttttggg gtcaggacga tgggtgcaga cagcatccac tctggtggct 240
gccccatcct tctcaggcct gagcaaggtc agtctgcaac cagagtacag agagctgaca 300
ctggtgttct tgaacaaggg cataagcaga ccctgaagga cacctcggcc gcgaccacgc 360
t 361

<210> 224

<211> 361

<212> DNA

<213> Homo sapiens

<400> 224

agcgtggctc cgcccgaggt gtccttcagg gtctgcttat gcccttgctc aagaacacca 60
gtgtcagctc tctgtactct ggttcagac tgaccttgct caggcctgag aaggatgggg 120
cagccaccag agtggatgct gtctgcaccc atcgtcctga ccccaaaagc cctggactgg 180
acagagagcg gctgtactgg aagctgagcc agctgaccca cggcatcact gagctgggcc 240
cctacaccct ggacagggac agtctctatg tcaatggttt caccatcgg agctctgtac 300
ccaccaccag caccggggtg gtcagcgagg agccattcaa cctgcccggg cggccgctcg 360
a 361

<210> 225

<211> 766

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 574, 610, 631, 643, 657, 660, 666, 688, 712, 735, 747

<223> n = A,T,C or G

<400> 225

agcgtggctc cgcccgaggt cctgtcagag tggcactggg agaagttcca ggaaccctga 60
actgtaaggg ttcttcatca gtgccaacag gatgacatga aatgatgtac tcagaagtgt 120
cctggaatgg ggcccatgag atggttgtct gagagagagc ttcttgctct acattcggcg 180
ggtatggtct tggcctatgc cttatggggg tggccgttgt gggcgggtgtg gtccgcctaa 240
aaccatgttc ctcaaagatc atttgttgcc caacactggg ttgtgacca gaagtgccag 300
gaagctgaat accatttcca gtgtcatacc cagggtgggt gacgaaaggg gtcttttgaa 360
ctgtggaagg aacatccaag atctctgttc catgaagatt ggggtgtgga agggttacca 420
gttggggaag ctgctctgtc tttttccttc caatcagggg ctgctcttc tgattattct 480
tcagggcaat gacataaatt gtatattcgg tcccggttcc aggccagtaa tagtagctc 540
tgtgacacca gggcggggcc gagggaccct tctnttgga gagaccagct tctcatactt 600
gatgatgagn ccggtaatcc tggcacgtgg nggttgcatg atnccaccaa ggaaatnggn 660
ggggngggac ctgcccggcg gccgttcnaa agcccaattc cacacacttg gnggcctgac 720
tatggatccc actcngtcca acttgngnga atatggcata actttt 766

<210> 226

<211> 364

<212> DNA

<213> Homo sapiens

<400> 226

tcgagcggcc gcccgggcag gtccttgacc ttttcagcaa gtgggaagg gtaatccgtc 60
tcacagaca agccaggac tcgtttgtac ccgttgatga tagaatggg tactgatgca 120
acagttgggt agccaatctg cagacagaca ctggcaacat tgcggacacc ctccaggaag 180
cgagaatgca gagtttctc tgtgatatca agcacttcag ggtttagat gctgccattg 240
tcgaacacct gctggatgac cagcccaaag gagaagggg agatgttgag catgttcagc 300
agcgtggctt cgctggctcc cactttgtct ccagtcttga tcagacctcg gcccgacca 360
cgct 364

<210> 227
<211> 275
<212> DNA
<213> Homo sapiens

<400> 227
agcgtggtcg cggccgaggt ctgtcctaca gtcctcagga ctctactccc tcagcagcgt 60
ggtgaccgtg ccctccagca acttcggcac ccagacctac acctgcaacg tagatcacia 120
gcccagcaac accaaggtgg acaagagagt tgagcccaaa tcttgtgaca aaactcacac 180
atgccaccg tggccagcac ctgaactcct ggggggaccg tcagtcttcc tcttcccccg 240
catccccctt ccaaacctgc ccggcgggcc gctcg 275

<210> 228
<211> 275
<212> DNA
<213> Homo sapiens

<400> 228
cgagcgggccg cccgggcagg tttggaaggg ggatgcgggg gaagaggaag actgacggtc 60
ccccaggag ttcaggtgct gggcacgggtg ggcattgtgt agttttgtca caagatttg 120
gctcaactct cttgtccacc ttggtgttgc tgggcttgtg atctacgttg caggtgtagg 180
tctgggtgcc gaagttgctg gagggcacgg tcaccacgct gctgagggag tagagtctg 240
aggactgtag gacagacctc ggccgcgacc acgct 275

<210> 229
<211> 40
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 1, 4, 5, 13, 15, 17, 29
<223> n = A,T,C or G

<400> 229
nggnnggtcc ggnncngncag gaccactcnt cttcgaata 40

<210> 230
<211> 208
<212> DNA
<213> Homo sapiens

<400> 230
agcgtggtcg cggccgaggt cctcacttgc ctctgcaaa gcaccgatag ctgcgctctg 60
gaagcgaga tctgttttaa agtcctgagc aatttctcgc accagacgct ggaagggag 120
tttgcaatc agaagttcag tggacttctg ataacgtcta atttcacgga gcgccacagt 180
accagacct gcccgggcgg ccgctcga 208

<210> 231
<211> 208
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 33
<223> n = A,T,C or G

<400> 231
 tcgagcggcc gcccgggcag gtccctggtag tngggcgctc cgtgaaatta gacgttatca 60
 gaagtccact gaacttctga ttccgaaact tcccttccag cgtctggtgc gagaaattgc 120
 tcaggacttt aaaacagatc tgcgcttcca gagcgagct atcgggtgctt tgcaggaggc 180
 aagtgaggac ctcggccgcg accacgct 208

<210> 232
 <211> 332
 <212> DNA
 <213> Homo sapiens

<400> 232
 tcgagcggcc gcccgggcag gtccacatcg gcagggtcgg agccctggcc gccatactcg 60
 aactggaatc catcggtcat gctctcgccg aaccagacat gcctcttgtc cttgggggttc 120
 ttgctgatgt accagttctt ctggggccaca ctgggctgag tggggtacac gcaggtctca 180
 ccagctctcca tgttgacaga gactttgatg gcattccaggt tgcagccttg gttgggggtca 240
 atccagtact ctccactctt ccagtcagag tggcacatct tgaggtcacg gcaggtgcgg 300
 gcgggggttct tgacctcggc cgcgaccacg ct 332

<210> 233
 <211> 415
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 6, 15, 19, 21
 <223> n = A,T,C or G

<400> 233
 gtgggnttga accnttttna nctccgcttg gtaccgagct cggatccact agtaacggcc 60
 gccagtgtgc tgggaattcgg cttagcgtgg tcgcgggccga ggtcaagaac cccgcccgcg 120
 cctgccgtga cctcaagatg tgccactctg actggaagag tggagagtac tggattgacc 180
 ccaaccaagg ctgcaacctg gatgccatca aagtcttctg caacatggag actggtgaga 240
 cctgcgtgta cccactcag ccagtggtg cccagaagaa ctggtacatc agcaagaacc 300
 ccaaggacaa gaggcagtgc tggttcggcg agagcatgac cgatggattc cagttcagat 360
 atggcgggcca gggctccgac cctgccgatg tggacctgcc cggcgggccg ctgca 415

<210> 234
 <211> 776
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 505, 550, 574, 601, 604, 608, 612, 649, 656, 657, 680, 711,
 750, 776
 <223> n = A,T,C or G

<400> 234
 agcgtggtcg cggccgaggt ctgggatgct cctgctgtca cagtgagata ttacaggatc 60
 acttacggag aaacaggagg aaatagccct gtccaggagt tcaactgtgc tgggagcaag 120
 tctacagcta ccatcagcgg ccttaaacct ggagttgatt ataccatcac tgtgtatgct 180
 gtcactggcc gtggagacag ccccgcaagc agcaagccaa ttccattaa ttaccgaaca 240
 gaaattgaca aaccatcca gatgcaagt accgatgttc aggacaacag cattagtgtc 300
 aagtggctgc cttcaagttc ccctgttact ggttacagag taaccaccac tcccaaaaat 360
 ggaccaggac caacaaaaac taaaactgca ggtccagatc aaacagaaat gactattgaa 420
 ggcttgacgc ccacagtgga gtatgtggtt aagtgtctat gtcagaatc caagcgaga 480

gaagtcagcc tctgggtcag actgnaagta accaaccattg atcgccctaaa ggactggcat 540
tcactgatgn ggaatgccgat tccatcaaaa ttgnttgga aaaccacacag gggcaagtgt 600
ncangtcnag gnggacctac tcgagccctg aggatggaat ccttgactnt tccttnncc 660
gatggggaaa aaaaaccttn aaaacttgaa ggacctgccc gggcgccgt ncaaaaccca 720
attccacccc cttggggcg ttctatgggn cccactcgga ccaaacttg ggtaan 776

<210> 235

<211> 805

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 637, 684, 705, 724, 733, 756, 778, 793, 796, 804

<223> n = A,T,C or G

<400> 235

tcgagcggcc gcccgggcag gtccttgca gtcctgcagt tcttcttcac catcagggtgc 60
aggaatagc tcatggattc catcctcagg gtcgagtag gtcaccctgt acctggaaac 120
ttgccctgt gggctttccc aagcaatgt gatggaatcg gcatccacat cagtgaatgc 180
cagtccttta gggcgatcaa tgttggttac tgcagctga accagaggct gactctctcc 240
gcttggttc tgagcataga cactaaccac atactccact gtgggctgca agccttcaat 300
agtcatttct gtttgatctg gacctgcagt tttagtttt gtgggtcctg gtccattttt 360
gggagtggtg gttactctgt aaccagtaac aggggaactt gaaggcagcc acttgacact 420
aatgctgttg tcctgaacat cggctcactg catctgggat ggtttgtcaa tttctgttcg 480
gtaattaatg gaaattggct tgctgcttg gggccttgtc tccacggcca gtgacagcat 540
acacagtgt ggtataatca actccagggt taagccgctg atggtagctg aaactttgct 600
ccaggcacia gtgaactcct gacagggcta tttcctnctg ttctccgtaa gtgatcctgt 660
aatactcac tgggacagca ggangcattc caaaacttcg ggcngaccc cctaagccga 720
attntgcaat atncatcaca ctggcggcg ctcgancatt cattaaaagg cccaatcnc 780
cctataggga gntantaca attng 805

<210> 236

<211> 262

<212> DNA

<213> Homo sapiens

<400> 236

tcgagcggcc gcccgggcag gtcacttttg gtttttggtc atgttcggtt ggtcaaagat 60
aaaaactaag tttgagagat gaatgcaaag gaaaaaata ttttcaaag tccatgtgaa 120
attgtctccc attttttttg cttttgagg ggttcagttt gggttgcttg tctgtttccg 180
ggttgggggg aaagtgtgtt ggggtggagg gagccagggt gggatggagg gagtttacag 240
gaagcagaca gggccaacgt cg 262

<210> 237

<211> 372

<212> DNA

<213> Homo sapiens

<400> 237

agcgtggtcg cgcccgaggt cctcaccaga ggtgccacct acaacatcat agtggaggca 60
ctgaaagacc agcagaggca taagggtcgg gaagagggtt ttaccgtgg caactctgtc 120
aacgaaggct tgaaccaacc tacggatgac tcgtgctttg acccctacac agtttcccat 180
tatgccgttg gagatgagt ggaacgaatg tctgaatcag gctttaaact gttgtgccag 240
tgcttaggct ttggaagtgg tcatttcaga tgtgattcat ctagatgggt ccatgacaat 300
ggtgtgaact acaagattgg agagaagtgg gaccgtcagg gagaaaatgg acctgcccg 360
cgggccgctc ga 372

<210> 238
<211> 372
<212> DNA
<213> Homo sapiens

<400> 238
tcgagcggcc gcccgggcag gtccattttc tccctgacgg tccactttct ctccaattctt 60
gtagttcaca ccattgtcat ggcaccatct agatgaatca catctgaaat gaccacttcc 120
aaagcctaag cactggcaca acagtttaaa gcctgattca gacattcgtt cccactcatc 180
tccaacggca taatgggaaa ctgtgtaggg gtcaaagcac gagtcacccg taggttggtt 240
caagccttcg ttgacagagt tgcccacggg aacaacctct tcccgaacct tatgcctctg 300
ctggtctttc agtgcctcca ctatgatgtt gtaggtggca cctctggtga ggacctcggc 360
cgcgaccacg ct 372

<210> 239
<211> 720
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 478, 557, 563, 566, 620, 660, 663, 672, 673, 684, 693, 695
<223> n = A,T,C or G

<400> 239
tcgagcggcc gcccgggcag gtccaccata agtcctgata caaccacgga tgagctgtca 60
ggagcaaggt tgatttcttt cattggtccg gtcttctcct tgggggtcac ccgcactcga 120
tatccagtga gctgaacatt ggggtggtgc cactgggcgc tcaggcttgt ggggtgtgacc 180
tgagtgaact tcaggtcagt tgggtgcagga atagtggta ctgcagtctg aaccagaggc 240
tgactctctc cgcttgatt ctgagcatag acactaacca catactccac tgtgggctgc 300
aagccttcaa tagtcatttc tgtttgatct ggacctgcag ttttagtttt tgttggtcct 360
ggtccatttt tgggagtggg ggttactctg taaccagtaa caggggaaact tgaaggcagc 420
cacttgacac taatgctgtt gtcctgaaca tcggtcactt gcatctggga tggtttgnca 480
atctctgttc ggtaattaat ggaaattggc ttgctgcttg cggggctgtc tccacggcca 540
gtgacagcat acacagngat ggnatnatca actccaagtt taaggccctg atggtaactt 600
taaaacttgc cccagccagn gaacttccgg acagggtatt tcttctggtt ttccgaaagn 660
gancctggaa tnnctctcct ggancagaag gancntccaa aacttgggcc ggaaccctt 720

<210> 240
<211> 691
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 564, 582, 640, 651, 666, 669, 690
<223> n = A,T,C or G

<400> 240
agcgtggtcg cgcccgaggt cctgtcagag tggcactggt agaagttcca ggaaccctga 60
actgtaaggg ttcttcatca gtgccaacag gatgacatga aatgatgtac tcagaagtgt 120
cctggaatgg ggcccatgag atgggtgtct gagagagagc ttcttgcctt acattcggcg 180
ggtatggtct tggcctatgc cttatggggg tggccgttgt gggcgggtgtg gtccgcctaa 240
aaccatgttc ctcaaagatc atttgttgcc caaactgagg ttgctgacca gaagtgccag 300
gaagctgaat accattttcca gtgtcatacc cagggtgggt gacgaaaggg gtcttttgaa 360
ctgtggaagg aacatccaag atctctggtc catgaagatt ggggtgtgga agggttacca 420
gttggggaag ctgctctgtc tttttccttc caatcagggg ctgctcttct tgattattct 480


```

tcagggcaat gacataaatt gtatattcgg ttcccgggtc caggccagta atagtagcct 540
cttgtgacac caggcggggc ccanggacca cttctctggg angagacca gcttctcata 600
cttgatgatg taacccggta atcctgcacg tggcggctgn catgatacca ncaaggaatt 660
gggtgnggng gacctgcccg gcggccctcn a 691

```

<210> 241

<211> 808

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 680, 715, 721, 728, 735, 749, 757, 762, 772, 776, 779, 781, 792, 796, 800, 808

<223> n = A,T,C or G

<400> 241

```

agcgtggtcg cggccgaggt ctgggatgct cctgctgtca cagtgaagata ttacaggatc 60
acttacggag aaacaggagg aaatagccct gtccaggagt tcaactgtgcc tgggagcaag 120
tctacagcta ccatcagcgg ccttaaacct ggagttgatt ataccatcac tgtgtatgct 180
gtcactggcc gtggagacag ccccgaagc agcaagccaa ttccattaa ttaccgaaca 240
gaaattgaca aaccatccca gatgcaagt accgatgttc aggacaacag cattagtgtc 300
aagtggctgc cttcaagttc ccctgttact ggttacagag taaccaccac tcccaaaaat 360
ggaccaggac caacaaaaac taaaactgca ggtccagatc aaacagaaat gactattgaa 420
ggcttgacgc ccacagtga gtatgtggtt agtgtctatg ctcagaatcc aagcggagag 480
agtcagcctc tggttcagac tgcagtaacc actattcctg caccaactga cctgaagttc 540
actcaggtca caccacaag cctgagccgc cagtggacac caccatgt tcaactactg 600
gatatcgagt gcgggtgacc cccaaggaga agaccggac ccatgaaaga aatcaacctt 660
gctcctgaca gctcatccgn ggggttatca ggacttatgg gggactgcc cggcnggccg 720
ntcgaaancg aattntgaaa tttccttcnc actggngggc gnttcgagct tnctntana 780
nggcccaatt cncctntagn gggtcgtn 808

```

<210> 242

<211> 26

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 22

<223> n = A,T,C or G

<400> 242

agcgtggtcg cggccgaggt cnagga

26

<210> 243

<211> 697

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 496, 541, 624, 662, 679, 688

<223> n = A,T,C or G

<400> 243

```

tcgagcggcc gcccgggcag gtccaccaca cccaattcct tgctggatc atggcagccg 60
ccacgtgcca ggattaccgg ctacatcatc aagtatgaga agcctgggtc tctcccaga 120

```

```

gaagtgggtcc ctcggccccc ccctgggtgtc acagaggcta ctattactgg cctggaaccg 180
ggaaccgaat atacaatttta tgtcattgcc ctgaagaata atcagaagag cgagcccctg 240
attggaagga aaaagacaga cgagcttccc caactggtaa cccttccaca cccaatctt 300
catggaccag agatcttgga tgttccttcc acagttcaaa agaccccttt cgtcaccac 360
cctgggtatg aacttgaaa tgggtattcag cttcctggca cttctggtca gcaaccag 420
gttgggcaac aatgatctt tgaggaacat ggttttaggc ggaccacac gccacaacg 480
ggcaccacca taaggnatag gccaaagaca taccgcgcg aatgtaggac aagaagctct 540
ntctcaacaa ccatctcatg ggccccattc caggacactt ctgagtacat catttcatgt 600
catcctggtg ggcacttgat gaanaaccct tacagttcag ggctcctgga acttctacca 660
gngccacttc tgacagganc ttgggcgnga ccaccct 697

```

<210> 244

<211> 373

<212> DNA

<213> Homo sapiens

<400> 244

```

agcgtgggtcg cgcccgaggt ccattttctc cctgacggtc ccacttctct ccaatcttgt 60
agttcacacc attgtcatgg caccatctag atgaatcaca tctgaaatga ccaattccaa 120
agcctaagca ctggcacaac agtttaagc ctgattcaga cattcggtcc cactcatctc 180
caacggcata atgggaaact gtgtaggggt caaagcacga gtcattccgta gggtgggtca 240
agccttcggt gacagagttg cccacggtaa caacctctc ccgaacctta tgccctctgt 300
ggtctttcag tgcctccact atgatgttgt aggtggcacc tctggtgagg acctgcccgg 360
gcggcccgcgt cga 373

```

<210> 245

<211> 307

<212> DNA

<213> Homo sapiens

<400> 245

```

agcgtgggtcg cgcccgaggt gtgccccaga ccaggaattc ggcttcgacg ttggccctgt 60
ctgcttctctg taaactccct ccattcccaac ctggctccct cccacccaac caactttccc 120
cccaaccgga aaacagacaa gcaacccaaa ctgaaccccc tcaaaagcca aaaaaatggg 180
agacaatttc acatggactt tggaaaatat ttttttcctt tgcatcctc tctcaaaact 240
agtttttatc tttgaccaac cgaacatgac caaaaaccaa aagtgcctg cccgggcggc 300
cgctcga 307

```

<210> 246

<211> 372

<212> DNA

<213> Homo sapiens

<400> 246

```

tcgagcggcc gcccgggcag gtctcacca gaggtgccac ctacaacatc atagtggagg 60
cactgaaaga ccagcagagg cataaggttc gggaagaggt tgttaccgtg ggcaactctg 120
tcaacgaagg cttgaaccaa cctacggatg actcgtgctt tgaccctac acagtttccc 180
attatgccgt tgagatgag tgggaacgaa tgtctgaatc aggccttaaa ctgttggtgc 240
agtgtctagg ctttggaagt ggtcatttca gatgtgattc atctagatgg tgccatgaca 300
atgggtgtgaa ctacaagatt ggagagaagt gggaccgtca gggagaaaat ggacctcggc 360
cgcgaccacg ct 372

```

<210> 247

<211> 348

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature
<222> 284, 297, 299, 322, 325, 338, 342, 345
<223> n = A,T,C or G

<400> 247
tcgagcggcc gcccgggcag gtaccggggt ggtcagcgag gagccattca cactgaactt 60
caccatcaac aacctgcggt atgaggagaa catgcagcac cctggctcca ggaagttcaa 120
caccacggag agggtccttc agggcctgct cagggtccctg ttcaagagca ccagtgttgg 180
ccctctgtac tctggctgca gactgacttt gctcagacct gagaaacatg gggcagccac 240
tggagtggac gccatctgca cctccgcct tgatcccaact ggtinctggac tggacanana 300
gcggctatac ttgggagctg anccnaacct ttggcgngna cncnctt 348

<210> 248
<211> 304
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 125
<223> n = A,T,C or G

<400> 248
gaggactggc tcagctccca gtatagccgc tctctgtcca gtccaggacc agtgggatca 60
aggcggaggg tgcagatggc gtccactcca gtggctgccc catgtttctc aagtctgagc 120
aaagnacagtc tgcagccaga gtacagaggg ccaacactgg tgctcttgaa cagggacctg 180
agcaggccct gaaggaccct ctccgtggtg ttgaacttcc tggagccagg gtgctgcatg 240
ttctctcat accgcagggt gttgatggtg aagttcagtg tgaatggctc ctgctgacc 300
accc 304

<210> 249
<211> 400
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 308, 310, 312, 320, 331, 336, 383, 392, 396
<223> n = A,T,C or G

<400> 249
agcgtggtcg cgcccgaggt ccaccacacc caattccttg ctggtatcat ggcagccgcc 60
acgtgccagg attaccggct acatcatcaa gtatgagaag cctgggtctc ctcccagaga 120
agtggtcctt cggcccgcct ctggtgtcac agaggctact attactggcc tggaaaccggg 180
aaccgaatat acaatttatg tcattgccct gaagaataat cagaagagcg agcccctgat 240
tggaaaggaaa aagacagacg agcttcccca actggttaacc cttccacacc ccaatcttca 300
tggaccanan ancttggatn gtcctttcac nggttnaaaa aacccttttc gccccccac 360
cttgggggatt aaccttggga aanggggatt tnacnnttcc 400

<210> 250
<211> 400
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 338, 357, 361, 369, 388, 394
<223> n = A,T,C or G

```

<400> 250
tcgagcgggcc gcccgggcag gtcctgtcag agtggcactg gtagaagttc caggaaccct 60
gaactgtaag ggttcttcat cagtgccaac aggatgacat gaaatgatgt actcagaagt 120
gtcctggaat ggggcccatg agatggttgt ctgagagaga gcttcttgtc ctacattcgg 180
cgggtatggt cttggcctat gccttatggg ggtggccggt gtgggcggtg tgggtccgct 240
aaaacccatgt tcctcaaaga tcatttggtg cccaacactg ggttgctgac cagaagtgcc 300
aggaagctga ataccatttc cagtgtcata cccagggngg gtgaccaaag ggggtcnttt 360
ngacctggng aaaggaacca tccaaaanct ctgncccatg 400

```

```

<210> 251
<211> 514
<212> .DNA
<213> Homo sapiens

```

```

<220>
<221> misc feature
<222> 8, 107, 312, 338, 351, 352, 357, 363, 366, 373, 380, 405,
421, 444, 508
<223> n = A,T,C or G

```

```

<400> 251
agcgtggncg cggccgaggt ctgaggatgt aaactcttcc caggggaagg ctgaagtgct 60
gaccatggtg ctactgggtc cttctgagtc agatatgtga ctgatngaa ctgaagtagg 120
tactgtagat ggtgaagtct ggggtgccct aaatgctgca tctccagagc cttccatcat 180
taccgtttct tcttttgcta tgggatgaga cactgttgag tattctctaa agtcaccact 240
gaaatcttcc tccaaaggaa aacctgtgga aaagcccctt atttctgcc cataatttgg 300
ttctccta at cncctgaaa tcactatttc cctggaangt ttgggaaaaa nngggcnacc 360
tgncantgga aantggatan aaagatccca ccattttacc caacnagcag aaagtgggaa 420
nggtaccgaa aagctccaag taanaaaaag gagggaagta aaggtcaagt gggcaccagt 480
ttcaaacaaa actttcccca aactatanaa ccca 514

```

```

<210> 252
<211> 501
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc feature
<222> 20, 21, 25, 44, 343, 347, 356, 362, 387, 391, 398, 409, 428,
430, 453, 494
<223> n = A,T,C or G

```

```

<400> 252
aagcggcgc cgggcaggn ncagnagtgc cttcgggact gggntcacc ccaggtctgc 60
ggcagttgtc acagcgccag ccccgctggc ctccaaagca tgtgcaggag caaatggcac 120
cgagatattc cttctgccac tgttctccta cgtggtatgt cttcccatca tcgtaacacg 180
ttgcctcatg agggtcacac ttgaattctc ctttccggt cccaagacat gtgcagctca 240
tttggtcgtc tctatagttt ggggaaagt tgttgaaact gtgccactga cctttacttc 300
ctccttctct actggagctt tccgtacct ccaacttctgc tngtggnaaa aaggnggaa 360
cntcttatca atttcattgg acagtanccc nctttctncc caaaacatnc aagggaatat 420
attgattncn agagcggatt aaggaacaac ccnaattatg ggggccagaa ataaaggggg 480
ctttccaca ggtnttttcc t 501

```

```

<210> 253
<211> 226
<212> DNA
<213> Homo sapiens

```

<400> 253

```

tcgagcggcc gcccgggcag gtctgcaggc tattgtaagt gttctgagca catatgagat 60
aacctgggcc aagctatgat gttcgatacg ttaggtgtat taaatgcact tttgactgcc 120
atctcagtgg atgacagcct tctcactgac agcagagatc ttctcactg tgccagtggg 180
caggagaaaag agcatgctgc gactggacct cggccgcgac cacgct 226

```

<210> 254

<211> 226

<212> DNA

<213> Homo sapiens

<400> 254

```

agcgtggtcg cggccgaggt ccagtcgcag catgctcttt ctctgcccc ctggcacagt 60
gaggaagatc tctgctgtca gtgagaaggc tgtcatccac tgagatggca gtcaaaagtg 120
catttaatac acctaacgta tcgaacatca tagcttggcc caggttatct catatgtgct 180
cagaacactt acaatagcct gcagacctgc ccggcgggcc gctcga 226

```

<210> 255

<211> 427

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 327, 403

<223> n = A,T,C or G

<400> 255

```

cgagcggccg cccgggcagg tccagactcc aatccagaga accaccaagc cagatgtcag 60
aagctacacc atcacagggt tacaaccagg cactgactac aagatctacc tgtacacctt 120
gaatgacaat gtcggagct cccctgtggt catcgacgcc tccactgccca ttgatgcacc 180
atccaacctg cgtttcctgg ccaccacacc caattccttg ctggtatcat ggcagccgcc 240
acgtgccagg attaccggct acatcatcaa gtatgagaag cctgggtctc ctcccagaga 300
agtggtcctt cggccccgcc ctggtgncac agaagctact attactggcc tggaaccggg 360
aaccgaatat acaatttatg tcattgccct gaagaataat canaagagcg agcccctgat 420
tggaagg 427

```

<210> 256

<211> 535

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 347, 456, 475

<223> n = A,T,C or G

<400> 256

```

agcgtggtcg cggccgaggt cctgtcagag tggcactggt agaagttcca ggaaccctga 60
actgtaaggg ttcttcatca gtgccaacag gatgacatga aatgatgtac tcagaagtgt 120
cctggaatgg ggcccatgag atggttgtct gagagagagc ttcttgcctt gtctttttcc 180
ttccaatcag gggctcgtct ttctgattat tcttcagggc aatgacataa attgtatatt 240
cgggtccccg ttccaggcca gtaatagtag cctctgtgac accagggcgg ggccgaggga 300
ccacttctct gggaggagac ccaggcttct catacttgat gatgtanccg gtaatcctgg 360
caccgtggcg gctgccatga taccagcaag gaattgggtg tggaggccaa gaaacgcagg 420
ttggatggtg catcaatggc agtggaggcg tcgatnacca caggggagct ccgancattg 480
tcattcaagg tggacaggta gaatcttgta atcagggtgcc tggtttgtaa acctg 535

```

<210> 257
<211> 544
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 495, 511
<223> n = A,T,C or G

<400> 257
tcgagcggcc gcccgggcag gtttcgtgac cgtgacctcg aggtggacac caccctcaag 60
agcctgagcc agcagatcga gaacatccgg agcccagagg gcagccgcaa gaaccccgcc 120
cgcacctgcc gtgacctcaa gatgtgccac tctgactgga agagtggaga gtactggatt 180
gacccaacc aaggctgcaa cctggatgcc atcaaagtct tctgcaacat ggagactggg 240
gagacctgcg tgtacccac tcagcccagt gtggcccaga agaactggta catcagcaag 300
aacccaagg acaagaagca tgtctgggtc ggcgaaagca tgaccgatgg attccagttc 360
gagtatggcg gccagggctc cgacctgcc gatgtggacc tcggccgcga ccacgctaag 420
cccgaattcc agcacactgg cggccgttac tagtgggatc cgagcttcgg taccaagctt 480
ggcgtaatca tgggncatag ctgtttcctg ngtgaaaatg gtattccgct tcacaatttc 540
ccac 544

<210> 258
<211> 418
<212> DNA
<213> Homo sapiens

<400> 258
agcgtggtcg cggccgaggt ccacatcggc agggtcggag ccctggccgc catactcgaa 60
ctggaatcca tcggtcatgc tctcgccgaa ccagacatgc ctcttgctct tggggttctt 120
gctgatgtac cagttcttct gggccacact gggctgagtg ggttacacgc aggtctcacc 180
agtctccatg ttgcagaaga ctttcatggc atccaggttg cagccttggt tggggtaaat 240
ccagtactct ccactcttcc agtcagagtg gcacatcttg aggtcacggc aggtgcgggc 300
ggggttcttg cggtgcctct ctgggtcccg gatgttctcg atctgctggc tcaagctctt 360
gaaggggtgt gtccacctcg aggtcacggt cacgaaacct gcccgggcgg ccgctcga 418

<210> 259
<211> 377
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 320, 326, 342, 352
<223> n = A,T,C or G

<400> 259
agcgtggtcg cggccgaggt caagaacccc gcccgcacct gccgtgacct caagatgtgc 60
cactctgact ggaagagtgg agagtactgg attgacccca accaaggctg caacctggat 120
gccatcaaaag tcttctgcaa catggagact ggtgagacct gcgtgtaccc cactcagccc 180
agtgtggccc agaagaactg gtacatcagc aagaacccca aggacaagag gcatgtctgg 240
ttcggcgaga gcatgaccga tggattccag ttcgagtatg gcggccaggg ctccgaccct 300
gccgatgtgg acctgcccg n gccggnccgc tcgaaaagcc cnaatttcca gncacacttg 360
gccggccggt actactg 377

<210> 260
<211> 332

<212> DNA

<213> Homo sapiens

<400> 260

```
tcgagcggcc gcccgggcag gtccacatcg gcagggtcgg agccctggcc gccatactcg 60
aactggaatc catcggtcat gctctcgccg aaccagacat gcctcttgtc cttgggggttc 120
ttgctgatgt accagttctt ctgggccaca ctgggctgag tggggtagac gcagggtctca 180
ccagtctcca tgttgacagaa gactttgatg gcatccaggt tgcagccttg gttgggggtca 240
atccagtact ctccactctt ccagtcagag tggcacatct tgaggtcacg gcagggtgcgg 300
gcgggggttct tgacctcggc cgcgaccacg ct                                     332
```

<210> 261

<211> 94

<212> DNA

<213> Homo sapiens

<400> 261

```
cgagcggccg cccgggcagg tccccccct ttttttttt ttttttttt ttttttttt 60
ttttttttt ttttttttt ttttttttt tttt                                     94
```

<210> 262

<211> 650

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 412, 582, 612, 641, 646

<223> n = A,T,C or G

<400> 262

```
agcgtggtcg cggccgaggt ctggcattcc ttcgacttct ctccagccga gtttcccaga 60
acatcacata tcaactgaaa aatagcattg catacatgga tcaggccagt ggaaatgtaa 120
agaagccct gaagctgatg gggcacaatg aaggtgaatt caaggctgaa ggaaatagca 180
aattcaccta cacagtctcg gaggatggtt gcacgaaaca cactggggaa tggagcaaaa 240
cagtctttga atatcgaa caagaggctg tgagactacc tattgtagat attgcaccct 300
atgacattgg tggctctgat caagaatttg gtgtggacgt tggccctggt tgctttttat 360
aaaccaaact ctatctgaaa tcccaacaaa aaaaatttaa ctccatattg gntcctcttg 420
ttctaattct ggcaaccagt gcaagtgaac gacaaaattc cagttattta tttccaaaat 480
gtttggaac agtataattt gacaaagaaa aaaggatact tctcttttt tggctggtcc 540
accaaataca attcaaaagg ctttttggtt ttatttttt anccaattcc aatttcaaaa 600
tgtctcaatg gngcttataa taaaataaac tttcaccctt ntttntgat 650
```

<210> 263

<211> 573

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 453, 458, 544

<223> n = A,T,C or G

<400> 263

```
agcgtggtcg cggccgaggt ctgggatgct cctgctgtca cagtgaata ttacaggatc 60
acttacggag aaacaggagg aaatagccct gtccaggagt tcaactgtgc tgggagcaag 120
tctacagcta ccatacagcg ccttaaacct ggagttgatt ataccatcac tgtgtatgct 180
gtcactggcc gtggagacag ccccgcaagc agcaagccaa tttccattaa ttaccgaaca 240
```

gaaattgaca aaccatccca gatgcaagt accgatgttc aggacaacag cattagtgtc 300
aagtggctgc cttcaagtcc cctgttact ggttacagaa gtaaccacca ctcccaaaaa 360
tggaccagga ccaacaaaaa ctaaaactgc aggtccagat caaacagaaa atggactatt 420
gaaggcttgc agcccacagt ggaagtatgt ggntaggngt ctatgctcag aatcccaagc 480
cggagaaagt cagccttctg gtttagactg cagtaaccaa cattgatcgc cctaaaggac 540
tggncattca cttggatggt ggatgtccaa ttc 573

<210> 264

<211> 550

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 39, 174, 352, 526

<223> n = A,T,C or G

<400> 264

tcgagcggcc gcccgggcag gtccttgcat ctctgcagng tcttcttcac catcaggtgc 60
agggaaatagc tcatggattc catcctcagg gctcgagtag gtcaccctgt acctggaaac 120
ttgcccctgt gggctttccc aagcaatttt gatggaatcg acatccacat cagnaatgc 180
cagtccttta gggcgatcaa tgttggttac tgcagtctga accagaggct gactctctcc 240
gcttggtattc tgagcataga cactaaccac atactccact gtgggctgca agccttcaat 300
agtcatttct gtttgatctg gacctgcagt ttttaagtttt tgggtggtcct gncccatttt 360
tggaagtgg ggggttactc tgtaaccagt aacaggggaa cttgaaggca gccacttgac 420
actaatgctg ttgtcctgaa catcggtcac ttgcatctgg ggatggtttt gacaatttct 480
ggttcggcaa attaatggaa attggcttgc tgcttggcgg ggctgnctcc acgggccagt 540
gacagcatac 550

<210> 265

<211> 596

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 347, 352, 353, 534, 555, 587

<223> n = A,T,C or G

<400> 265

tcgagcggcc gcccgggcag gtccttgcat ctctgcagt tcttcttcac catcaggtgc 60
agggaaatagc tcatggattc catcctcagg gctcgagtag gtcaccctgt acctggaaac 120
ttgcccctgt gggctttccc aagcaatttt gatggaatcg acatccacat cagtgaatgc 180
cagtccttta gggcgatcaa tgttggttac tgcagtctga accagaggct gactctctcc 240
gcttggtattc tgagcataga cactaaccac atactccact gtgggctgca agccttcaat 300
agtcatttct gtttgatctg gacctgcagt ttttaagtttt tggttggnct gncccatttt 360
tggggaagggt gtggttactc ttgtaaccag taacagggga actgaagca gccacttgac 420
actaatgctg gtggcctgaa catcggtcac ttgcatctgg gatggtttgg tcaatttctg 480
ttcggttaatt aatgggaaat tggttactg gcttgcgggg gctgtctcca cggncagtga 540
caagcataca caggngatgg gtataatcaa ctccaggttt aaggccnctg atggta 596

<210> 266

<211> 506

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 393, 473

<223> n = A,T,C or G

<400> 266

```

agcgtggtcg cggccgaggt ctgggatgct cctgctgtca cagtgaata ttacaggatc 60
acttacggag aaacaggagg aaatagccct gtccaggagt tctactgtgc tgggagcaag 120
tctacagcta ccatcagcgg ccttaaacct ggagttgatt ataccatcac tgtgtatgct 180
gtcactggcc gtggagacag ccccgcaagc agtaagccaa tttccattaa ttaccgaaca 240
gaaattgaca aaccatccca gatgcaagt accgatgttc aggacaacag cattagtgtc 300
aagtggctgc cttcaagtgc cctgttact gggtacagag taaccaccac tcccaaaaat 360
gggaccagga ccaacaaaaa actaaaactg canggtccag atcaaacaga aatgactatt 420
gaaggcttgc agcccacagt ggagtatgtg gggtagtgtc tatgtctaga atnccaagcg 480
gagagagtca gcctctggtt cagact                                     506

```

<210> 267

<211> 548

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 346, 358, 432, 510, 512

<223> n = A,T,C or G

<400> 267

```

togagcggcc gcccgggcag gtcagcgtc tcaggacgtc accaccatgg cctgggctct 60
gtcctcctc accctcctca ctcagggcac agggtcctgg gccagtcctg ccctgactca 120
gcctccctcc gcgtccgggt ctctggaca gtcagtcacc atctcctgca ctggaaccag 180
cagtgaaggt ggtgcttatg aatttgtctc ctggtacca caacaccacag gcaaggcccc 240
caaactcatg atttctgagg tctaagcg gccctcaggg gtccctgatc gcttctctgg 300
ctccaagtct ggcaacacgg cctccctgac cgtctctggg ctccangctg aggatgangc 360
tgattattac tggaagctca tatgcaggca acaacaattg ggtgttcggc ggaaggggacc 420
aagctgaccg tntaaggctc aagcccaagg cttgcccccc tcggtcactc tgttccacc 480
ctcctctgaa gaagctttca agccaacaan gncacactgg gtgtgtctca taagtggact 540
ttctaccc                                     548

```

<210> 268

<211> 584

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 98, 380, 421, 454, 495, 506, 512, 561, 565, 579

<223> n = A,T,C or G

<400> 268

```

agcgtggtcg cggccgaggt ctgtagcttc tgtgggactt ccactgctca ggcgtcaggc 60
tcaggtagct gctggccgcg tacttggtgt tgetttgntt ggagggtgtg gtggtctcca 120
ctcccgcctt gacggggctg ctatctgect tccaggccac tgtcacggct cccgggtaga 180
agtcaactat gagacacacc agtgtggcct tgttggcttg aagctcctca gaggagggtg 240
ggaacagagt gaccgagggg gcagccttgg gctgacctag gacggtcagc ttggtccctc 300
cgccgaacac ccaattgttg ttgcctgcat atgagctgca gtaataatca gcctcatcct 360
cagcctggag cccagagacn gtcaaggag gcccggtgtt gccaaagactt ggaagccaga 420
naagcgatca gggaccctcg agggcgctt tacngacctc aaaaaatcat gaatttgggg 480
ggcctttgcc tggngtttgg ttggnacca gnaaaacaaa atttcataaa gcaccaacgt 540
cactgctggt ttccagtgcg ngaanatggt gaactgaant gtcc                                     584

```

<210> 269
<211> 368
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 265, 329
<223> n = A,T,C or G

<400> 269
agcgtggtcg cgcccgaggt ccagcatcag gagccccgcc ttgccggctc tggatcatgc 60
ctttcttttt gtggcctgaa acgatgtcat caattcgag tagcagaact gccgtctcca 120
ctgctgtctt ataagtctgc agcttcacag ccaatggctc ccatatgcc agttccttca 180
tgtccaccaa agtaccgctc tcaccattta caccocaggt ctcacagttc tcctgggtgt 240
gcttggcccg aagggaggtg agtanacgga tgggtgtggt cccacagttc tggatcaggg 300
tacaggaat gacctctagg gcctgggcna caagccctgt atggacctgc ccggcggggc 360
ccgctcga 368

<210> 270
<211> 368
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 54, 163, 219, 229, 316
<223> n = A,T,C or G

<400> 270
tcgagcggcc gcccgggcag gtccatacag ggctgttgcc caggccctag aggnccattcc 60
ttgtaccctg atccagaact gtgggaccag caccatccgt ctacttacct cccttcgggc 120
caagcacacc caggagaact gtgagacctg ggggtgaaat gngagacgg gtacttttgt 180
ggacatgaag gaactgggca tatgggagcc attggctgng aagctgcana cttataagac 240
agcagtggag acggcagttc tgctactgag aattgatgac atcgtttcag gccacaaaaa 300
gaaaggcgat gaccanagcc ggcaaggcgg ggcttcctga tgctggacct cggccgccga 360
ccacgctt 368

<210> 271
<211> 424
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 279, 329, 362, 384, 400
<223> n = A,T,C or G

<400> 271
agcgtggtcg cgcccgaggt ccactagagg tctgtgtgcc attgcccagg cagagtctct 60
gcgttacaaa ctctaggag ggcttgctgt gcggagggcc tgctatggtg tgctgcggtt 120
catcatggag agtggggcca aaggctgcga ggttggtgtg tctgggaaac tccgaggaca 180
gagggctaaa tccatgaagt ttgtggatgg cctgatgac cacagcggag accctgttaa 240
ctactacgtt gacactgctg tgcgccacgt gttgctcana cagggtgtgc tgggcatcaa 300
ggtgaagatc atgtgccct gggaccanc tggcaaaaat ggcccttaaa aacccttgc 360
cntgaccacg tgaaccattt gtnggaaccc caagatgaan atacttgccc accaccccc 420
attc 424

<210> 272
<211> 541
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 422, 442, 510, 513, 515, 525
<223> n = A,T,C or G

<400> 272
tcgagcggcc gcccgggcag gtctgccaag gagaccctgt tatgctgtgg ggactggctg 60
gggcatggca ggcggtctg gcttcccacc cttctgttct gagatggggg tggggggcag 120
tatctcatct ttgggttcca caatgtcac gtggtcaggc aggggcttct tagggccaat 180
cttaccagtt ggggtcccagg gcagcatgat cttcaccttg atgcccagca caccctgtct 240
gagcaacacg tggcgcacag cagtgtcaac gtagtagtta acaggggtctc cgctgtggat 300
catcaggcca tccacaaact tcatggattt agccctctgt cctcggagtt tcccaaaaca 360
ccacaacctc gccagccttt gggccccact tcttcatgaa tgaaaccgca gcacaccatt 420
ancaaggccc ttccgcacag gnaagccctt cctaaggagt ttgttaaacy caaaaaactc 480
ttgcctgggg caaatgggca cacagacctn tantnggacc ttggnccgcy aaccaccgct 540
t 541

<210> 273
<211> 579
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 223, 265, 277, 308, 329, 346, 360, 366, 429, 448, 517, 524,
531, 578
<223> n = A,T,C or G

<400> 273
agcgtggctc gggccgaggt ctggccctcc tggcaaggct ggtgaagatg gtcaccctgg 60
aaaaccggga cgacctggtg agagaggagt tgttggacca cagggtgctc gtggtttccc 120
tggaaactct ggacttcctg gcttcaaagg cattagggga cacaatggc tggatggatt 180
gaaagggacag cccggtgctc ctggtgtgaa ggggtgaacct gngcccctg gtgaaaatgg 240
aactccaggt caaacaggag cccgngggct tcctggngag agaggacgtg ttggtgcccc 300
tggcccanac ctgcccgggc ggccgctcna aaagccgaaa tccagnacac tggcgggcgn 360
tactantgga atccgaactt cggtagcaaa gcttggccgt aatcatggcc atagcttgtt 420
ccctggggng gaaatttgta ttccgctncc aattccacac aacataccga acccggaag 480
cattaaagtg taaaagccct gggggggcct aaatgangtg agcntaactc ncattttaatt 540
ggcgttgccg ttcactgccc cgcttttcca gtccgggna 579

<210> 274
<211> 330
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 171
<223> n = A,T,C or G

<400> 274
tcgagcggcc gcccgggcag gtctgggcca ggggcaccaa cacgtcctct ctcaccagga 60
agcccacggg ctctgtttg acctggagtt ccattttcac caggggcacc aggttcaccc 120

```

ttcacaccag gagcaccggg ctgtcccttc aatccatcca gaccattgtg ncccctaattg 180
cctttgaagc caggaagtcc aggagttcca gggaaaccac gagcacctg tggccaaca 240
actcctctct caccagggtcg tccgggtttt ccagggtgac catcttcacc agccttgcca 300
ggagggccag acctcgccg cgaccacgct                                     330

```

```

<210> 275
<211> 97
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 2, 35, 72
<223> n = A,T,C or G

```

```

<400> 275
ancgtggtcg cgcccgaggc cctcaccaga ggtgncacct acaacatcat agtggaggca 60
ctgaaagacc ancagaggca taagggttcg gaagagg                                     97

```

```

<210> 276
<211> 610
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 358, 360, 363, 382, 424, 433, 464, 468, 477, 491, 499, 511,
558, 584, 588, 590
<223> n = A,T,C or G

```

```

<400> 276
tcgagcggcc gcccgggcag gtccattttc tccctgacgg toccacttct ctccaattctt 60
gtagttcaca ccattgtcat ggcaccatct agatgaatca catctgaaat gaccacttcc 120
aaagcctaag cactggcaca acagtttaaa gcctgattca gacattcgtt cccactcatc 180
tccaacggca taatgggaaa ctgtgtaggg gtcaaagcac gagtcacccg taggttggtt 240
caagccttcg ttgacagagt tgtccacggt aacaacctct tcccgaacct tatgcctctg 300
ctggtctttc agtgccctca ctatgatgtt gtaggtggca cctctggtga ggacctcngn 360
ccngaacaac gcttaagccc gnattctgca gaataatccc atcacacttg gcggccgctt 420
cgancatgca tcntaaaagg ggccccaatt tcccccttat aagngaancg gtatttncca 480
atttcaactg ncccgccgnt ttacaaaacg ncggtgaact ggggaaaaac cctggcggtt 540
acccaacttt aatcgccntt ggcagcacia tcccccttt tcgnccanctn tgggcgtaaa 600
taaccgaaaa                                     610

```

```

<210> 277
<211> 38
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 2, 5, 18, 21, 31
<223> n = A,T,C or G

```

```

<400> 277
ancngnggtcg cgcccgangt nttttttctt nttttttt                                     38

```

```

<210> 278
<211> 443

```

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 156, 212, 233, 245, 327, 331, 336, 361, 364, 381, 391, 397,
419, 437

<223> n = A,T,C or G

<400> 278

```
agcgtggtcg cggccgaggt ctgaggttac atgcgtggtg gtggacgtga gccacgaaga 60
ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa 120
gccgcgggag gagcagtaca acagcacgta ccgggnggtc agcgtcctca ccgtcctgca 180
ccagaattgg ttgaatggca aggagtacaa gngcaagggt tccaacaaag ccntcccagc 240
ccccntcgaa aaaaccattt ccaaagccaa agggcagccc cgagaaccac aggtgtacac 300
cctgccccca tcccgggagg aaaagancaa naaccnggtt cagccttaac ttgcttggtc 360
naangctttt tatccaacg nacttcccc ntggaantgg gaaaaaccaa tgggccaanc 420
cgaaaaacaa ttacaanaac ccc 443
```

<210> 279

<211> 348

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 219, 256, 291, 297, 307, 314, 317

<223> n = A,T,C or G

<400> 279

```
tcgagcggcc gcccgggcag gtgtcggagt ccagcacggg aggcgtggtc ttgtagttgt 60
tctccggctg ccattgctc tcccactcca cggcgatgtc gctgggatag aagcctttga 120
ccaggcaggt caggctgacc tggttcttgg tcatctctc ccgggatggg ggcaggggtga 180
acacctgggg ttctcggggc ttgccctttg gttttgaana tggttttctc gatgggggct 240
ggaagggctt tgttgnaaac cttgcacttg actccttgcc attcaccag ncctggngca 300
ggacggnag gacnctnacc acacggaacc gggctggtgg actgctcc 348
```

<210> 280

<211> 149

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 18, 34, 51, 118, 120, 140

<223> n = A,T,C or G

<400> 280

```
agcgtggtcg cggacgangt cctgtcagag tggnaactgg agaagttcca ngaaccctga 60
actgtaaggg ttcttcatca gtgccaacag gatgacatga aatgatgtac tcagaagnn 120
cctggaatgg ggcccatgan atggttgcc 149
```

<210> 281

<211> 404

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature
 <222> 383, 386, 388, 393
 <223> n = A,T,C or G

<400> 281
 tcgagcggcc gcccgggcag gtccaccaca cccaattcct tgctggtatc atggcagccg 60
 ccacgtgccg ggattaccgg ctacatcadc aagtatgaga agcctgggtc tcctcccaga 120
 gaagtgggtc ctcggccccg ccctgggtgc acagaggcta ctattactgg cctggaaccg 180
 ggaaccgaat atacaattta tgtcattgcc ctgaagaata atcagaagag cgagcccctg 240
 attggaagga aaaagacaga cgagcttccc caactggtaa cccttccaca cccaatctt 300
 catggaccag agatcttgga tgctccttcc acagttcaaa agaccctttt cggcaccccc 360
 cctgggtatg aacctgggaa aanggnantt aanccttctt ggca 404

<210> 282
 <211> 507
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 320, 341, 424, 450, 459, 487, 498
 <223> n = A,T,C or G

<400> 282
 agcgtggtcg cggccgaggt ctgggatgct cctgctgtca cagtgaagata ttacaggatc 60
 acttacggag aaacaggagg aaatagccct gtccaggagt tcactgtgcc tgggagcaag 120
 tctacagcta ccatcagcgg ccttaaaccct ggagttgatt ataccatcac tgtgtatgct 180
 gtactgtgcc gtggagacag ccccgcaagc agcaagccaa ttccattaa ttaccgaaca 240
 gaaattgaca aaccatccca gatgcaagtg accgatgttc aggacaacag cattagtgtc 300
 aagtggctgc cttcaaggtn ccctgggtact gggttacaga ntaaccacca ctccccaaaa 360
 tggaccagga accacaaaaa cttaaactgc aggggtccaga tcaaaacaga aatgactatt 420
 gaangcttgc agcccacagt gggagtatgn gggtagtgnc tatgcttcag aatccaagcg 480
 gaaaaangtc aagccttntg ggttcaa 507

<210> 283
 <211> 325
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 216, 292, 303, 304
 <223> n = A,T,C or G

<400> 283
 tcgagcggcc gcccgggcag gtcccttcag ctctgcagtg tcttcttcac catcaggtgc 60
 agggaaatagc tcatggattc catcctcagg gctcgagtag gtcaccctgt acctggaac 120
 ttgcccctgt gggctttccc aagcaatttt gatggaatcg acatccacat cagtgaatgc 180
 cagtccctta gggcgatcaa tggttggttac tgcagnctga accagaggct gactctctcc 240
 gcttggattc tgagcataga cactaaccac atactccact gtgggctgca ancttcaat 300
 aanncatttc tgtttgatct ggacc 325

<210> 284
 <211> 331
 <212> DNA
 <213> Homo sapiens

<220>

<221> misc_feature

<222> 54, 59, 63, 121, 312, 327

<223> n = A,T,C or G

<400> 284

```
tcgagcggcc gcccgggcag gtctggtggg gtcctggcac acgcacatgg gggngttgnt 60
ctnatccagc tgcccagccc ccattggcga gtttgagaag gtgtgcagca atgacaacaa 120
naccctcgac tcttcctgcc atttctttgc cacaaagtgc accctggagg gcaccaagaa 180
gggccacaag ctccacctgg actacatcgg gccttgcaaa tacatcccc cttgcctgga 240
ctctgagctg accgaattcc cccttgcgca tgcgggactg gctcaagaac cgtcctggca 300
cccttgatat anagggatga agacacnacc c 331
```

<210> 285

<211> 509

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 316, 319, 327, 329, 339, 344, 357, 384, 398, 427, 443, 450, 478

<223> n = A,T,C or G

<400> 285

```
agcgtggtcg cgcccgaggt ctgtcctaca gtcctcagga ctctactccc tcagcagcgt 60
ggtgaccgtg ccctccagca acttcggcac ccagacctac acctgcaacg tagatcacia 120
gccagcaac accaagggtg acaagagagt tgagcccaaa tcttgtagaca aaactcacac 180
atgccaccg tgcccagcac ctgaactcct ggggggaccg tcagtcttcc tcttcccccg 240
catccccctt ccaaacctgc ccgggcggcc gctcgaaagc cgaattccag cacactggcg 300
gccggtacta gtgganccna acttggnanc caacctggng gaantaatgg gcataanctg 360
tttctggggg gaaattggtg tccngtttac aattcccnca caacatacga gccggaagca 420
taaaagncta aaagcctggg ggnngcctan tgaagtgaag ctaaaactcac attaattngc 480
gttgccgctc actggcccgc ttttccagc 509
```

<210> 286

<211> 336

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 188, 251, 267

<223> n = A,T,C or G

<400> 286

```
tcgagcggcc gcccgggcag gtttggaagg gggatgcggg ggaagaggaa gactgacggt 60
ccccccagga gttcaggtgc tgggcacggt gggcatgtgt gagttttgtc acaagatttg 120
ggctcaactc tcttgccac cttggtgttg ctgggcttgt gatctacgtt gcaggtgtag 180
gtctggngc cgaagttgct ggagggcacg gtcaccacgc tgctgagggg gtagagtcct 240
gaggactgta ngacagacct cgcccgngac cagcctaagc cgaattctgc agatatccat 300
cacactggcg gccgctccga gcatgcattt tagagg 336
```

<210> 287

<211> 30

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature
<222> 8, 18
<223> n = A,T,C or G

<400> 287
agcgtggncg cggacganga caacaacccc

30

<210> 288
<211> 316
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 22, 130
<223> n = A,T,C or G

<400> 288
tcgagcggcc gcccgggcag gnccacatcg gcagggtcgg agccctggcc gccatactcg 60
aactggaatc catcggtcat gctcttgccg aaccagacat gcctcttgtc cttgggggttc 120
ttgctgatgn accagttctt ctgggccaca ctgggctgag tgggggtacac gcaggtctca 180
ccagtctcca tgttgagaa gactttgatg gcatccaggt tgcagccttg gttgggggtca 240
atccagtact ctccactctt ccagtcagag tggcacatct tgaggtcacg gcaggtgcgg 300
ggggggttct tgacct 316

<210> 289
<211> 308
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 36, 165, 191, 195, 218, 235
<223> n = A,T,C or G

<400> 289
agcgtggtcg cggccgaggt ccagcctgga gataanggtg aaggtggtgc ccccggaactt 60
ccaggtatag ctggacctcg tggtagccct ggtgagagag gtgaaactgg cctccagga 120
cctgctggtt tccctggtgc tcctggacag aatggtgaac ctggnngtaa aggagaaaga 180
ggggctccgg ntganaaagg tgaaggaggc cctcctgnat tggcaggggc cccangactt 240
agaggtggag ctggccccc tggccccgaa ggaggaaagg gtgctgctgg tctcctggg 300
ccacctg 308

<210> 290
<211> 324
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 184
<223> n = A,T,C or G

<400> 290
tcgagcggcc gcccgggcag gtctgggcca ggaggaccaa taggaccagt aggaccctt 60
gggccatctt tccctgggac accatcagca cctggaccgc ctggttcacc cttgtcacc 120
tttgaccag gacttccaag acctcctctt tctccaggca ttcttgacg accaggagta 180
ccancagcac caggtggccc aggaggacca gcagcaccct ttctctcttc gggaccaggg 240

ggaccagctc cacctctaag tcctggggcc cctgccaatc caggagggcc tccttcacct 300
ttctcacccg gagccccctct ttct 324

<210> 291
<211> 278
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 249, 267
<223> n = A,T,C or G

<400> 291
tcgagcggcc gcccgggcag gtccaccggg atattcgggg gtctggcagg aatgggaggc 60
atccagaacg agaaggagac catgcaaagc ctgaacgacc gcctggcctc ttacctggac 120
agagtgagga gcctggagac cgacaaccgg aggctggaga gcaaaatccg ggagcacttg 180
gagaagaagg gaccccaggt cagagactgg agccattact tcaagatcat cgaggacctg 240
agggtcana tcttcgcaa tactgcngac aatgcccg 278

<210> 292
<211> 299
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 6, 19, 25, 51, 53, 61, 63, 70, 109, 136, 157, 241, 276
<223> n = A,T,C or G

<400> 292
atgcgnggtc gcgcccgang accanctctg gctcactatt gactctaaag nntcaccag 60
nanttacggn cattgccaat ctgcagaacg atgcgggcat tgtccgcant atttgcaag 120
atctgagccc tcaggnccctc gatgatcttg aagtaanggc tccagtctct gacctggggt 180
cccttcttct ccaagtgtc ccggattttg ctctccagcc tccggttctc ggtctccaag 240
ncttctcact ctgtccagga aaagaggcca ggcggncgat cagggtcttt gcatggact 299

<210> 293
<211> 101
<212> DNA
<213> Homo sapiens

<400> 293
agcgtggtcg cggccgaggt tgtacaagct tttttttttt tttttttttt tttttttttt 60
tttttttttt tttttttttt tttttttttt tttttttttt t 101

<210> 294
<211> 285
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 64, 103, 110, 237, 282
<223> n = A,T,C or G

<400> 294
tcgagcggcc gcccgggcag gtctgccaac accaagattg gcccccgccg catccacaca 60

```

gttngtgtgc ggggaggtaa caagaaatac cgtgccctga ggntggacgn ggggaatttc 120
tcctggggct cagagtgttg tactcgtaaa acaaggatca tcgatgttgt ctacaatgca 180
tctaataacg agctgggtcg taccaagacc ctggtgaaga attgcatcgt gctcatngac 240
agcacaccgt accgacagtg ggtaccgaag tcccactatg cncct 285

```

<210> 295
 <211> 216
 <212> DNA
 <213> Homo sapiens

```

<400> 295
tcgagcggcc gcccgggcag gtccaccaca cccaattcct tgctggtatc atggcagccg 60
ccacgtgccca ggattaccgg ctacatcatc aagtatgaga agcctgggtc tcctcccaga 120
gaagtgggtcc ctcggtcccg ccctggtgtc acagaggcta ctattactgg cctggaaccg 180
ggaaccgaat atacaattta tgtcattgcc ctgaag 216

```

<210> 296
 <211> 414
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 7, 10, 33, 61, 62, 63, 88, 109, 122, 255, 298, 307, 340,
 355, 386, 393
 <223> n = A,T,C or G

```

<400> 296
agcgtgntcn cggccgagga tggggaagct cgnctgtctt tttccttcca atcaggggct 60
nnntcttctg attattcttc agggcaanga cataaattgt atattcgnt cccggttcca 120
gnccagtaat agtagcctct gtgacaccag ggcggggccg agggaccact tctctgggag 180
gagaccaggt cttctcatac ttgatgatga agccggtaat cctggcacgt gggcgggtgc 240
catgatacca ccaangaatt ggggtgtgtg gacctgcccg ggcggggccg tcgaaaaanc 300
gaattcntgc aagaatatcc atcacacttg ggcggggccg tcgaaccatg catcntaaaa 360
gggcccgaat ttcccccta ttagngnaag ccncatttaa caaattccac ttgg 414

```

<210> 297
 <211> 376
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 312, 326, 335, 361
 <223> n = A,T,C or G

```

<400> 297
tcgagcggcc gcccgggcag gtctcgcggt cgcactggtg atgctggtcc tgttggtccc 60
cccggccctc ctggacctcc tgggtccccc ggtcctccca gcgctggtt cgacttcagc 120
ttcctgcccc agccacctca agagaaggct cagcatggtg gccgctacta ccgggctgat 180
gatgccaatg tggttcgtga ccgtgacctc gaggtggaca ccacctcaa gagccttgag 240
ccagcagaat cgaaaacatt cggaaccxaa gaagggaag cccgcaaaga aaccccgccc 300
gcacctggcc gngaacctcc aagaangtgc ccacntcttg actgggaaaa aaagggaaaa 360
ntacttgga ttggac 376

```

<210> 298
 <211> 357
 <212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 345, 346

<223> n = A,T,C or G

<400> 298

```
agcgtggtcg cggccgaggt ccacatcggc agggctcggag ccctggccgc cataactcgaa 60
ctggaatcca tcggtcatgc tctcgccgaa ccagacatgc ctcttgctct tggggttctt 120
gctgatgtac cagttcttct gggccacact gggctgagtg gggtaacacg aggtctcacc 180
agtctccatg ttgcagaaga ctttgatggc atccagggtg cagccttggg tgggggtcaat 240
ccagtactct ccactcttcc agtcagaagt ggcacatctt gaggtcacgg caggggtgcgg 300
gcgggggttct tgcgggctgc cttctcgggc tcccggaatg ttctnngaac ttgctgg 357
```

<210> 299

<211> 307

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 281, 285, 306

<223> n = A,T,C or G

<400> 299

```
agcgtggtcg cggccgaggt ccactagagg tctgtgtgcc attgcccagg cagagtctct 60
gcgttacaaa ctctaggag ggcttgctgt gcggagggcc tgctatggtg tgctgcggtt 120
catcatggag agtggggcca aaggctgcga ggttggtgtg tctgggaaac tccgaggaca 180
gaggggtaaa tccatgaagt ttgtggatgg cctgatgatc cacagcggag accctgttaa 240
ctactacgtt gacacttgct tgtgcgccac gtgttgctca nacanggggt ggctgggcat 300
caaggng 307
```

<210> 300

<211> 351

<212> DNA

<213> Homo sapiens

<400> 300

```
tcgagcggcc gcccgggcag gtctgccaag gagaccctgt tatgctgtgg ggactggctg 60
gggcatggca ggcggctctg gcttcccacc cttctgttct gagatggggg tgggtgggcag 120
tatctcatct ttgggttcca caatgctcac gtggtcaggc aggggcttct tagggccaat 180
cttaccagtt gggccccagg gcagcatgat cttcaccttg atgccagca caccctgtct 240
gagcaaacag tggcgcacag caagtgtcaa cgtaagtaag ttaacagggt ctccgctgtg 300
gatcatcagg ccatccacaa acttcatgga tttaaccttc tgcctcggg g 351
```

<210> 301

<211> 330

<212> DNA

<213> Homo sapiens

<400> 301

```
tcgagcggcc gcccgggcag gtgtttcaga ggttccaagg tccactgtgg aggtcccagg 60
agtgtctggt gtgggcacag aggtccgatg ggtgaaacca ttgacataga gactgttctt 120
gtccagggtg taggggccca gctctttgat gccattggcc agttggctca gctcccagta 180
cagccgctct ctgttgagtc cagggctttt ggggtcaaga tgatggatgc agatggcatc 240
cactocagtg gctgtccat cttctcggc cctgagagag gtcagtctgc agccagagta 300
cagagggcca aactggtgt tctttgaata 330
```

<210> 302
<211> 317
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 129, 295
<223> n = A,T,C or G

<400> 302
agcgtggtcg cggccgaggt ctgtactggg agctaagcaa actgaccaat gacattgaag 60
agctggggccc ctacaccctg gacaggaaca gtctctatgt caatgggttc acccatcaga 120
gctctgtgnc caccaccagc actcctggga cctccacagt ggatttcaga acctcagga 180
ctccatcttc cctctccagc cccacaatta tggctgctgg ccctctcctg gtaccattca 240
ccctcaactt caccatcacc aacctgcagt atggggagga catgggtcac cctgnetcca 300
ggaagttcaa caccaca 317

<210> 303
<211> 283
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 139, 146, 195
<223> n = A,T,C or G

<400> 303
tcgagcggcc gcccgacag gtctgggcgg atagcaccgg gcatattttg gaatggatga 60
ggctctggcac cctgagcagt ccagcgagga cttggtctta gttgagcaat ttggctagga 120
ggatagtatg cagcacggnt ctgagnctgt gggatagctg ccatgaagta acctgaagga 180
ggtgctggct ggtanggggt gattacaggg ttgggaacag ctcgtacact tgccattctc 240
tgcatatact ggtagtgag gtgagcctgg ccctcttctt ttg 283

<210> 304
<211> 72
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 59
<223> n = A,T,C or G

<400> 304
agcgtggtcg cggccgaggt gagccacagg tgaccggggc tgaagctggg gctgctggnc 60
ctgctggtcc tg 72

<210> 305
<211> 245
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 5, 11, 22, 98, 102

<223> n = A,T,C or G

<400> 305

```
cagcngctcc nacggggcct gngggacca caacaccgtt ttcaccctta ggccctttgg 60
ctcctctttc tccttttagca ccaggttgac cagcagcncc ancaggacca gcaaattccat 120
tgggggccagc aggaccgacc tcaccacgtt caccagggct tccccgagga ccagcaggac 180
cagcaggacc agcagcccca gcttcgcccc ggtcacctgt ggctcacctc ggccgcgacc 240
acgct 245
```

<210> 306

<211> 246

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 144, 159

<223> n = A,T,C or G

<400> 306

```
tcgagcggtc gcccgggcag gtccaccggg atagccgggg gtctggcagg aatgggaggc 60
atccagaacg agaaggagac catgcaaagc ctgaacgacc gcctggcctc ttacctggac 120
agagtgagga gcctgggagc cganaaccgg aggctggana gcaaaatccg ggagcacttg 180
gagaagaagg gaccccaggt caagagactg gagccattac ttcaagatca tcgagggacc 240
tgagg 246
```

<210> 307

<211> 333

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 5

<223> n = A,T,C or G

<400> 307

```
agcgnnggtc cgcccgaggt ccagctctgt ctcatcttg actctaaagt catcagcagc 60
aagacgggca ttgtcaatct gcagaacgat gcgggcattg tccgcagtat ttgcgaagat 120
ctgagccctc aggtcctcga tgatcttgaa gtaatggctc cagtctctga cctgggggtc 180
cttcttctcc aagtgtccc ggattttgct ctccagcctc cggttctcgg tctccagggt 240
cctcactctg tccaggtaag aaggcccagg cggtcgttca ggctttgcat ggtctccttc 300
tcgttctgga tgctcccat tcctgccaga ccc 333
```

<210> 308

<211> 310

<212> DNA

<213> Homo sapiens

<400> 308

```
tcgagcggcc gcccgggcag gtcaggaagc acattggtct tagagccact gcctcctgga 60
ttccacctgt gctgcggaca tctccaggga gtgcagaagg gaagcaggtc aaactgctca 120
gatcagtcag actggctgtt ctcagttctc acctgagcaa ggtcagctg cagccagagt 180
acagagggcc aacactggtg ttcttgaaca agggcttgag cagaccctgc agaaccctct 240
tccgtggtgt tgaacttcct ggaaaccagg gtgttgcatg ttttctctca taatgcaagg 300
ttggtgatgg 310
```

<210> 309

<211> 429
<212> DNA
<213> Homo sapiens

<400> 309
agcgtggtcg cggccgaggt ccacatcggc agggtcggag ccctggccgc catactcgaa 60
ctggaatcca tcggatcatgc tctcgccgaa ccagacatgc ctcttgctct tggggttctt 120
gctgatgtac cagttcttct gggccacact gggctgagtg ggttacaccg caggtctcac 180
cagtctccat gttgcagaag actttgatgg catccagggt gcagccttgg ttgggggtcaa 240
tccagtactc tccactcttc cagtcagaag tgggcacatc ttgagggtcac cggcaggtgc 300
cgggccgggg gttcttgccg cttgccctct gggctccgga tgtctctgat ctgcttggtc 360
caggctcttg aggggtgggtg tccacctcga ggtcacggtc accgaaacct gcccgggcgg 420
cccgtcga 429

<210> 310
<211> 430
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 342
<223> n = A,T,C or G

<400> 310
tcgagcggtc gcccgggcag gtttcgtgac cgtgacctcg aggtggacac caccctcaag 60
agcctgagcc agcagatcga gaacatccgg agcccagagg gcagccgcaa gaaccccgcc 120
cgcacctgcc gtgacctcaa gatgtgccac tctgactgga agagtggaga gtactggatt 180
gaccccaacc aaggctgcaa cctggatgcc atcaaagtct tctgcaacat ggagactggt 240
gagacctgcy tgtacccac tcagcccagt gtgggcccag aagaaactgg tacatcagca 300
aggaaccca aggacaagag gcattgtctt ggttcggcga gnagcatgac ccgatggatt 360
ccagtttcga gtattggcgg ccagggttc cggaccttg ccgatgtgga cctcgccgcg 420
gaccacgct 430

<210> 311
<211> 2996
<212> DNA
<213> Homo sapiens

<400> 311
cagccaccgg agtggatgcc atctgcaccc accgccctga cccacaggc cctgggctgg 60
acagagagca gctgtatttg gagctgagcc agctgaccca cagcatcact gagctgggcc 120
cctacaccct ggacagggac agtctctatg tcaatgggtt cacacagcgg agctctgtgc 180
ccaccactag cattcctggg acccccacag tggacctggg aacatctggg actccagttt 240
ctaaacctgg tccctcggct gccagccctc tctgggtgct attcactctc aacttcacca 300
tcaccaacct gcggtatgag gagaacatgc agcacctgg ctccaggaag ttcaaacacca 360
cggagagggt ccttcagggc ctggtccctg ttcaagagca ccagtgttg ccctctgtac 420
tctggctgca gactgacttt gctcaggcct gaaaaggatg ggacagccac tggagtggat 480
gccatctgca cccaccaccc tgaccccaa agccctaggc tggacagaga gcagctgtat 540
tgggagctga gccagctgac ccacaatate actgagctgg gccctatgc cctggacaac 600
gacagcctct ttgtcaatgg tttcactcat cggagctctg tgtccaccac cagcactcct 660
gggaccccca cagtgtatct gggagcatct aagactccag cctcgatatt tggcccttca 720
gctgccagcc atctcctgat actattcacc ctcaacttca ccatcactaa cctgcggtat 780
gaggagaaca tgtggcctgg ctccagggaag ttcaacacta cagagagggt ccttcagggc 840
ctgctaaggc ccttgttcaa gaacaccagt gttggccctc tgtactctgg ctgcaggctg 900
accttgctca ggccagagaa agatggggaa gccaccggag tggatgccat ctgacccac 960
cgccctgacc ccacaggccc tgggctggac agagagcagc tgtatttga cctgagccg 1020
ctgaccaca gcactactga gctgggcccc tacacactgg acagggacag tctctatgtc 1080

```

aatggtttca cccatcggag ctctgtacc accaccagca ccgggggtggt cagcgaggag 1140
ccattcacac tgaacttcac catcaacaac ctgcgctaca tggcggacat gggccaaccc 1200
ggctccctca agttcaacat cacagacaac gtcatgaagc acctgctcag tcctttgttc 1260
cagaggagca gcctgggtgc acggtacaca ggctgcaggg tcatcgact aaggtctgtg 1320
aagaacggtg ctgagacacg ggtggacctc ctctgcacct acctgcagcc cctcagcggc 1380
ccaggtctgc ctatcaagca ggtgttccat gagctgagcc agcagacca tggcatcacc 1440
cggctggggc cctactctct ggacaaagac agcctctacc ttaacggta caatgaacct 1500
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gaagccacaa cagccatggg gtaccacctg aagacctca cactcaactt caccatctcc 1620
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aatttcaca ttgtcaactg gaacctcagt aatccagacc ccacatctc agagtacatc 2040
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ggagaataca acgtccagca acagtcccca ggctactacc agtcacacct agacctggag 2880
gatctgcaat gactggaact tgccggtgcc tggggtgcct ttccccagc cagggtccaa 2940
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<210> 312

<211> 914

<212> PRT

<213> Homo sapiens

<400> 312

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Met Ser Met Val Ser His Ser Gly Ala Leu Cys Pro Pro Leu Ala Phe
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Leu Gly Pro Pro Gln Trp Thr Trp Glu His Leu Gly Leu Gln Phe Leu
  20             25             30
Asn Leu Val Pro Arg Leu Pro Ala Leu Ser Trp Cys Tyr Ser Leu Ser
  35             40             45
Thr Ser Pro Ser Pro Thr Cys Gly Met Arg Arg Thr Cys Ser Thr Leu
  50             55             60
Ala Pro Gly Ser Ser Thr Pro Arg Arg Gly Ser Phe Arg Ala Trp Ser
  65             70             75             80
Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu
  85             90             95
Thr Leu Leu Arg Pro Glu Lys Asp Gly Thr Ala Thr Gly Val Asp Ala
 100            105            110
Ile Cys Thr His His Pro Asp Pro Lys Ser Pro Arg Leu Asp Arg Glu
 115            120            125
Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Asn Ile Thr Glu Leu
 130            135            140
Gly Pro Tyr Ala Leu Asp Asn Asp Ser Leu Phe Val Asn Gly Phe Thr

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145					150					155				160
His	Arg	Ser	Ser	Val	Ser	Thr	Thr	Ser	Thr	Pro	Gly	Thr	Pro	Thr
				165						170				175
Tyr	Leu	Gly	Ala	Ser	Lys	Thr	Pro	Ala	Ser	Ile	Phe	Gly	Pro	Ser
			180					185					190	
Ala	Ser	His	Leu	Leu	Ile	Leu	Phe	Thr	Leu	Asn	Phe	Thr	Ile	Thr
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Leu	Arg	Tyr	Glu	Glu	Asn	Met	Trp	Pro	Gly	Ser	Arg	Lys	Phe	Asn
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Thr	Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu	Arg	Pro	Leu	Phe	Lys	Asn
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Ser	Val	Gly	Pro	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Thr	Leu	Leu	Arg
			245						250					255
Glu	Lys	Asp	Gly	Glu	Ala	Thr	Gly	Val	Asp	Ala	Ile	Cys	Thr	His
		260					265						270	
Pro	Asp	Pro	Thr	Gly	Pro	Gly	Leu	Asp	Arg	Glu	Gln	Leu	Tyr	Leu
	275						280					285		
Leu	Ser	Gln	Leu	Thr	His	Ser	Ile	Thr	Glu	Leu	Gly	Pro	Tyr	Thr
	290					295					300			
Asp	Arg	Asp	Ser	Leu	Tyr	Val	Asn	Gly	Phe	Thr	His	Arg	Ser	Ser
	305				310					315				320
Pro	Thr	Thr	Ser	Thr	Gly	Val	Val	Ser	Glu	Glu	Pro	Phe	Thr	Leu
			325						330					335
Phe	Thr	Ile	Asn	Asn	Leu	Arg	Tyr	Met	Ala	Asp	Met	Gly	Gln	Pro
		340						345					350	
Ser	Leu	Lys	Phe	Asn	Ile	Thr	Asp	Asn	Val	Met	Lys	His	Leu	Leu
	355					360					365			
Pro	Leu	Phe	Gln	Arg	Ser	Ser	Leu	Gly	Ala	Arg	Tyr	Thr	Gly	Cys
	370				375					380				
Val	Ile	Ala	Leu	Arg	Ser	Val	Lys	Asn	Gly	Ala	Glu	Thr	Arg	Val
	385				390				395					400
Leu	Leu	Cys	Thr	Tyr	Leu	Gln	Pro	Leu	Ser	Gly	Pro	Gly	Leu	Pro
			405						410					415
Lys	Gln	Val	Phe	His	Glu	Leu	Ser	Gln	Gln	Thr	His	Gly	Ile	Thr
		420						425					430	
Leu	Gly	Pro	Tyr	Ser	Leu	Asp	Lys	Asp	Ser	Leu	Tyr	Leu	Asn	Gly
	435					440					445			
Asn	Glu	Pro	Gly	Pro	Asp	Glu	Pro	Pro	Thr	Thr	Pro	Lys	Pro	Ala
	450				455						460			
Thr	Phe	Leu	Pro	Pro	Leu	Ser	Glu	Ala	Thr	Thr	Ala	Met	Gly	Tyr
	465				470				475					480
Leu	Lys	Thr	Leu	Thr	Leu	Asn	Phe	Thr	Ile	Ser	Asn	Leu	Gln	Tyr
		485						490					495	
Pro	Asp	Met	Gly	Lys	Gly	Ser	Ala	Thr	Phe	Asn	Ser	Thr	Glu	Gly
		500						505					510	
Leu	Gln	His	Leu	Leu	Arg	Pro	Leu	Phe	Gln	Lys	Ser	Ser	Met	Gly
	515					520						525		
Phe	Tyr	Leu	Gly	Cys	Gln	Leu	Ile	Ser	Leu	Arg	Pro	Glu	Lys	Asp
	530				535					540				
Ala	Ala	Thr	Gly	Val	Asp	Thr	Thr	Cys	Thr	Tyr	His	Pro	Asp	Pro
	545				550					555				560
Gly	Pro	Gly	Leu	Asp	Ile	Gln	Gln	Leu	Tyr	Trp	Glu	Leu	Ser	Gln
			565					570						575
Thr	His	Gly	Val	Thr	Gln	Leu	Gly	Phe	Tyr	Val	Leu	Asp	Arg	Asp
	580						585					590		
Leu	Phe	Ile	Asn	Gly	Tyr	Ala	Pro	Gln	Asn	Leu	Ser	Ile	Arg	Gly
	595					600					605			
Tyr	Gln	Ile	Asn	Phe	His	Ile	Val	Asn	Trp	Asn	Leu	Ser	Asn	Pro

610	615	620
Pro Thr Ser Ser Glu Tyr Ile Thr Leu Leu Arg Asp Ile Gln Asp Lys		
625	630	635
Val Thr Thr Leu Tyr Lys Gly Ser Gln Leu His Asp Thr Phe Arg Phe		640
	645	650
Cys Leu Val Thr Asn Leu Thr Met Asp Ser Val Leu Val Thr Val Lys		655
	660	665
Ala Leu Phe Ser Ser Asn Leu Asp Pro Ser Leu Val Glu Gln Val Phe		670
	675	680
Leu Asp Lys Thr Leu Asn Ala Ser Phe His Trp Leu Gly Ser Thr Tyr		685
	690	695
Gln Leu Val Asp Ile His Val Thr Glu Met Glu Ser Ser Val Tyr Gln		700
705	710	715
Pro Thr Ser Ser Ser Ser Thr Gln His Phe Tyr Leu Asn Phe Thr Ile		720
	725	730
Thr Asn Leu Pro Tyr Ser Gln Asp Lys Ala Gln Pro Gly Thr Thr Asn		735
	740	745
Tyr Gln Arg Asn Lys Arg Asn Ile Glu Asp Ala Leu Asn Gln Leu Phe		750
	755	760
Arg Asn Ser Ser Ile Lys Ser Tyr Phe Ser Asp Cys Gln Val Ser Thr		765
	770	775
Phe Arg Ser Val Pro Asn Arg His His Thr Gly Val Asp Ser Leu Cys		780
	785	790
Asn Phe Ser Pro Leu Ala Arg Arg Val Asp Arg Val Ala Ile Tyr Glu		800
	805	810
Glu Phe Leu Arg Met Thr Arg Asn Gly Thr Gln Leu Gln Asn Phe Thr		815
	820	825
Leu Asp Arg Ser Ser Val Leu Val Asp Gly Tyr Phe Pro Asn Arg Asn		830
	835	840
Glu Pro Leu Thr Gly Asn Ser Asp Leu Pro Phe Trp Ala Val Ile Leu		845
	850	855
Ile Gly Leu Ala Gly Leu Leu Gly Leu Ile Thr Cys Leu Ile Cys Gly		860
	865	870
Val Leu Val Thr Thr Arg Arg Arg Lys Lys Glu Gly Glu Tyr Asn Val		875
	880	885
Gln Gln Gln Cys Pro Gly Tyr Tyr Gln Ser His Leu Asp Leu Glu Asp		890
	900	905
Leu Gln		910

<210> 313

<211> 656

<212> DNA

<213> Homo sapiens

<400> 313

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tgacgtttgt ctacgactcc tcggagaaaa ccacttcaa agacgcagtc agtgctggga 180
agcacacagc caactcgac cacctctctg ccttggtcac ccccgctggg aagtcctatg 240
agtgtcaagc tcaacaaacc atttcaactg cctctagtga tccgcagaag acggtcacca 300
tgatcctgtc tgcggtccac atccaacctt ttgacattat ctgagatttt gtcttcagtg 360
aagagcataa atgccagtg gatgagcggg agcaactgga agaaaccttg ccctgattt 420
tggggctcat cttgggcctc gtcacatggt taacactcgc gatttaccac gtccaccaca 480
aatgactgc caaccaggtg cagatccctc gggacagatc ccagtataag cacatgggct 540
agaggccgtt aggcaggcac cccctattcc tgctcccca actggatcag gtagaacaac 600
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<210> 314
 <211> 519
 <212> DNA
 <213> Homo sapiens

<400> 314
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 gttaaggat ggtctcgggt gttaggccca ctagaataaa ctgagtccaa tacctctaca 180
 cagttatgtt taactgggct ctctgacacc gggaggaagg tggcgggggt taggtgttgc 240
 aaacttcaat ggttatgcgg ggatgttcac agagcaagct ttggtatcta gctagtctag 300
 cattcattag ctaatgggtg cctttgggtat ttattaaaat caccacagca tagggggact 360
 ttatgttttag gttttgtcta agagttagct tatctgcttc ttgtgctaac agggctattg 420
 ctaccaggga ctttgacat gggggccagc gtttgaaac ctcatctagt tttttgaga 480
 gataggccac tggccttgga cctcggccgc gaccacgt 519

<210> 315
 <211> 441
 <212> DNA
 <213> Homo sapiens

<400> 315
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 aaaagttccc atgttgatta catgtaaata gtcacatata tacaatgaag gcagtttctt 120
 cagaggcaac cagggtttat agtgctaggt aaatgtcatc tcttttgtgc tactgactca 180
 ttgtcaaacg tctctgcact gttttcagcc tctccacgtt gcctctgtcc tgcttcttag 240
 ttctttcttt gtgacaaacc aaaagaataa gaggatttag aacaggactg cttttcccct 300
 atgatttaaa aattccaatg actttcgccc ttgggagaaa tttccaagga aatctctctc 360
 gctcgctctc tccgttttcc tttgtgagct tctgggggag ggtagtggt gactttttga 420
 tacgaaaaaa tgcattttgt g 441

<210> 316
 <211> 247
 <212> DNA
 <213> Homo sapiens

<400> 316
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 ggcgggatac tccattatgg cccctcgccc tgtagggctg gaatagttag aaaaggcaac 120
 ccagtctagc ttgtaagaa gagagacatg cccccaacct cggcgccctt ttctctcacg 180
 atctgctgtc cttacttcag cgactgcagg agcttcacct gcaagaaaac agcattgagc 240
 tgctgac 247

<210> 317
 <211> 409
 <212> DNA
 <213> Homo sapiens

<400> 317
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 cacgatgtgg gatgaacagc agccttgggt ttagagccag ggtgtccatg gatttgaccc 120
 gaatgtccc tggaggccct gtggcgagga caggcactgg atggtccaga cctctgggt 180
 ggaggagtgg tggagccagg actgggcctt cagccatgag ggctagaata acctgacctc 240
 ttgcatctta aactgggtc attaatgaca cctttccagt ggatgttgca aaaaccaaca 300
 ctgtcaggaa cctggccctg ggagggtcga ggtgagctca caaggagagg tcaagccaag 360
 ccaaagggtg ggkaacacac aacaccaggg gaaaccagcc cccaaacca 409

<210> 318
<211> 320
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> 6, 17, 24, 271
<223> n = A,T,C or G

<400> 318
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cctcacgagg tcaggggaac ccttgtagaa ctccaccagc agcatcatct cgtgaaggat 120
gtcattgggtc aggaagctgt cctggacgta ggccatctcc acatccatgg ggatgccata 180
gtcactgggc ctttgctcgg gaggaggcat caccagaaa ggcgagatct tggactcggg 240
gcctgggttg ccagaatagt aaggggagca naggaggcg aggcagggtt ggaagccatt 300
gctggagccc tgcagccgca 320

<210> 319
<211> 212
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> 172
<223> n = A,T,C or G

<400> 319
tgaagcaata gcgcccccat tttacaggcg gagcatggaa gccagagagg tgggtggggg 60
agggggtcct tccctggctc aggcagatgg gaagatgagg aagccgctga agacgctgtc 120
ggcctcagag ccctggtaaa tgtgaccctt tttgggtctt ttttcaacc anacctgggtc 180
acctctgtgc agacctcggc cgcgaccacg ct 212

<210> 320
<211> 769
<212> DNA
<213> Homo sapiens

<400> 320
tggagggtgta gcagtgagag gagatytcag gcaagagtgt cacagcagag ccctaaascc 60
tccaactcac cagtgaagaga tgagactgcc cagtactcag ccttcatctc ctggggccacc 120
tggagggcgt ctttctccat cagcgcatatc tgagcagggg tactcagatc cttcttggaa 180
ctacaagga agagaagcac actggaaggg tcattctcct tcagggcatc ggccagccac 240
tgctgccat gggagggtgga aagtaaggga tgagtgaatc tgcagggccc ctccactga 300
cattcatagg cccaattacc cctctctggt tctacatgc attcttcttc ttcctgacca 360
cccctctgtt ctgaaccctc tcttcccga gcctccatt atattgcagg atgctcactt 420
acttggtatg ttccagagat gccacatcat tcaggttgaa gacaatgatg atggcttgga 480
agagtggcag aaacagcccc aggttgacag ggaagacact actgctcatt tcccacatcc 540
ttccagctcc atatgagaaa gccatgtgca ctctgagacc cacctacccc acttcacca 600
gccccttacc ttgagctcct ctatagtagg ttgatgcaat gcatttgaac ctctcctgcc 660
cagcggatc ccaactggaa ggaaggaaga gtgaagcaca ggtatgtatc ttgggggggtg 720
tgggtgctgg ggagaaggga tagctggaag ggggtgtgga gcaactcaca 769

<210> 321
<211> 690
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 633, 666
<223> n = A,T,C or G

<400> 321
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cctactcccc cggaggcaac tgggaggtca acgggaagac aatcatcccc tataagaagg 120
gtgcctgggtg ttgcgtctgc acagccagtg tctcaggctg cttcaaagcc tgggaccatg 180
cagggggggct ctgtgaggtc cccaggaatc cttgtcgcag gagctgccag aaccatggac 240
gtctcaacat cagcacctgc cactgccact gtccccctgg ctacacgggc agatactgcc 300
aagtgaggtg cagcctgcag tgtgtgcacg gccggttccg ggaggaggag tgctcgtgcy 360
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cctgtgacct gaggatcgac ggagactgct tcatgggtgc ttcagaggca gacacctatt 480
acagaagcca ggatgaaatg tcagaggaat ggcgggggtgc tggcccagat caagagccag 540
aaagtgcagg acatcctcgc cttctatctg ggccgcctgg agaccacca cgaggtgact 600
gacagtgact ttgagaccag gaacttctgg atnnggctca cctacaagac cgccaaggac 660
tccttncgct ggccacaggg ggagcaccag 690

<210> 322
<211> 104
<212> DNA
<213> Homo sapiens

<400> 322
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acgctcacat cacggacatc atggagcagg accaccacct ggtc 104

<210> 323
<211> 118
<212> DNA
<213> Homo sapiens

<400> 323
gggccttggg cgcttcctaaa tgacccagga ggtgggtctgc gacgaatgcc ctaatgtcaa 60
actagtgaat gaagaacgaa cactggaagt agaaatagag cctgggggtga gagacgga 118

<210> 324
<211> 354
<212> DNA
<213> Homo sapiens

<400> 324
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agcgggtctgt atggacccag gcttgtcaaa ctgtactata cacatcgtga cagtcaccat 120
taacggagat gatgccgaaa acgcaaggcc gaagccaaag ccaggggatg gagagtttgt 180
ggaagtcatc tctttaccca agaatgacct gctgcagaga cttgatgctc tggtagctga 240
agaacatctc acagtggacg ccagggtcta ttcctacgct ctagcgtga aacatgcaaa 300
tgcaaagcca tttgaagtgc ctttcttgaa attttaagcc caaatatgac actg 354

<210> 325
<211> 642
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> 1

<223> n = A,T,C or G

<400> 325

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cccactgata ccaagaccaa tgaaagagac acagttaagc agcaatccat ctcatattcca 120
ggcacttcaa taggtcgctg attggctcctt gcaccagcag tggtagtcgt acctatttca 180
gagaggctctg aaattcaggt tcttagtttg ccagggacag gccctacctt atattttttt 240
ccatcttcat catccacttc tgcttacagt ttgctgctta caataactta atgatggatt 300
gagttatctg ggtggctctt agccatctgg gcagtgtggt tctgtctaac caaagggcat 360
tggcctcaaa ccctgcattt ggtttagggg ctaacagagc tcctcagata atcttcacac 420
acatgtaact gctggagatc ttattctatt atgaataaga aacgagaagt ttttccaaag 480
tgttagtcag gatctgaagg ctgtcattca gataaccag cttttccttt tggcttttag 540
cccattcaga ctttgccaga gtcaagccaa ggattgcttt tttgctacag ttttctgcca 600
aatggcctag ttcctgagta cctggaaacc agagagaaag ag 642
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<210> 326

<211> 455

<212> DNA

<213> Homo sapiens

<400> 326

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tccgtgagga tgagcttcga gtccttcacc aggcactgca ggggcacagt cacgtcaatc 60
accttcacct tctcgctctt cctgctcttg tcattgacaa acttcccgtg ccaggcattg 120
acgatgatga ggccattctt ggactcttct gcctcaatta tccttcggac agattcctgc 180
atcagccgga cagcggaactc cgctcttgc ttcttctgca gcacatcggt ggccggcgtt 240
tccctctgct tctccaattc cttctctttc tgagccctga ggtatggttt gatgatcaga 300
cggtgcatgg caaagtagac cactagaggc ccacgggtgg catagaacat ggcgctgggc 360
agaagctggg ccgtcaagtg aataggggag aagtatgtct gactggccct gttgagcttg 420
actttgagag aaacgccttg tggaactcca acgct 455
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<210> 327

<211> 321

<212> DNA

<213> Homo sapiens

<400> 327

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ttcactgtga actcgagtc ctcgatgaac tcgcacagat gtgacagccc tgtctccttg 60
ctctctgagt tctcttcaat gatgctgatg atgcagteca cgatagcgcg cttataactca 120
aagccaccct cttcccgag catggtgaac aggaagtcca taaggacggc gtgtttgcga 180
ggatatttct gacacagggc actgatggcc tggacaacca ccaccttgaa ttcattccgag 240
atttctgaca tgaaggagga gatctgcttc atgaggcggt cgatgctgct ctcgctgccc 300
gtcttaagga ggggtggtgat g 321
```

<210> 328

<211> 476

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 302, 311

<223> n = A,T,C or G

<400> 328

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tgcaggaggg gccatggggg ctgtgaatgg gatgcagccc catggtgtcc ctgataaatc 60
cagtgtgcag tctgatgaag tctgggtggg tgtggtctac gggctggcag ctaccatgat 120
ccaaggagta atgcactcct tttcccatct ctccaccatc tgtatcctgg ccmagaaaaa 180
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cttccttca aaccaaccaa aatttccttt caaaggcata acccaaatgc catccttggt 240
ccggtctaataaagcctccc ccatttttcc cctggatatgc attcccaggc tccctggcct 300
tncagggtctt nctgtctgtg ggtcatagtt tatctcctcc cacttgctgg gagtccttg 360
aaggcaaaga ctctactgcc tccatctatc cagtggaggt ggctcttcag aggggtgcaa 420
gttagtatgt atgactgtca tctctcccaa cagggcctga cttggsaggg cttcca 476

<210> 329

<211> 340

<212> DNA

<213> Homo sapiens

<400> 329

cgaggagat tgccagcacc ctgatggaga gtgagatgat ggagatcttg tcagtgttag 60
ctaagggtga ccacagccct gtcacaaggg ctgctgcagc ctgcctggac aaagcagtgg 120
aatatgggct tatccaaccc aaccaagatg gagagtggag gggttgctcc tgggcccagg 180
gctcatgcac acgctaccta ttgtggcacg gagagtaagg acggaagcag ctttggctgg 240
tggtggctgg catgcccatt actcttgccc atcctcgctt gctgcctag gatgtcctct 300
gttctgagtc agcggccacg ttcagtcaca cagccctgct 340

<210> 330

<211> 277

<212> DNA

<213> Homo sapiens

<400> 330

tgtcaccatc acattggtgc caaataccca gaagacatcg tagatgaaga gtccgcccag 60
caggatgcag ccagtgtgta cattgttgag gtgcaggagc tctactccat taagggagaa 120
ggccaggcca aaaagggtgt tggcaatcca gtgcttcctc agcaggatcc agacgccaac 180
gatgtgtctc aggccaggc acaccaggtc cttggtgtca aattcataat tgatgatctc 240
ctccttgttt tcccagaacc ctgtgtgaag agcagac 277

<210> 331

<211> 136

<212> DNA

<213> Homo sapiens

<400> 331

ttgcttccca cctcctttct ctgtcctctc ctgaggttct gccttacaat ggggacactg 60
atacaaacca cacacacaat gaggatgaaa acagataaca ggtaaaatga cctcacctgc 120
ccgggcggcc gctcga 136

<210> 332

<211> 184

<212> DNA

<213> Homo sapiens

<400> 332

ttgtgagata aacgcagata ctgcaatgca ttaaaacgct tgaaatactc atcagggtatg 60
ttgtgatctt tattgttgct taagtagaga gttagaagag agacaggag accagaaggc 120
agtctggcta tctgattgaa gctcaagtca aggtattcga gtgatttaag accttataaa 180
gcag 184

<210> 333

<211> 384

<212> DNA

<213> Homo sapiens

<400> 333

cggaaaactt cgaggaattg ctcaaagtgc tgggggtgaa tgtgatgctg aggaagattg 60
ctgtggctgc agcgtccaag ccagcagtg agatcaaaca ggaggagac actttctaca 120
tcaaaacctc caccaccgtg cgcaccacag agattaactt caagggtggg gaggagtgtg 180
aggagcagac tgtggatggg aggccctgta agagcctggt gaaatgggag agtgagaata 240
aatggctctg tgagcagaag ctctgaagg gagaggggcc caagacctcg tggaccagag 300
aactgaccaa cgatggggaa ctgacctga ccatgacggc ggatgacgtt gtgtgcacca 360
gggtctacgt ccgagagtga gcgg 384

<210> 334
<211> 169
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 2, 165
<223> n = A,T,C or G

<400> 334
cnacaaacag agcagacacc ctggatccgg tcctgctact ggccaggacg gctggaccgt 60
aaaattgaat ttccacttcc tgaccgccgc cagaagagat tgattttctc cactatcact 120
agcaagatga acctctctga ggaggttgac ttggaagact atgtngccc 169

<210> 335
<211> 185
<212> DNA
<213> Homo sapiens

<400> 335
ccagggttgc agcccaggct gcacatcagg ggactgcctc gcaatacttc atgctgttgc 60
tgctgactga tgggtgctgtg acggatgtgg aagccacacg tgaggctgtg gtgcgtgcct 120
cgaacctgcc catgtcagtg atcattgtgg gtgtgggtgg tgctgacttt gaggccatgg 180
agcag 185

<210> 336
<211> 358
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 26
<223> n = A,T,C or G

<400> 336
ctgcccctgc cttacggcgg ccaganacac acccaggatg gcattggccc caaacttggg 60
tttgttctca gtcccatcca actccagcat caggttgtcc agtttctctt gctccaccac 120
agagagacct gagctgatga gggctggcgo gatgtggag ttgatgtggt ccaactgcctt 180
caggacacct ttgcctaagt aacgtgttt gtctccatcc ctcagctcca gggcctcata 240
gatgcccgta gaggctccac tgggcactgc agcccgaaa agacctttgg cagtataag 300
atccacctcc actgtggggt tcccgcggga gtccaggatc tcccggggcc agatcttc 358

<210> 337
<211> 271
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature

<222> 17

<223> n = A,T,C or G

<400> 337

```
cacaaagcca ccagccnggg aaatcagaat ttacttgatg caactgactt gtaatagcca 60
gaaatcctgc ccagcatggg attcagaacc tggctgcaa ccaaaccac cgtcaaagtt 120
catacaggat aaaacaaatt caattgcctt ttccacatta atagcatcaa gttccccc 180
caaagccaaa gttgccaccg cacaaaaaga gaattctgtg tcaatttctc cctactttat 240
aaaagtagat ttttcacatc ccatgaagca g                                     271
```

<210> 338

<211> 326

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 15, 17, 18

<223> n = A,T,C or G

<400> 338

```
ctgtgctccc gactngnnca tctcaggtag caccgactgc actgggaggg gccctctggg 60
gggaaaggct ccacggggca gggatacatc tcgaggccag tcatcctctg gaggcagccc 120
aatcagggtca aagattttgc ccaactgggc ggcttcagag ttccacaga agagaggctt 180
tcgacgaaac atctctgcaa agatacagcc aacactccac atgtccacag gtgttgcata 240
tgtggactgc agaagaactt cgggagctcg gtaccagagt gtaacaacca cgggtgtaag 300
tgccatctgg tagctgtaga ttctgg                                     326
```

<210> 339

<211> 260

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 47, 54, 60, 69, 90, 91, 96, 113, 117, 119, 195

<223> n = A,T,C or G

<400> 339

```
ttcacctgag gactcatttc gtgccctttg ttgacttcaa gcaaagncct tcanggtctn 60
caaggacgnc acatttcac ttgcgaatgn nctcanggct catcttgag aanaagnanc 120
ccaagtgtg gatccagac tcgggggtaa ccttgtgggt aagagctcat ccagtttatg 180
ctttaggacg tccanctact cgggggagct ggaagcctgc gtggatgcgg cctgtctgga 240
cctcggccgc gaccacgcta                                     260
```

<210> 340

<211> 220

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 15, 18

<223> n = A,T,C or G

<400> 340

```
ctggaagccc ggctngnct ggcagcgga ggagccaggc aggttcacgc agcgggtgctg 60
```


gcagtagcgg tagcggcact cgtctatgtc cacacactcg ggcccgatct tgcggtaacc 120
 atcagggcag gtgcactgat aggagccagg caagttatgg cagtcctggc tggggcgaca 180
 gtcgtgcagg gcctgggcac actcgtccac atccacacag 220

<210> 341

<211> 384

<212> DNA

<213> Homo sapiens

<400> 341

ctgtaccag gggagcgaga gctgactatc ccagcctcgg ctaatgtatt ctacgccatg 60
 gatggagctt cacacgattt cctcctgcgg cagcggcgaa ggtcctctac tgctacaccg 120
 ggcgtcacca gtggcccgtc tgcctcagga actcctcga gtgagggagg agggggctcc 180
 tttcccagga tcaaggccac agggaggaag attgcacggg cactgttctg aggaggaagc 240
 cccgttggct tacagaagtc atggtgttca taccagatgt gggtagccat cctgaatggt 300
 ggcaattata tcacattgag acagaaattc agaaaggag ccagccacc tggggcagtg 360
 aagtgcact ggtttaccag acag 384

<210> 342

<211> 245

<212> DNA

<213> Homo sapiens

<400> 342

ctggctaagc tcatcattgt tactggtggg caccatgtcc ttgaagcttc aggcaagcaa 60
 tgtaaccaac aagaatgacc ccaagtcct caactctcga gtcttcattg gaaacctcaa 120
 cacagctctg gtgaagaaat cagatgtgga gaccatcttc tctaagtatg gccgtgtggc 180
 cggctgttct gtgcacaagg gctatgcctt tgttcagtac tccaatgagc gccatgcccg 240
 ggcag 245

<210> 343

<211> 611

<212> DNA

<213> Homo sapiens

<400> 343

caaaaaaaaa caagatttaa tttttttatt tgcactgaaa aactaatcat aactgttaat 60
 tctcagccat ctttgaagct tgaaagaaga gtctttggta ttttgtaaac gttagcagac 120
 tttcctgcc a gtgtcagaaa atcctattta tgaatcctgt cggatttcct tggatatctga 180
 aaaaaatacc aaatagtacc atacatgagt tatttctaag tttgaaaaat aaaaagaaat 240
 tgcatacacac taattacaaa atacaagttc tggaaaaaat atttttcttc atttttaaac 300
 tttttttaac taataatggc tttgaaagaa gaggcttaat ttgggggtgg taactaaaat 360
 caaaagaaat gattgacttg agggctctctg tttggtgaaga atacatcatt agcttaata 420
 agcagcagaa ggtagtttt aattatgtag cttctgttaa tattaagtgt tttttgtctg 480
 ttttacctca atttgaacag ataagtttgc ctgcatgctg gacatgcctc agaaccatga 540
 atagcccgt a ctatgcttg ggaacatgga tcttagagtc ctttggaata agttcttata 600
 taaatacccc c 611

<210> 344

<211> 311

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 1, 275, 284, 296, 297, 300

<223> n = A,T,C or G

<400> 344
nctcgaaaaa gcccaagaca gcagaagcag acacctccag tgaactagca aagaaaagca 60
aagaagtatt cagaaaagag atgtcccagt tcatcgtcca gtgcctgaac ccttaccgga 120
aacctgactg caaagtggga agaattacca caactgaaga ctttaaacad ctggctcgca 180
agctgactca cgggtgttatg aataaggagc tgaagtactg taagaatcct gaggacctgg 240
agtgcattga gaattgaaa cacaaaacca aggantacat taanaagtac atgcannan 300
tttggggctt g 311

<210> 345
<211> 201
<212> DNA
<213> Homo sapiens

<400> 345
cacacggtca tcccgactgc caacctggag gcccaggccc tgtggaagga gccgggcagc 60
aatgtcacca tgagtgtgga tgctgagtgt gtgcccattg tcagggacct tctcaggtac 120
ttctactccc gaaggattga catcacctg tcgtcagtca agtgcttcca caagctggcc 180
tctgcctatg gggccaggca g 201

<210> 346
<211> 370
<212> DNA
<213> Homo sapiens

<400> 346
ctgctccagg gcgtgggtgtg ccttcgtggc ctctgcctcc tccgaggagc caggctgtgt 60
tctcttcaga atgttctgga gcagcagttt gaggcgggtg atgcgttgga agggcagaat 120
cagaaaggac ttgagggaaa ggcgctggca gacggggtcg ctctccagct tctccaagac 180
ctcccggaaa ttgctgttgc tattcatcag gctctggaag gtgcgttcct gataggtctg 240
gttgggtgaca taaggcaggt agacccggcg gaagtctggg gcgtgggtca ggactacgtc 300
acatacttgg aaggagaaga tattgttctc aaagttctct tccaggtctg aaaggaacgt 360
ggcgtgacg 370

<210> 347
<211> 416
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 416
<223> n = A,T,C or G

<400> 347
ctgttggtgt gtgtatggac gtgggcttta ccatgagtaa ctccattcct ggtatagaat 60
ccccatttga acaagcaaag aaggtgataa ccatgtttgt acagcgacag gtgtttgctg 120
agaacaagga tgagattgct ttagtcctgt ttggtacaga tggcactgac aatccccctt 180
ctggtgggga tcagtatcag aacatcacag tgcacagaca tctgatgcta ccagattttg 240
atttgcctga ggacattgaa agcaaaatcc aaccagggtc tcaacaggct gacttcctgg 300
atgcactaat cgtgagcatg gatgtgattc aacatgaaac aataggaaag aagtttgag 360
aagaggcata ttgaaatatt cactgacctc aagcagcccg attcagcaaa agtcan 416

<210> 348
<211> 351
<212> DNA
<213> Homo sapiens

<400> 348

```
gtacaggaga ggatggcagg tgcagagcgg gcaactgagct ctgcagggtga aagggtcgg 60
cagttggatg ctctcctgga ggctctgaaa ttgaaacggg caggaaatag tctggcagcc 120
tctacagcag aagaaacggc aggcagtgcc caggacgag caggagacag atgccttcct 180
cttgtctcaa ctgcaaagag gcgttccttc ctctttcact aatcctcctc agcacagacc 240
ctttacgggt gtcaggctgg gggacagtaa ggtctttccc ttcccacaa gccatatctc 300
aggctgtctc agtgggggga aaccttggac aataccggg ctttcttggg c 351
```

<210> 349

<211> 207

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 1

<223> n = A,T,C or G

<400> 349

```
nccgggacat ctccaccctc aacagtggca agaagagcct ggagactgaa cacaaggcct 60
tgaccagtga gattgcaactg ctgcagtcca ggctgaagac agagggctct gatctgtgcg 120
acagagtgag cgaatgcag aagctggatg cacaggtaa ggagctggtg ctgaagtcgg 180
cggtggaggc tgagcgcctg gtggtcg 207
```

<210> 350

<211> 323

<212> DNA

<213> Homo sapiens

<400> 350

```
ccatacaggg ctgttgccca ggccctagag gtcattcctc gtaccctgat ccagaactgt 60
ggggccaagca ccatccgtct acttacctcc cttcgggcca agcacacca ggagaactgt 120
gagacctggg gtgtaaatgg tgagacgggt actttggtgg acatgaagga actgggcata 180
tgaggagccat tggctgtgaa gctgcagact tataagacag cagtggagac ggcagttctg 240
ctactgcgaa ttgatgacat cgtttcaggc cacgaaaaga aaggcgatga ccagagccgg 300
caaggcgggg ctcctgatgc tgg 323
```

<210> 351

<211> 353

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 12, 25, 39, 42

<223> n = A,T,C or G

<400> 351

```
cgccgcaccc cntggtccct tccantccct tttcctttnt cngggaacgt gtatgcggtt 60
tgtttttgtt ttgtagggtt ttttcccttc tccacctctc cctgtctctt ttgtccatg 120
ttgtccgttt ctgtggggtt aggtttatgt ttttaatcat ctgaggtcac gtctatttcc 180
tccggactcg cctgcttggg ggcgattctc caccggttaa tatggtgcgt cccttttttc 240
ttttgttgcg aatctgagcc ttcttccctc agcttctgcc ttttgaactt tgttcttcgg 300
ttctgaaacc atacttttac ctgagtttcc gtgaggctga ggctgtgtgc caa 353
```

<210> 352

<211> 467

<212> DNA

<213> Homo sapiens

<400> 352

ctgcccacac tgatcacttg cgagatgtcc ttaggggtaca agaacaggaa ttgaagtctg 60
aatttgagca gaacctgtct gagaaactct ctgaacaaga attacaattt cgtcgtctca 120
gtcaagagca agttgacaac ttactcttg atataaatac tgcctatgcc agactcagag 180
gaatcgaaac ggctgttcag agccatgcag ttgctgaaga ggaagccaga aaagcccacc 240
aactctggct ttcagtggag gcattaaagt acagcatgaa gacctcatct gcagaaacac 300
ctactatccc gctgggtagt gcagttgagg ccatcaaagc caactgttct gataatgaat 360
tcacccaagc ttttaaccga gctatccctc cagagtccct gaccgtggg gtgtacagt 420
aagagaccct tagagccgt ttctatgctg ttcaaaaact ggccga 467

<210> 353

<211> 350

<212> DNA

<213> Homo sapiens

<400> 353

ctgctgcagc cacagtagtt cctcccatgg tgggtggccc tcctggtcct gctggcccag 60
gaaatctgtc cccaccaaga acagcccctg gaaaacggcc ccgtcctcta ccacctgtg 120
gaaatgctgc acgggaactg cctcctggag gaccagcttt acctcccca gacattgtc 180
ctgattgtgt agtttctctg gactgcattt caaattgact caggaactgt ttattgcatg 240
gagttacaac aggattctga ccatgaagtt ctcttttagg taacagatcc attactttt 300
ttgaagatgc ttcagatcca acaccaacaa gggcaaacc ctttgactgg 350

<210> 354

<211> 351

<212> DNA

<213> Homo sapiens

<400> 354

atthagatga gatctgaggc atggagacat ggagacagta tacagactcc tagatttaag 60
ttttagggtt tttgctttc taatcaccaa ttcttatata caatgtatat tttagactcg 120
agcagatgat catcttcac ttaagtcatt ccttttgact gagtatggca ggattagagg 180
gaatggcagt atagatcaat gtcttttct gtaaagtata ggaaaaacca gagaggaaaa 240
aaagagctga caattggaag gtagtagaaa attgacgata atttcttctt aacaaataat 300
agttgtatat acaaggaggc tagtcaacca gattttattt gttgagggcg a 351

<210> 355

<211> 308

<212> DNA

<213> Homo sapiens

<400> 355

ttttggcgca agttttacag attttattaa agtcgaagct attggtcttg gaagatgaaa 60
atgcaaagt t gatgagggt gaattgaagc cagatacctt aataaaatta tatcttggtt 120
ataaaaaataa gaaattaagg gttacatca atgtgccaat gaaaaccgaa cagaagcagg 180
aacaagaaac cacacacaaa aacatcgagg aagaccgcaa actactgatt caggcgccca 240
tcgtgagaat catgaagatg aggaagggtc tgaaacacca gcagttactt ggcgaggtcc 300
tactcag 308

<210> 356

<211> 207

<212> DNA

<213> Homo sapiens

<400> 356

ctgtcccaag tgctcccaga aggcaggatt ctgaagacca ctccagcgat atgttcaact 60
atgaagaata ctgcaccgcc aacgcagtca ctgggccttg ccgtgcatcc ttcccacgt 120

ggtagctttga cgtggagagg aactcctgca ataacttcat ctatggaggc tgccggggca 180
ataagaacag ctaccgctct gaggagg 207

<210> 357
<211> 188
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 25, 29
<223> n = A,T,C or G

<400> 357
tcgaccacgc cctcgtagcg catgngctnc aggacgatgc tcagagtgat gaacaccccg 60
gtgcgggcca cgccagcact gcagtgcacc gtgataggcc catcctgtcc aaactgctcc 120
ttggtcttat gcacctgccc gatgaagtca atgaatccct cgcctgtctt gggcacgccc 180
tgctctgg 188

<210> 358
<211> 291
<212> DNA
<213> Homo sapiens

<400> 358
ctgggagcat cggcaagcta ctgccttaaa atccgatctc cccgagtgca caatttctgt 60
cccttttaag gggtcacac actaaagatt tcacatgaaa gggttgat tgatttgagc 120
aggcaggcgg tacgtgacag gggctgcatg caccgggtgt cagagagaaa cagaacaggg 180
cagggaattt cacaatgttc ttctatacaa tggctggaat ctatgaataa catcagtttc 240
taagttatgg gttgattttt aactactggg tttaggccag gcaggcccag g 291

<210> 359
<211> 117
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 79, 98, 100
<223> n = A,T,C or G

<400> 359
gccaccacac tccagcctgg gcaatacagc aagactgtct caaaaaaaaa aaaaaaaaaa 60
cccaaaaaaa ctcaaaaang taatgaatga taccgaangn gccttttcta gaaaaag 117

<210> 360
<211> 394
<212> DNA
<213> Homo sapiens

<400> 360
ctgttctctt ggggtggtcc agttctagag tgggagaaag ggagtcaggc gcattgggaa 60
tcgtggttcc agtctggttg cagaatctgc acatttgcca agaaattttc cctgtttgga 120
aagtttgccc cagctttccc gggcacacca ccttttgtec caagtgtctg ccggtcgacc 180
aatctgcttg ccacacattg accaagccag acccggttca cccagctcga ggatcccagg 240
ttgaagagtg gccccttgag gccctggaag gaccaatcac tggacttctt cccttgagag 300
tcagaggcca cccgtgattc tgctgcacc ttatcattga tctgcagtga tttctgcaaa 360
tcaagagaaa ctctgcaggg cactcccctg tttc 394

<210> 361
<211> 394
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 28, 31
<223> n = A,T,C or G

<400> 361
ctgggcggtat agcaccgggc atattttntt natggatgag gtctggcacc ctgagcagtc 60
cagcgaggac ttggtcttag ttgagcaatt tggctaggag gatagtatgc agcacggttc 120
tgagtctgtg ggatagctgc catgaagtaa cctgaaggag gtgctggctg gtaggggttg 180
attacagggt tgggaacagc tcgtacactt gccattctct gcatatactg gttagtgagg 240
tgagcctggc gctcttcttt gcgctgagct aaagctacat acaatggctt tgtggacctc 300
ggccgcgacc acgctaagcc gaattccagc acactggcgg ccgttactag tggatccgag 360
ctcggtagca agcttggcgt aatcatggct atag 394

<210> 362
<211> 268
<212> DNA
<213> Homo sapiens

<400> 362
ctgcgcgttg accagtcagc ttccgggtgt gactggagca gggcttgtcg tcttcttcag 60
agtcactttg caggggttgg tgaagctgct cccatccatg tacagctccc agtctactga 120
tgtttaagga tgggtctcgt ggtaggccc actagaataa actgagtcca atacctctac 180
acagttatgt ttaactggc tctctgacac cgggaggaag gtggcggggg ttaggtgttg 240
caaaactcaa tggttatgcg gggatggt 268

<210> 363
<211> 323
<212> DNA
<213> Homo sapiens

<400> 363
ccttgacctt ttcagcaagt gggaagggtg aatccgtctc cacagacaag gccaggactc 60
gtttgtaccc gttgatgata gaatggggta ctgatgcaac agttgggtag ccaatctgca 120
gacagacact ggcaacattg cggacaccct ccaggaagcg agaatgcaga gtttcctctg 180
tgatatcaag cacttcaggg ttgtagatgc tgccattgtc gaacacctgc tggatgacca 240
gcccaaagga gaagggggag atgttgagca tgttcagcag cgtggcttcg ctggctccca 300
ctttgtctcc agtcttgatc aga 323

<210> 364
<211> 393
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 29
<223> n = A,T,C or G

<400> 364
ccaagctctc catcgctccc gtgcgcagng gctactgggg gaacaagatc ggcaagcccc 60
acactgtccc ttgcaagggt acaggccgct ggggtctgtg gctggtaagc ctcactactg 120

```

caccagggg cactggcatc gtctccgcac ctgtgcctaa gaagctgctc atgatggctg 180
gcatcgatga ctgctacacc tcagcccggg gctgcactgc caccctgggc aacttcgcca 240
aggccacctt tgatgccatt tctaagacct acagctacct gacccccgac ctctggaagg 300
agactgtatt caccaagtct ccctatcagg agttcactga ccacctcgtc aagaccaca 360
ccagagtctc cgtgcagcgg actcaggctc cag

```

```

<210> 365
<211> 371
<212> DNA
<213> Homo sapiens

```

```

<400> 365
cctcctcaga gcggtagctg ttcttattgc cccggcagcc tccatagatg aagttattgc 60
aggagttcct ctccacgtca aagtaccagc gtgggaagga tgcacggcaa ggcccagtga 120
ctgcgttggc ggtgcagtat tcttcatagt tgaacatata gctggagtgg tcttcagaat 180
cctgccttct gggagcactt gggacagagg aatccgctgc attcctgctg gtggacctcg 240
gccgcgacca cgctaagccg aattccagca cactggcggc cgttactagt ggatccgagc 300
tcggtaccaa gcttgccgta atcatggta tagctgtttc ctgtgtgaaa ttgttatccg 360
ctcacattc c

```

```

<210> 366
<211> 393
<212> DNA
<213> Homo sapiens

```

```

<400> 366
atttcttggc agatgggagc tctttggtga agactccttt cgggaaaagt tttttggctt 60
cttcttcagg gatggttga aggaccatca cactatcccc atccttccaa tcaactgggg 120
tggaaccctt tttttctgct gtcagctgga gagagatgac taccctgaga atctcatcaa 180
agttcctgcc agtggtagct gggtagagga tagacagctt cagcttctta tcaggaccaa 240
aaacaaacac cacacgagct gccacaggca tgcccttttc atccttctct gctggatcca 300
gcatgcccaa caggatggca agctccgat tcctatcatc gatgatggga aaaggtaact 360
tttctgtggg ctcttcacaa ttgtaagcat tga

```

```

<210> 367
<211> 327
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc feature
<222> 34, 54, 55
<223> n = A,T,C or G

```

```

<400> 367
ccagctctgt ctcatacttg actctaaagt cttnagcagc aagacgggca ttgnnaatct 60
gcagaacgat gcgggcattg tccacagtat ttgcgaagat ctgagccctc aggtcctcga 120
tgatcttgaa gtaatggctc cagtctctga cctgggggtcc cttcttctcc aagtgtctcc 180
ggattttgct ctccagcctc cggttctcgg tctccaggct cctcactctg tccaggtaag 240
aggccaggcg gtcgttcagg ctttgcattg tctccttctc gttctggatg cctcccatte 300
ctgccagacc cccggctatc ccggtgg

```

```

<210> 368
<211> 306
<212> DNA
<213> Homo sapiens

```

```

<220>

```

<221> misc_feature

<222> 24

<223> n = A,T,C or G

<400> 368

```
ctggagaagg acttcagcag tttnaagaag tactgccaag tcatccgtgt cattgcccac 60
acctgatgc gcctgcttcc tctgcgccag aagaaggccc acctgatgga gatccagggtg 120
aacggaggca ctgtggccga gaagctggac tgggcccgcg agaggcttga gcagcaggta 180
cctgtgaacc aagtgtttgg gcaggatgag atgatcgacg tcatcggggt gaccaagggc 240
aaaggctaca aaggggtcac cagtcgttgg cacaccaaga agctgccccg caagaccac 300
cgagga 306
```

<210> 369

<211> 394

<212> DNA

<213> Homo sapiens

<400> 369

```
tcgaccaca ccggaacacg gagagctggg ccagcattgg cacttgatag gatttcccg 60
cggtgccac gaaagtgcgt ttctttgtgt tctcgggttg gaaccgtgat ttccacagac 120
ccttgaaata cactgcgttg acgaggacca gtctggtgag cacaccatca ataagatctg 180
gggacagcag attgtcaatc atatccctgg tttcattttt aacctatgca ttgatggaat 240
cacaggcaga ggctggatcc tcaaagttca cattccggac ctacactgg aacacatctt 300
tgttccttgt aacaaaaggc acttcaattt cagaggcatt cttaacaaac acggcggttag 360
ccactgtcac aatgtcttta ttcttcttgg agac 394
```

<210> 370

<211> 653

<212> DNA

<213> Homo sapiens

<400> 370

```
ccaccacacc caattccttg ctggtatcat ggcagccgcc acgtgccagg attacgggt 60
acatcatcaa gtatgagaag cctgggtctc ctcccagaga agtggtcctt cggccccgcc 120
ctggtgtcac agaggctact attactggcc tggaaaccggg aaccgaatat acaatttatg 180
tcattgccct gaagaataat cagaagagcg agcccctgat tggaaaggaaa aagacagacg 240
agcttcccc actggtaacc cttccacacc ccaatcttca tggaccagag atcttggatg 300
ttccttccac agttcaaaag acccctttcg tcaccacacc tgggtatgac actggaaatg 360
gtattcagct tcctggcact tctggtcagc aaccagtggt tgggcaacaa atgatctttg 420
aggaacatgg ttttaggcgg accacaccgc ccacaacggc caccaccata aggcataggc 480
caagaccata cccgccgaat gtaggacaag aagctctctc tcagacaacc atctcatggg 540
ccccattcca ggacacttct gagtacatca tttcatgtca tcctgttggc actgatgaag 600
aacccttaca gttcagggtt cctggaactt ctaccagtgc cactctgaca gga 653
```

<210> 371

<211> 268

<212> DNA

<213> Homo sapiens

<400> 371

```
ctgcccagcc cccattggcg agtttgagaa ggtgtgcagc aatgacaaca agaccttcca 60
ctcttctcgc cacttctttg ccacaaagtg caccctggag ggcaccaaga agggccacaa 120
gtctccactg gactacatcg ggccttgcaa atacatcccc ccttgcttgg actctgagct 180
gaccgaattc cccctgcgca tgcgggactg gctcaagaac gtcctggtca cctgttatga 240
gagggatgag gacaacaacc ttctgact 268
```

<210> 372

<211> 392

<212> DNA

<213> Homo sapiens

<400> 372

```
gctgggtgccc ctgggtgaacg tggacctcct ggattggcag gggccccagg acttagaggt 60
ggaactggtc cccctgggtcc cgaaggagga aagggtgctg ctggtcctcc tgggccacct 120
ggtgctgctg gtactcctgg tctgcaagga atgcctggag aaagaggagg tcttggaagt 180
cctgggtccaa aggggtgacaa ggggtgaacca ggcggtccag gtgctgatgg tgtcccaggg 240
aaagatggcc caaggggtcc tactggtcct attggtcctc ctggcccagc tggccagcct 300
ggagataagg gtgaaggtgg tgcccccgga cttccaggta tagctggacc tcgtggtagc 360
cctgggtgaga gaggtgaaac ctcggccgag ac 392
```

<210> 373

<211> 388

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 30

<223> n = A,T,C or G

<400> 373

```
ccaagcgctc agatcggtcaa ggggcaccan ttttgatctg ccagtgacac agccccacaa 60
ccaggtcagc gatgaagta tcttcagtct cccccgaacg atgagacacc atgacgcccc 120
aaccattggc ctgggccagc ttgcacgcct gaagagactc ggtcacggag ccaatctggt 180
tgactttgag caggaggcag ttgcaggact tctcgttcac ggccttggcg atcctctttg 240
ggttgggtcac tgtgagatca tccccacta cctggattcc tgcactggct gtgaacttct 300
gccaagctcc ccagtcaccc tgggtcaaagg gatcttcgat agacaccact gggtagtcct 360
tgatgaagga cttgtacagg tcagccag 388
```

<210> 374

<211> 393

<212> DNA

<213> Homo sapiens

<400> 374

```
ctgacgaccg cgtgaacccc tgcattgggg gtgtcatcct cttocatgag acactctacc 60
agaaggcgga tgatgggctg cccttcccc aagttatcaa atccaagggc ggtgttgtgg 120
gcatcaaggt agacaagggc gtggtcccc tggcagggac aaatggcgag actaccaccc 180
aagggttggg tgggctgtct gagcgctgtg cccagtacaa gaaggacgga gctgacttcg 240
ccaagtggcg ttgtgtgctg aagattgggg aacacacccc ctcagccctc gccatcatgg 300
aaaatgccaa tgttctggcc cgttatgccg gtatctgccg gcagaatggc attgtgcccc 360
tcgtggagcc tgagatcctc cctgatgggg acc 393
```

<210> 375

<211> 394

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 30, 33

<223> n = A,T,C or G

<400> 375

```
ccacaaatgg cgtgggtccat gtcacaccn ttnttctgca gcctccagcc aacagacctc 60
aggaaagagg ggatgaactt gcagactctg cgcttgagat cttcaaacia gcatcagcgt 120
```

tttccagggc ttcccagagg tctgtgcgac tagcccctgt ctatcaaaag ttattagaga 180
ggatgaagca ttagcttgaa gcactacagg aggaatgcac cacggcagct ctccgccaat 240
ttctctcaga ttccacaga gactgtttga atgttttcaa aaccaagtat cacacttta 300
tgtacatggg ccgcaccata atgagatgtg agccttgtgc atgtggggga ggagggagag 360
agatgtactt tttaatcat gttccccta aaca 394

<210> 376
<211> 392
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 30
<223> n = A,T,C or G

<400> 376
ctgcccagcc cccattggcg agtttgattn ggtgtgcagc aatgacaaca agaccttga 60
ctcttcctgc cacttctttg ccacaaagtg caccctggag ggcaccaaga agggccaca 120
gctccacctg gactacatcg ggccttgcaa atacatcccc ccttgccctgg actctgagct 180
gaccgaattc cccctgcgca tgcgggactg gctcaagaac gtccctgttca cctgtatga 240
gagggatgag gacaacaacc ttctgactga gaagcagaag ctgcggtga agaagatcca 300
tgagaatgag aagcgcctgg aggcaggaga ccacccctg gagctgctgg cccgggactt 360
cgagaagaac tataacatgt acatcttccc tg 392

<210> 377
<211> 292
<212> DNA
<213> Homo sapiens

<400> 377
caatgtttga tgcttaaccc cccaatttc tgtgagatgg atggccagtg caagcgtgac 60
ttgaagtgtt gcatgggcat gtgtgggaaa tcctgcgttt cccctgtgaa agcttgattc 120
ctgccatatg gaggaggtc tggagtcctg ctctgtgtgg tccaggtcct ttccaccctg 180
agacttggct ccaccactga taccctcctt tggggaaagg ctgggcacac agcaggcttt 240
caagaagtgc cagttgatca atgaataaat aaacgagcct atttctcttt gc 292

<210> 378
<211> 395
<212> DNA
<213> Homo sapiens

<400> 378
ctgctgcttc agcgaagggt ttctggcata tccaatgata aggctgcaa agactgttcc 60
aataccagca ccagaaccag ccactcctac tggtgcagca cctgcaccaa taaatttggc 120
agcagtatca atgtctctgc tgattgcact ggtctgaaac tccctttgga ttagctgaga 180
cacaccattc tgggcctga ttttctaag atagaactcc aactctttgc cctctagcac 240
atagccatct gctcggccac actgtcccgg ccttgaagcg atgcacgcaa gaagcttgcc 300
ctgctggaac tgctcctcca ggagactgct gattttggca ttctttttcc ttcatcata 360
tttctctga attttttaga tcgtttttt tttaa 395

<210> 379
<211> 223
<212> DNA
<213> Homo sapiens

<400> 379
ccagatgaaa tgctgccgca atggctgtgg gaaggtgtcc tgtgtcactc ccaatttctg 60

```

agctccagcc accaccaggc tgagcagtga ggagagaaag tttctgcctg gccctgcatc 120
tggttccagc ccacctgccc tccccttttt cgggactctg tattccctct tgggctgacc 180
acagcttctc cctttcccaa ccaataaagt aaccactttc agc 223

```

```

<210> 380
<211> 317
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc feature
<222> 30, 32
<223> n = A,T,C or G

```

```

<400> 380
tcgaccacag tattccaacc ctctgtgcn tngagaagt atggaggggtg ctgacaacca 60
gggtgcagga gaacaaggta gaccagttag gcagaatat tatcggggat atagaccacg 120
attccgcagg ggcctctctc gccaaagaca gcctagagag gacggcaatg aagaagataa 180
agaaaatcaa ggagatgaga cccaaggta gcagccacct caacgtcggg accgccgcaa 240
cttcaattac cgacgcagac gccagaaaa ccctaaacca caagatggca aagagacaaa 300
agcagccgat ccaccag 317

```

```

<210> 381
<211> 392
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc feature
<222> 29, 30, 31
<223> n = A,T,C or G

```

```

<400> 381
cctgaaggaa gagctggcct acctgaatnn naaccatgag gaggaaatca gtacgctgag 60
gggccaagtg ggaggccagg tcagtgtgga ggtggattcc gctccgggca ccgatctcgc 120
caagatcctg agtgacatgc gaagccaata tgaggatcat gccgagcaga accggaagga 180
tgctgaagcc tggttcacca gccggactga agaattgaac cgggaggtcg ctggccacac 240
ggagcagctc cagatgagca ggtccgaggt tactgacctg cggcgacccc ttcagggctc 300
tgagattgag ctgcagtcac agacctcggc cgcgaccacg ctaagccgaa ttccagcaca 360
ctggcggcgc ttactagtgg atccgagctc gg 392

```

```

<210> 382
<211> 234
<212> DNA
<213> Homo sapiens

```

```

<400> 382
cctcgatgtc taaatgagcg tggtaaagga tgggtgcctgc tggggctctcg tagatacctc 60
gggacttcat tccaatgaag cggttctcca cgatgtcaat acggcccacg ccatgcttgc 120
ccgcgacttc gttcaggtag atgaagagct ccaaggaggt ctgggtgggt gtgccatcct 180
tgacgttggt caccttcaca gggacccctt ttttgaactc catctccaga atgt 234

```

```

<210> 383
<211> 396
<212> DNA
<213> Homo sapiens

```

```

<220>

```

<221> misc_feature

<222> 66

<223> n = A,T,C or G

<400> 383

```

ccttgacctt ttcagcaagt gggaaggtgt tttccgtctc cacagacaag gccaggactc 60
gtttgnaccc gttgatgata gaatggggta ctgatgcaac agttgggtag ccaatctgca 120
gacagacact ggcaacattg cggacaccca ggatttcaat ggtgcccctg gagatttttag 180
tgggtgatacc taaagcctgg aaaaaggagg tcttctcggg cccgagacca gtgttctggg 240
ctggcacagt gacttcacat ggggcaatgg caccagcacg ggcagcagac ctgcccgggc 300
ggcgcctcga aagccgaatt ccagcacact ggcggccgtt actagtggat ccgagctcgg 360
taccaagctt ggcgtaatca tggtcatage tgtttc 396

```

<210> 384

<211> 396

<212> DNA

<213> Homo sapiens

<400> 384

```

gctgaatagg cacagagggc acctgtacac cttcagacca gtctgcaacc tcaggctgag 60
tagcagtga ctcaggagcg ggagcagtc attcaccctg aaattcctcc ttggtcactg 120
ccttctcagc agcagcctgc tcttcttttt caatctcttc aggatctctg tagaagtaca 180
gatcaggcat gacctcccat ggggtgtcac gggaaatgg gccacgcag cgcagaactt 240
cccagagccag catccaccac atcaaaccca ctgagtgage tcccttgttg ttgcatggga 300
tggcaatgtc cacatagcgc agaggagaat ctgtgttaca cagcgcaatg gtaggtaggt 360
taacataaga tgcctccgtg agaggctggt ggtcag 396

```

<210> 385

<211> 2943

<212> DNA

<213> Homo sapiens

<400> 385

```

cagccaccgg agtggatgcc atctgcaccc accgcccctga cccacagggc cctgggctgg 60
acagagagca gctgtatttg gagctgagcc agctgaccca cagcatcact gagctgggcc 120
cctacacccct ggacagggac agtctctatg tcaatggttt cacacagcgg agctctgtgc 180
ccaccactag cattcctggg acccccacag tggacctggg aacatctggg actccagttt 240
ctaaacctgg tccctcggct gccagccctc tcctgggtgct attcactctc aacttcacca 300
tcaccaacct gcggtatgag gagaacatgc agcaccctgg ctccaggaag ttcaacacca 360
cggagagggt ccttcagggc ctggctccctg ttcaagagca ccagtgttgg ccctctgtac 420
tctggctgca gactgacttt gctcaggcct gaaaaggatg ggacagccac tggagtggat 480
gccatctgca cccaccaccc tgaccccaaa agccctaggc tggacagaga gcagctgtat 540
tgggagctga gccagctgac ccacaatatc actgagctgg gccctatgc cctggacaac 600
gacagcctct ttgtcaatgg ttctactcat cggagctctg tgtccaccac cagcactcct 660
gggaccccca cagtgtatct gggagcatct aagactccag cctcgatatt tggcccttca 720
gctgccagcc atctcctgat actattcacc ctcaacttca ccatcactaa cctgcggtat 780
gaggagaaca tgtggcctgg ctccaggaag ttcaacacta cagagagggt ccttcagggc 840
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acctgtctca ggccagagaa agatggggaa gccaccggag tggatgcat ctgcacccac 960
cgccctgacc ccacaggccc tgggctggac agagagcagc tgtatttggg gctgagccag 1020
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aatggtttca cccatcgagg ctctgtaccc accaccagca ccggggtggt cagcgaggag 1140
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ggctccctca agttcaacat cacagacaac gtcattgaagc acctgctcag tctttgttc 1260
cagaggagca gcctgggtgc acggtacaca ggctgcaggg tcatcgcaact aaggtctgtg 1320
aagaacggtg ctgagacacg ggtggacctc ctctgcacct acctgcagcc cctcagcgcc 1380
ccaggtctgc ctatcaagca ggtgttccat gagctgagcc agcagaccca tggcatcacc 1440
cggctgggcc cctactctct ggacaaagac agcctctacc ttaacggtta caatgaacct 1500

```

```

ggtcagatg agcctcctac aactcccaag ccagccacca cattcctgcc tcctctgtca 1560
gaagccacaa cagccatggg gtaccacctg aagaccctca cactcaactt caccatctcc 1620
aatctccagt attcaccaga tatgggcaag ggctcagcta cattcaactc caccgagggg 1680
gtccttcagc acctgctcag acccttggtc cagaagagca gcatggggcc cttctacttg 1740
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acctgcacct accaccctga ccctgtgggc cccgggctgg acatacagca gctttactgg 1860
gagctgagtc agctgacca tgggtgcacc caactgggct tctatgtcct ggacagggat 1920
agcctcttca tcaatggcta tgcacccag aatttatcaa tccggggcga gtaccagata 1980
aatttcacaa ttgtcaactg gaacctcagt aatccagacc ccacatcctc agagtacatc 2040
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gacacattcc gcttctgcct ggtcaccaac ttgacgatgg actcctgtgt ggtcactgtc 2160
aaggcattgt tctcctccaa tttggacccc agcctgggtg agcaagtctt tctagataag 2220
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acagaaatgg agtcatcagt ttatcaacca acaagcagct ccagcaccca gcacttctac 2340
ctgaatttca ccatcaccaa cctaccatat tcccaggaca aagcccagcc aggcaccacc 2400
aattaccaga ggaacaaaag gaatttgag gatgcggcac cacaccggg tggactccct 2460
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tgtggatggg tattttccca acagaaatga gcccttaact gggaattctg accttccctt 2640
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gtgcccaggc tactaccagt cacacctaga cctggaggat ctgcaatgac tggaaactgc 2820
cgggtgcctgg ggtgcctttc cccagccag ggtccaaaga agcttggctg gggcagaaat 2880
aaaccatatt ggtcgaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2940
aaa

```

<210> 386

<211> 2608

<212> DNA

<213> Homo sapiens

<400> 386

```

gttcaagagc accagtgttg gccctctgta ctctggctgc agactgactt tgctcaggcc 60
tgaaaaggat gggacagcca ctggagtgga tgccatctgc acccaccacc ctgaccccaa 120
aagccctagg ctggacagag agcagctgta ttgggagctg agccagctga cccacaatat 180
cactgagctg ggccctatg ccctggacaa cgacagcctc tttgtcaatg gtttactca 240
tcggagctct gtgtccacca ccagcactcc tgggaccccc acagtgtatc tgggagcatc 300
taagactcca gcctcgatat ttggcccttc agctgccagc catctcctga tactattcac 360
cctcaacttc accatcacta acctgcggta tgaggagaac atgtggcctg gctccaggaa 420
gttcaacact acagagaggg tccttcaggg cctgctaagg cccttggtca agaaccaccg 480
tgttggccct ctgtactctg gctgcaggct gaccttgctc aggccagaga aagatgggga 540
agccaccgga gtgatgcca tctgcaccca ccgccctgac cccacaggcc ctgggctgga 600
cagagagcag ctgtatttgg agctgagcca gctgaccac agcatcactg agctggggcc 660
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caccaccagc accggggtgg tcagcgagga gccattcaca ctgaacttca ccatcaacaa 780
cctgcgtac atggcggaca tgggccaacc cggtccctc aagttcaaca tcacagacaa 840
cgtcatgaag cacctgctca gtcccttgtt ccagaggagc agcctgggtg cacggtacac 900
aggctgcagg gtcatcgcac taaggctctg gaagaacggt gctgagacac ggggtggacct 960
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cagcctctac cttaacgggtt acaatgaacc tggccagat gagcctccta caactcccaa 1140
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gaagaccctc aactcaact tcaccatctc caatctccag tattcaccag atatgggcaa 1260
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gaaggatggg gcagccactg gtgtggacac cacctgcacc taccacctg acctgtggg 1440
ccccggctg gacatacagc agctttactg ggaagtgagt cagctgacct atggtgtcac 1500
ccaactgggc ttctatgtcc tggacaggga tagcctcttc atcaatggct atgcacccca 1560

```

```

gaatttatca atccggggcg agtaccagat aaatttccac attgtcaact ggaacctcag 1620
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<210> 387

<211> 1761

<212> DNA

<213> Homo sapiens

<400> 387

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<210> 388

<211> 772

<212> PRT

<213> Homo sapiens

<400> 388

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Leu Gly Pro Pro Gln Trp Thr Trp Glu His Leu Gly Leu Gln Phe Leu
      20          25          30
Asn Leu Val Pro Arg Leu Pro Ala Leu Ser Trp Cys Tyr Ser Leu Ser
      35          40          45
Thr Ser Pro Ser Pro Thr Cys Gly Met Arg Arg Thr Cys Ser Thr Leu
      50          55          60
Ala Pro Gly Ser Ser Thr Pro Arg Arg Gly Ser Phe Arg Ala Trp Ser
      65          70          75          80
Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu
      85          90          95
Thr Leu Leu Arg Pro Glu Lys Asp Gly Thr Ala Thr Gly Val Asp Ala
      100          105          110
Ile Cys Thr His His Pro Asp Pro Lys Ser Pro Arg Leu Asp Arg Glu
      115          120          125
Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Asn Ile Thr Glu Leu
      130          135          140
Gly Pro Tyr Ala Leu Asp Asn Asp Ser Leu Phe Val Asn Gly Phe Thr
      145          150          155          160
His Arg Ser Ser Val Ser Thr Thr Ser Thr Pro Gly Thr Pro Thr Val
      165          170          175
Tyr Leu Gly Ala Ser Lys Thr Pro Ala Ser Ile Phe Gly Pro Ser Ala
      180          185          190
Ala Ser His Leu Leu Ile Leu Phe Thr Leu Asn Phe Thr Ile Thr Asn
      195          200          205
Leu Arg Tyr Glu Glu Asn Met Trp Pro Gly Ser Arg Lys Phe Asn Thr
      210          215          220
Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Leu Phe Lys Asn Thr
      225          230          235          240
Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro
      245          250          255
Glu Lys Asp Gly Glu Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg
      260          265          270
Pro Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Gln Leu Tyr Leu Glu
      275          280          285
Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu
      290          295          300
Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val
      305          310          315          320
Pro Thr Thr Ser Thr Gly Val Val Ser Glu Glu Pro Phe Thr Leu Asn
      325          330          335
Phe Thr Ile Asn Asn Leu Arg Tyr Met Ala Asp Met Gly Gln Pro Gly
      340          345          350
Ser Leu Lys Phe Asn Ile Thr Asp Asn Val Met Lys His Leu Leu Ser
      355          360          365
Pro Leu Phe Gln Arg Ser Ser Leu Gly Ala Arg Tyr Thr Gly Cys Arg
      370          375          380
Val Ile Ala Leu Arg Ser Val Lys Asn Gly Ala Glu Thr Arg Val Asp
      385          390          395          400
Leu Leu Cys Thr Tyr Leu Gln Pro Leu Ser Gly Pro Gly Leu Pro Ile
      405          410          415
Lys Gln Val Phe His Glu Leu Ser Gln Gln Thr His Gly Ile Thr Arg
      420          425          430

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Leu Gly Pro Tyr Ser Leu Asp Lys Asp Ser Leu Tyr Leu Asn Gly Tyr
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 Asn Glu Pro Gly Pro Asp Glu Pro Pro Thr Thr Pro Lys Pro Ala Thr
 450 455 460
 Thr Phe Leu Pro Pro Leu Ser Glu Ala Thr Thr Ala Met Gly Tyr His
 465 470 475 480
 Leu Lys Thr Leu Thr Leu Asn Phe Thr Ile Ser Asn Leu Gln Tyr Ser
 485 490 495
 Pro Asp Met Gly Lys Gly Ser Ala Thr Phe Asn Ser Thr Glu Gly Val
 500 505 510
 Leu Gln His Leu Leu Arg Pro Leu Phe Gln Lys Ser Ser Met Gly Pro
 515 520 525
 Phe Tyr Leu Gly Cys Gln Leu Ile Ser Leu Arg Pro Glu Lys Asp Gly
 530 535 540
 Ala Ala Thr Gly Val Asp Thr Thr Cys Thr Tyr His Pro Asp Pro Val
 545 550 555 560
 Gly Pro Gly Leu Asp Ile Gln Gln Leu Tyr Trp Glu Leu Ser Gln Leu
 565 570 575
 Thr His Gly Val Thr Gln Leu Gly Phe Tyr Val Leu Asp Arg Asp Ser
 580 585 590
 Leu Phe Ile Asn Gly Tyr Ala Pro Gln Asn Leu Ser Ile Arg Gly Glu
 595 600 605
 Tyr Gln Ile Asn Phe His Ile Val Asn Trp Asn Leu Ser Asn Pro Asp
 610 615 620
 Pro Thr Ser Ser Glu Tyr Ile Thr Leu Leu Arg Asp Ile Gln Asp Lys
 625 630 635 640
 Val Thr Thr Leu Tyr Lys Gly Ser Gln Leu His Asp Thr Phe Arg Phe
 645 650 655
 Cys Leu Val Thr Asn Leu Thr Met Asp Ser Val Leu Val Thr Val Lys
 660 665 670
 Ala Leu Phe Ser Ser Asn Leu Asp Pro Ser Leu Val Glu Gln Val Phe
 675 680 685
 Leu Asp Lys Thr Leu Asn Ala Ser Phe His Trp Leu Gly Ser Thr Tyr
 690 695 700
 Gln Leu Val Asp Ile His Val Thr Glu Met Glu Ser Ser Val Tyr Gln
 705 710 715 720
 Pro Thr Ser Ser Ser Thr Gln His Phe Tyr Leu Asn Phe Thr Ile
 725 730 735
 Thr Asn Leu Pro Tyr Ser Gln Asp Lys Ala Gln Pro Gly Thr Asn
 740 745 750
 Tyr Gln Arg Asn Lys Arg Asn Ile Glu Asp Ala Ala Pro His Arg Gly
 755 760 765
 Gly Leu Pro Val
 770

<210> 389

<211> 833

<212> PRT

<213> Homo sapiens

<400> 389

Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr
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 Leu Leu Arg Pro Glu Lys Asp Gly Thr Ala Thr Gly Val Asp Ala Ile
 20 25 30
 Cys Thr His His Pro Asp Pro Lys Ser Pro Arg Leu Asp Arg Glu Gln
 35 40 45

Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly
 50 55 60
 Pro Tyr Ala Leu Asp Asn Asp Ser Leu Phe Val Asn Gly Phe Thr His
 65 70 75 80
 Arg Ser Ser Val Ser Thr Thr Ser Thr Pro Gly Thr Pro Thr Val Tyr
 85 90 95
 Leu Gly Ala Ser Lys Thr Pro Ala Ser Ile Phe Gly Pro Ser Ala Ala
 100 105 110
 Ser His Leu Leu Ile Leu Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu
 115 120 125
 Arg Tyr Glu Glu Asn Met Trp Pro Gly Ser Arg Lys Phe Asn Thr Thr
 130 135 140
 Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Leu Phe Lys Asn Thr Ser
 145 150 155 160
 Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
 165 170 175
 Lys Asp Gly Glu Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Pro
 180 185 190
 Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Gln Leu Tyr Leu Glu Leu
 195 200 205
 Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp
 210 215 220
 Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Pro
 225 230 235 240
 Thr Thr Ser Thr Gly Val Val Ser Glu Glu Pro Phe Thr Leu Asn Phe
 245 250 255
 Thr Ile Asn Asn Leu Arg Tyr Met Ala Asp Met Gly Gln Pro Gly Ser
 260 265 270
 Leu Lys Phe Asn Ile Thr Asp Asn Val Met Lys His Leu Leu Ser Pro
 275 280 285
 Leu Phe Gln Arg Ser Ser Leu Gly Ala Arg Tyr Thr Gly Cys Arg Val
 290 295 300
 Ile Ala Leu Arg Ser Val Lys Asn Gly Ala Glu Thr Arg Val Asp Leu
 305 310 315 320
 Leu Cys Thr Tyr Leu Gln Pro Leu Ser Gly Pro Gly Leu Pro Ile Lys
 325 330 335
 Gln Val Phe His Glu Leu Ser Gln Gln Thr His Gly Ile Thr Arg Leu
 340 345 350
 Gly Pro Tyr Ser Leu Asp Lys Asp Ser Leu Tyr Leu Asn Gly Tyr Asn
 355 360 365
 Glu Pro Gly Pro Asp Glu Pro Pro Thr Thr Pro Lys Pro Ala Thr Thr
 370 375 380
 Phe Leu Pro Pro Leu Ser Glu Ala Thr Thr Ala Met Gly Tyr His Leu
 385 390 395 400
 Lys Thr Leu Thr Leu Asn Phe Thr Ile Ser Asn Leu Gln Tyr Ser Pro
 405 410 415
 Asp Met Gly Lys Gly Ser Ala Thr Phe Asn Ser Thr Glu Gly Val Leu
 420 425 430
 Gln His Leu Leu Arg Pro Leu Phe Gln Lys Ser Ser Met Gly Pro Phe
 435 440 445
 Tyr Leu Gly Cys Gln Leu Ile Ser Leu Arg Pro Glu Lys Asp Gly Ala
 450 455 460
 Ala Thr Gly Val Asp Thr Thr Cys Thr Tyr His Pro Asp Pro Val Gly
 465 470 475 480
 Pro Gly Leu Asp Ile Gln Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr
 485 490 495
 His Gly Val Thr Gln Leu Gly Phe Tyr Val Leu Asp Arg Asp Ser Leu
 500 505 510

Phe Ile Asn Gly Tyr Ala Pro Gln Asn Leu Ser Ile Arg Gly Glu Tyr
 515 520 525
 Gln Ile Asn Phe His Ile Val Asn Trp Asn Leu Ser Asn Pro Asp Pro
 530 535 540
 Thr Ser Ser Glu Tyr Ile Thr Leu Leu Arg Asp Ile Gln Asp Lys Val
 545 550 555 560
 Thr Thr Leu Tyr Lys Gly Ser Gln Leu His Asp Thr Phe Arg Phe Cys
 565 570 575
 Leu Val Thr Asn Leu Thr Met Asp Ser Val Leu Val Thr Val Lys Ala
 580 585 590
 Leu Phe Ser Ser Asn Leu Asp Pro Ser Leu Val Glu Gln Val Phe Leu
 595 600 605
 Asp Lys Thr Leu Asn Ala Ser Phe His Trp Leu Gly Ser Thr Tyr Gln
 610 615 620
 Leu Val Asp Ile His Val Thr Glu Met Glu Ser Ser Val Tyr Gln Pro
 625 630 635 640
 Thr Ser Ser Ser Ser Thr Gln His Phe Tyr Leu Asn Phe Thr Ile Thr
 645 650 655
 Asn Leu Pro Tyr Ser Gln Asp Lys Ala Gln Pro Gly Thr Thr Asn Tyr
 660 665 670
 Gln Arg Asn Lys Arg Asn Ile Glu Asp Ala Leu Asn Gln Leu Phe Arg
 675 680 685
 Asn Ser Ser Ile Lys Ser Tyr Phe Ser Asp Cys Gln Val Ser Thr Phe
 690 695 700
 Arg Ser Val Pro Asn Arg His His Thr Gly Val Asp Ser Leu Cys Asn
 705 710 715 720
 Phe Ser Pro Leu Ala Arg Arg Val Asp Arg Val Ala Ile Tyr Glu Glu
 725 730 735
 Phe Leu Arg Met Thr Arg Asn Gly Thr Gln Leu Gln Asn Phe Thr Leu
 740 745 750
 Asp Arg Ser Ser Val Leu Val Asp Gly Tyr Phe Pro Asn Arg Asn Glu
 755 760 765
 Pro Leu Thr Gly Asn Ser Asp Leu Pro Phe Trp Ala Val Ile Leu Ile
 770 775 780
 Gly Leu Ala Gly Leu Leu Gly Leu Ile Thr Cys Leu Ile Cys Gly Val
 785 790 795 800
 Leu Val Thr Thr Arg Arg Arg Lys Lys Glu Gly Glu Tyr Asn Val Gln
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 Gln Gln Cys Pro Gly Tyr Tyr Gln Ser His Leu Asp Leu Glu Asp Leu
 820 825 830
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<210> 390

<211> 438

<212> PRT

<213> Homo sapiens

<400> 390

Met Gly Tyr His Leu Lys Thr Leu Thr Leu Asn Phe Thr Ile Ser Asn
 1 5 10 15
 Leu Gln Tyr Ser Pro Asp Met Gly Lys Gly Ser Ala Thr Phe Asn Ser
 20 25 30
 Thr Glu Gly Val Leu Gln His Leu Leu Arg Pro Leu Phe Gln Lys Ser
 35 40 45
 Ser Met Gly Pro Phe Tyr Leu Gly Cys Gln Leu Ile Ser Leu Arg Pro
 50 55 60

Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Thr Thr Cys Thr Tyr His
 65 70 75 80
 Pro Asp Pro Val Gly Pro Gly Leu Asp Ile Gln Gln Leu Tyr Trp Glu
 85 90 95
 Leu Ser Gln Leu Thr His Gly Val Thr Gln Leu Gly Phe Tyr Val Leu
 100 105 110
 Asp Arg Asp Ser Leu Phe Ile Asn Gly Tyr Ala Pro Gln Asn Leu Ser
 115 120 125
 Ile Arg Gly Glu Tyr Gln Ile Asn Phe His Ile Val Asn Trp Asn Leu
 130 135 140
 Ser Asn Pro Asp Pro Thr Ser Ser Glu Tyr Ile Thr Leu Leu Arg Asp
 145 150 155 160
 Ile Gln Asp Lys Val Thr Thr Leu Tyr Lys Gly Ser Gln Leu His Asp
 165 170 175
 Thr Phe Arg Phe Cys Leu Val Thr Asn Leu Thr Met Asp Ser Val Leu
 180 185 190
 Val Thr Val Lys Ala Leu Phe Ser Ser Asn Leu Asp Pro Ser Leu Val
 195 200 205
 Glu Gln Val Phe Leu Asp Lys Thr Leu Asn Ala Ser Phe His Trp Leu
 210 215 220
 Gly Ser Thr Tyr Gln Leu Val Asp Ile His Val Thr Glu Met Glu Ser
 225 230 235 240
 Ser Val Tyr Gln Pro Thr Ser Ser Ser Ser Thr Gln His Phe Tyr Leu
 245 250 255
 Asn Phe Thr Ile Thr Asn Leu Pro Tyr Ser Gln Asp Lys Ala Gln Pro
 260 265 270
 Gly Thr Thr Asn Tyr Gln Arg Asn Lys Arg Asn Ile Glu Asp Ala Leu
 275 280 285
 Asn Gln Leu Phe Arg Asn Ser Ser Ile Lys Ser Tyr Phe Ser Asp Cys
 290 295 300
 Gln Val Ser Thr Phe Arg Ser Val Pro Asn Arg His His Thr Gly Val
 305 310 315 320
 Asp Ser Leu Cys Asn Phe Ser Pro Leu Ala Arg Arg Val Asp Arg Val
 325 330 335
 Ala Ile Tyr Glu Glu Phe Leu Arg Met Thr Arg Asn Gly Thr Gln Leu
 340 345 350
 Gln Asn Phe Thr Leu Asp Arg Ser Ser Val Leu Val Asp Gly Tyr Phe
 355 360 365
 Pro Asn Arg Asn Glu Pro Leu Thr Gly Asn Ser Asp Leu Pro Phe Trp
 370 375 380
 Ala Val Ile Leu Ile Gly Leu Ala Gly Leu Leu Gly Leu Ile Thr Cys
 385 390 395 400
 Leu Ile Cys Gly Val Leu Val Thr Thr Arg Arg Arg Lys Lys Glu Gly
 405 410 415
 Glu Tyr Asn Val Gln Gln Gln Cys Pro Gly Tyr Tyr Gln Ser His Leu
 420 425 430
 Asp Leu Glu Asp Leu Gln
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<210> 391

<211> 2627

<212> DNA

<213> Homo sapiens

<400> 391

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<210> 392

<211> 309

<212> PRT

<213> Homo sapiens

<400> 392

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His Ala Ser Ala His Ala Ser Gly Arg Gln Arg Gln Leu His Ser Ala
 1           5           10          15
Ser Thr Gln Ile Arg Trp Glu Pro Ser Pro Ala Met Ala Ser Leu Gly
          20          25          30
Gln Ile Leu Phe Trp Ser Ile Ile Ser Ile Ile Ile Leu Ala Gly
          35          40          45
Ala Ile Ala Leu Ile Ile Gly Phe Gly Ile Ser Gly Arg His Ser Ile
          50          55          60
Thr Val Thr Thr Val Ala Ser Ala Gly Asn Ile Gly Glu Asp Gly Ile

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65          70          75          80
Leu Ser Cys Thr Phe Glu Pro Asp Ile Lys Leu Ser Asp Ile Val Ile
      85          90          95
Gln Trp Leu Lys Glu Gly Val Leu Gly Leu Val His Glu Phe Lys Glu
      100          105          110
Gly Lys Asp Glu Leu Ser Glu Gln Asp Glu Met Phe Arg Gly Arg Thr
      115          120          125
Ala Val Phe Ala Asp Gln Val Ile Val Gly Asn Ala Ser Leu Arg Leu
      130          135          140
Lys Asn Val Gln Leu Thr Asp Ala Gly Thr Tyr Lys Cys Tyr Ile Ile
      145          150          155          160
Thr Ser Lys Gly Lys Gly Asn Ala Asn Leu Glu Tyr Lys Thr Gly Ala
      165          170          175
Phe Ser Met Pro Glu Val Asn Val Asp Tyr Asn Ala Ser Ser Glu Thr
      180          185          190
Leu Arg Cys Glu Ala Pro Arg Trp Phe Pro Gln Pro Thr Val Val Trp
      195          200          205
Ala Ser Gln Val Asp Gln Gly Ala Asn Phe Ser Glu Val Ser Asn Thr
      210          215          220
Ser Phe Glu Leu Asn Ser Glu Asn Val Thr Met Lys Val Val Ser Val
      225          230          235          240
Leu Tyr Asn Val Thr Ile Asn Asn Thr Tyr Ser Cys Met Ile Glu Asn
      245          250          255
Asp Ile Ala Lys Ala Thr Gly Asp Ile Lys Val Thr Glu Ser Glu Ile
      260          265          270
Lys Arg Arg Ser His Leu Gln Leu Leu Asn Ser Lys Ala Ser Leu Cys
      275          280          285
Val Ser Ser Phe Phe Ala Ile Ser Trp Ala Leu Leu Pro Leu Ser Pro
      290          295          300
Tyr Leu Met Leu Lys
305

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<210> 393

<211> 282

<212> PRT

<213> Homo sapiens

<400> 393

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Met Ala Ser Leu Gly Gln Ile Leu Phe Trp Ser Ile Ile Ser Ile Ile
  1          5          10          15
Ile Ile Leu Ala Gly Ala Ile Ala Leu Ile Ile Gly Phe Gly Ile Ser
      20          25          30
Gly Arg His Ser Ile Thr Val Thr Val Ala Ser Ala Gly Asn Ile
      35          40          45
Gly Glu Asp Gly Ile Leu Ser Cys Thr Phe Glu Pro Asp Ile Lys Leu
      50          55          60
Ser Asp Ile Val Ile Gln Trp Leu Lys Glu Gly Val Leu Gly Leu Val
      65          70          75          80
His Glu Phe Lys Glu Gly Lys Asp Glu Leu Ser Glu Gln Asp Glu Met
      85          90          95
Phe Arg Gly Arg Thr Ala Val Phe Ala Asp Gln Val Ile Val Gly Asn
      100          105          110
Ala Ser Leu Arg Leu Lys Asn Val Gln Leu Thr Asp Ala Gly Thr Tyr
      115          120          125
Lys Cys Tyr Ile Ile Thr Ser Lys Gly Lys Gly Asn Ala Asn Leu Glu
      130          135          140
Tyr Lys Thr Gly Ala Phe Ser Met Pro Glu Val Asn Val Asp Tyr Asn

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145              150              155              160
Ala Ser Ser Glu Thr Leu Arg Cys Glu Ala Pro Arg Trp Phe Pro Gln
              165              170              175
Pro Thr Val Val Trp Ala Ser Gln Val Asp Gln Gly Ala Asn Phe Ser
              180              185              190
Glu Val Ser Asn Thr Ser Phe Glu Leu Asn Ser Glu Asn Val Thr Met
              195              200              205
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Cys Met Ile Glu Asn Asp Ile Ala Lys Ala Thr Gly Asp Ile Lys Val
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Thr Glu Ser Glu Ile Lys Arg Arg Ser His Leu Gln Leu Leu Asn Ser
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 Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Arg Val
 20 25 30
 Asp Ala Val Cys Thr His Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp
 35 40 45
 Arg Glu Arg Leu Tyr Trp Lys Leu Ser Gln Leu Thr His Gly Ile Thr
 50 55 60
 Glu Leu Gly Pro Tyr Thr Leu Asp Arg His Ser Leu Tyr Val Asn Gly
 65 70 75 80
 Phe Thr His Gln Ser Ser Met Thr Thr Thr Arg Thr Pro Asp Thr Ser
 85 90 95
 Thr Met His Leu Ala Thr Ser Arg Thr Pro Ala Ser Leu Ser Gly Pro
 100 105 110
 Thr Thr Ala Ser Pro Leu Leu Val Leu Phe Thr Ile Asn Phe Thr Ile
 115 120 125
 Thr Asn Leu Arg Tyr Glu Glu Asn Met His His Pro Gly Ser Arg Lys
 130 135 140
 Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Val Phe
 145 150 155 160
 Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu
 165 170 175
 Leu Arg Pro Lys Lys Asp Gly Ala Ala Thr Lys Val Asp Ala Ile Cys
 180 185 190
 Thr Tyr Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu
 195 200 205
 Tyr Trp Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro
 210 215 220
 Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr Gln Arg
 225 230 235 240
 Ser Ser Val Pro Thr Ser Ile Pro Gly Thr Pro Thr Val Asp Leu
 245 250 255
 Gly Thr Ser Gly Thr Pro Val Ser Lys Pro Gly Pro Ser Ala Ala Ser
 260 265 270
 Pro Leu Leu Val Leu Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Arg
 275 280 285
 Tyr Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr
 290 295 300
 Glu Arg Val Leu Gln Gly Leu Leu Arg Ser Leu Phe Lys Ser Thr Ser


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      770              775              780
Thr Thr Cys Thr Tyr His Pro Asp Pro Val Gly Pro Gly Leu Asp Ile
785              790              795              800
Gln Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Gly Val Thr Gln
      805              810              815
Leu Gly Phe Tyr Val Leu Asp Arg Asp Ser Leu Phe Ile Asn Gly Tyr
      820              825              830
Ala Pro Gln Asn Leu Ser Ile Arg Gly Glu Tyr Gln Ile Asn Phe His
      835              840              845
Ile Val Asn Trp Asn Leu Ser Asn Pro Asp Pro Thr Ser Ser Glu Tyr
      850              855              860
Ile Thr Leu Leu Arg Asp Ile Gln Asp Lys Val Thr Thr Leu Tyr Lys
865              870              875              880
Gly Ser Gln Leu His Asp Thr Phe Arg Phe Cys Leu Val Thr Asn Leu
      885              890              895
Thr Met Asp Ser Val Leu Val Thr Val Lys Ala Leu Phe Ser Ser Asn
      900              905              910
Leu Asp Pro Ser Leu Val Glu Gln Val Phe Leu Asp Lys Thr Leu Asn
      915              920              925
Ala Ser Phe His Trp Leu Gly Ser Thr Tyr Gln Leu Val Asp Ile His
      930              935              940
Val Thr Glu Met Glu Ser Ser Val Tyr Gln Pro Thr Ser Ser Ser Ser
945              950              955              960
Thr Gln His Phe Tyr Pro Asn Phe Thr Ile Thr Asn Leu Pro Tyr Ser
      965              970              975
Gln Asp Lys Ala Gln Pro Gly Thr Thr Asn Tyr Gln Arg Asn Lys Arg
      980              985              990
Asn Ile Glu Asp Ala Leu Asn Gln Leu Phe Arg Asn Ser Ser Ile Lys
      995              1000              1005
Ser Tyr Phe Ser Asp Cys Gln Val Ser Thr Phe Arg Ser Val Pro Asn
1010              1015              1020
Arg His His Thr Gly Val Asp Ser Leu Cys Asn Phe Ser Pro Leu Ala
1025              1030              1035              1040
Arg Arg Val Asp Arg Val Ala Ile Tyr Glu Glu Phe Leu Arg Met Thr
      1045              1050              1055
Arg Asn Gly Thr Gln Leu Gln Asn Phe Thr Leu Asp Arg Ser Ser Val
      1060              1065              1070
Leu Val Asp Gly Tyr Ser Pro Asn Arg Asn Glu Pro Leu Thr Gly Asn
      1075              1080              1085
Ser Asp Leu Pro Phe Trp Ala Val Ile Phe Ile Gly Leu Ala Gly Leu
      1090              1095              1100
Leu Gly Leu Ile Thr Cys Leu Ile Cys Gly Val Leu Val Thr Thr Arg
1105              1110              1115              1120
Arg Arg Lys Lys Glu Gly Glu Tyr Asn Val Gln Gln Gln Cys Pro Gly
      1125              1130              1135
Tyr Tyr Gln Ser His Leu Asp Leu Glu Asp Leu Gln
      1140              1145

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<210> 459

<211> 1156

<212> PRT

<213> Homo sapiens

<400> 459

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Glu Arg Val Leu Gln Gly Leu Leu Met Pro Leu Phe Lys Asn Thr Ser
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Val Ser Ser Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu

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945          950          955          960
Tyr Gln Pro Thr Ser Ser Ser Ser Thr Gln His Phe Tyr Pro Asn Phe
          965          970          975
Thr Ile Thr Asn Leu Pro Tyr Ser Gln Asp Lys Ala Gln Pro Gly Thr
          980          985          990
Thr Asn Tyr Gln Arg Asn Lys Arg Asn Ile Glu Asp Ala Leu Asn Gln
          995          1000          1005
Leu Phe Arg Asn Ser Ser Ile Lys Ser Tyr Phe Ser Asp Cys Gln Val
1010          1015          1020
Ser Thr Phe Arg Ser Val Pro Asn Arg His His Thr Gly Val Asp Ser
1025          1030          1035          1040
Leu Cys Asn Phe Ser Pro Leu Ala Arg Arg Val Asp Arg Val Ala Ile
          1045          1050          1055
Tyr Glu Glu Phe Leu Arg Met Thr Arg Asn Gly Thr Gln Leu Gln Asn
          1060          1065          1070
Phe Thr Leu Asp Arg Ser Ser Val Leu Val Asp Gly Tyr Ser Pro Asn
          1075          1080          1085
Arg Asn Glu Pro Leu Thr Gly Asn Ser Asp Leu Pro Phe Trp Ala Val
          1090          1095          1100
Ile Phe Ile Gly Leu Ala Gly Leu Leu Gly Leu Ile Thr Cys Leu Ile
1105          1110          1115          1120
Cys Gly Val Leu Val Thr Thr Arg Arg Arg Lys Lys Glu Gly Glu Tyr
          1125          1130          1135
Asn Val Gln Gln Gln Cys Pro Gly Tyr Tyr Gln Ser His Leu Asp Leu
          1140          1145          1150
Glu Asp Leu Gln
          1155

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<210> 460
 <211> 79
 <212> PRT
 <213> Homo sapiens

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<400> 460
Met Ser Met Val Ser His Ser Gly Ala Leu Cys Pro Pro Leu Ala Phe
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Leu Gly Pro Pro Gln Trp Thr Trp Glu His Leu Gly Leu Gln Phe Leu
          20          25          30
Asn Leu Val Pro Arg Leu Pro Ala Leu Ser Trp Cys Tyr Ser Leu Ser
          35          40          45
Thr Ser Pro Ser Pro Thr Cys Gly Met Arg Arg Thr Cys Ser Thr Leu
          50          55          60
Ala Pro Gly Ser Ser Thr Pro Arg Arg Gly Ser Phe Arg Ala Trp
65          70          75

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<210> 461
 <211> 313
 <212> PRT
 <213> Homo sapiens

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<400> 461
Met Pro Leu Phe Lys Asn Thr Ser Val Ser Ser Leu Tyr Ser Gly Cys
 1          5          10          15
Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Arg Val
          20          25          30
Asp Ala Val Cys Thr His Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp

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35	40	45			
Arg Glu Arg Leu Tyr Trp Lys	Leu Ser Gln Leu Thr His Gly Ile Thr				
50	55	60			
Glu Leu Gly Pro Tyr Thr Leu	Asp Arg His Ser Leu Tyr Val Asn Gly				
65	70	75		80	
Phe Thr His Gln Ser Met Thr Thr Thr Arg Thr Pro Asp Thr Ser					
85	90		95		
Thr Met His Leu Ala Thr Ser Arg Thr Pro Ala Ser Leu Ser Gly Pro					
100	105		110		
Thr Thr Ala Ser Pro Leu Leu Val Leu Phe Thr Ile Asn Phe Thr Ile					
115	120		125		
Thr Asn Leu Arg Tyr Glu Glu Asn Met His His Pro Gly Ser Arg Lys					
130	135		140		
Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Val Phe					
145	150		155		160
Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu					
165	170		175		
Leu Arg Pro Lys Lys Asp Gly Ala Ala Thr Lys Val Asp Ala Ile Cys					
180	185		190		
Thr Tyr Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu					
195	200		205		
Tyr Trp Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro					
210	215		220		
Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr Gln Arg					
225	230		235		240
Ser Ser Val Pro Thr Thr Ser Ile Pro Gly Thr Pro Thr Val Asp Leu					
245	250		255		
Gly Thr Ser Gly Thr Pro Val Ser Lys Pro Gly Pro Ser Ala Ala Ser					
260	265		270		
Pro Leu Leu Val Leu Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Arg					
275	280		285		
Tyr Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr					
290	295		300		
Glu Arg Val Leu Gln Gly Leu Leu Arg					
305	310				

<210> 462

<211> 2996

<212> DNA

<213> Homo sapiens

<400> 462

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cctacaccct ggacagggac agtctctatg tcaatggttt cacacagcgg agctctgtgc 180
ccaccactag cattcctggg acccccacag tggacctggg aacatctggg actccagttt 240
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gccatctgca cccaccaccc tgaccccaaa agccctaggc tggacagaga gcagctgtat 540
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<210> 463

<211> 3557

<212> DNA

<213> Homo sapiens

<400> 463

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<210> 464

<211> 2712

<212> DNA

<213> Homo sapiens

<400> 464

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<210> 465

<211> 1175

<212> DNA

<213> Homo sapiens

<400> 465

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gctcagtcct ttgttccaga ggagcagcct ggggtgcacgg tacacaggct gcaggggtcat 780
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<210> 466

<211> 1959

<212> DNA

<213> Homo sapiens

<400> 466

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```

<210> 467

<211> 1636

<212> DNA

<213> Homo sapiens

<400> 467

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cccaagccag ccaccacatt cctgcctcct ctgtcagaag ccacaacagc catgggggtac 240
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<210> 468
 <211> 231
 <212> DNA
 <213> Homo sapiens

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<400> 468
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atcaaccaac aagcagctcc agcaccagc acttctacct gaatttcacc atcaccaacc 120
taccatattc ccaggacaaa gccagccag gcaccaccaa ttaccagagg aacaaaagga 180
atattgagga tgcgctcaac caactcttcc gaaacagcag catcgagagt t 231

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<210> 469
 <211> 607
 <212> DNA
 <213> Homo sapiens

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<400> 469
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aggtgcaggt ggtgtccaca ccagtggctg cccatcctt ctcaggccag gtgctgaagg 180
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ccaggttcat tgtaaccgtt aaggtagagg ctgtctttgt ccagagagta ggggccagc 420
cggtgatgc catgggtctg ctggctcagc tcatggaaca cctgcttgat aggagacct 480
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tggaaaca 607

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<210> 470
 <211> 981
 <212> DNA

<213> Homo sapiens

<400> 470

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ggacaattcc caacttttcc c 981
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<210> 471

<211> 959

<212> DNA

<213> Homo sapiens

<400> 471

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cagccagagt acagagggcc aacactgggt ttcttgaaca agggccttag caggccctga 120
aggaccctct ctgtagtgtt gaacttcctg gagccaggcc acatgttctc ctcataccgc 180
aggttagtga tgggtgaagt gaggggtgaat agtatcagga gatggctggc agctgaaggg 240
ccaaatatcg aggtggagt cttagatgct ccagataca ctgtgggggt cccaggagt 300
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<210> 472

<211> 1315

<212> DNA

<213> Homo sapiens

<400> 472

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gtcaatggtt tcacccatcg gacctctgtg cccaccacca gactcctgg gacctccaca 180
gtggaccttg gaacctcagg gactccattc tccctcccaa gccccgcaac tgctggccct 240
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catcgccctg gctccaggaa gttcaacacc actgagaggg tcctgcagac tctgcttggg 360
cctatgttca agaaccagc tgttggcctt ctgtactctg gctgcagact gaccttgctc 420
agggtccaga aggatggagc agccactgga gtggatgcca tctgcaccca ccgtcttgac 480
```



```
ccccaaaagcc ctggagtggga cagggagcag ctatactggg agctgagcca gctgaccaat 540
ggcatcaaag agctggggccc ctacacbcctg gacaggaaca gtctctatgt caatggtttc 600
acccattgga tccctgtgcc caccagcagc actcctggga cctccacagt ggaccttggg 660
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accacggagc ggtcctgca ggtctcgctt ggtcccatgt tcaagaacac tacga 1315
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<210> 473

<211> 689

<212> DNA

<213> Homo sapiens

<400> 473

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tgaaaccatt gacatagaga ctgttccggt ccagggtgta ggggccagc tcagtgatgc 180
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<210> 474

<211> 495

<212> DNA

<213> Homo sapiens

<400> 474

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aggtcaatgc taccctgggt caatgaaccg agtttcatgg tacagggaca attgaagatt 180
ttctatcagc atcctcacat caggaaagaa tgccctgagg gaacacagtc catgatggta 240
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taggggcca gctcttcaat gtcattggtc agtttgctta gctcccagta cagctgctcc 480
ctgttgagtc caggg 495
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<210> 475

<211> 192

<212> DNA

<213> Homo sapiens

<400> 475

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ccggtgcctg gggatagcct cttcatcaat ggctatgcac cccagaattt atcaatccgg 120
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ggcgagtacc agataaattt ccacattgtc aactggaacc tcagtaatcc agaccccaca 180
tcctcagagt ac 192

<210> 476
<211> 500
<212> DNA
<213> Homo sapiens

<400> 476
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atgtttctca ggtctgagca 500

<210> 477
<211> 191
<212> DNA
<213> Homo sapiens

<400> 477
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agaagtaggc cttttggaaa tatataaagt tctccacttt tgaacatgtt gtttctttcc 180
cacctccacg a 191

<210> 478
<211> 914
<212> PRT
<213> Homo sapiens

<400> 478
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Asn Leu Val Pro Arg Leu Pro Ala Leu Ser Trp Cys Tyr Ser Leu Ser
35 40 45
Thr Ser Pro Ser Pro Thr Cys Gly Met Arg Arg Thr Cys Ser Thr Leu
50 55 60
Ala Pro Gly Ser Ser Thr Pro Arg Arg Gly Ser Phe Arg Ala Trp Ser
65 70 75 80
Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu
85 90 95
Thr Leu Leu Arg Pro Glu Lys Asp Gly Thr Ala Thr Gly Val Asp Ala
100 105 110
Ile Cys Thr His His Pro Asp Pro Lys Ser Pro Arg Leu Asp Arg Glu
115 120 125
Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Asn Ile Thr Glu Leu
130 135 140
Gly Pro Tyr Ala Leu Asp Asn Asp Ser Leu Phe Val Asn Gly Phe Thr
145 150 155 160
His Arg Ser Ser Val Ser Thr Thr Ser Thr Pro Gly Thr Pro Thr Val
165 170 175

Tyr Leu Gly Ala Ser Lys Thr Pro Ala Ser Ile Phe Gly Pro Ser Ala
 180 185 190
 Ala Ser His Leu Leu Ile Leu Phe Thr Leu Asn Phe Thr Ile Thr Asn
 195 200 205
 Leu Arg Tyr Glu Glu Asn Met Trp Pro Gly Ser Arg Lys Phe Asn Thr
 210 215 220
 Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Leu Phe Lys Asn Thr
 225 230 235 240
 Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro
 245 250 255
 Glu Lys Asp Gly Glu Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg
 260 265 270
 Pro Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Gln Leu Tyr Leu Glu
 275 280 285
 Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu
 290 295 300
 Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val
 305 310 315 320
 Pro Thr Thr Ser Thr Gly Val Val Ser Glu Glu Pro Phe Thr Leu Asn
 325 330 335
 Phe Thr Ile Asn Asn Leu Arg Tyr Met Ala Asp Met Gly Gln Pro Gly
 340 345 350
 Ser Leu Lys Phe Asn Ile Thr Asp Asn Val Met Lys His Leu Leu Ser
 355 360 365
 Pro Leu Phe Gln Arg Ser Ser Leu Gly Ala Arg Tyr Thr Gly Cys Arg
 370 375 380
 Val Ile Ala Leu Arg Ser Val Lys Asn Gly Ala Glu Thr Arg Val Asp
 385 390 395 400
 Leu Leu Cys Thr Tyr Leu Gln Pro Leu Ser Gly Pro Gly Leu Pro Ile
 405 410 415
 Lys Gln Val Phe His Glu Leu Ser Gln Gln Thr His Gly Ile Thr Arg
 420 425 430
 Leu Gly Pro Tyr Ser Leu Asp Lys Asp Ser Leu Tyr Leu Asn Gly Tyr
 435 440 445
 Asn Glu Pro Gly Pro Asp Glu Pro Pro Thr Thr Pro Lys Pro Ala Thr
 450 455 460
 Thr Phe Leu Pro Pro Leu Ser Glu Ala Thr Thr Ala Met Gly Tyr His
 465 470 475 480
 Leu Lys Thr Leu Thr Leu Asn Phe Thr Ile Ser Asn Leu Gln Tyr Ser
 485 490 495
 Pro Asp Met Gly Lys Gly Ser Ala Thr Phe Asn Ser Thr Glu Gly Val
 500 505 510
 Leu Gln His Leu Leu Arg Pro Leu Phe Gln Lys Ser Ser Met Gly Pro
 515 520 525
 Phe Tyr Leu Gly Cys Gln Leu Ile Ser Leu Arg Pro Glu Lys Asp Gly
 530 535 540
 Ala Ala Thr Gly Val Asp Thr Thr Cys Thr Tyr His Pro Asp Pro Val
 545 550 555 560
 Gly Pro Gly Leu Asp Ile Gln Gln Leu Tyr Trp Glu Leu Ser Gln Leu
 565 570 575
 Thr His Gly Val Thr Gln Leu Gly Phe Tyr Val Leu Asp Arg Asp Ser
 580 585 590
 Leu Phe Ile Asn Gly Tyr Ala Pro Gln Asn Leu Ser Ile Arg Gly Glu
 595 600 605
 Tyr Gln Ile Asn Phe His Ile Val Asn Trp Asn Leu Ser Asn Pro Asp
 610 615 620
 Pro Thr Ser Ser Glu Tyr Ile Thr Leu Leu Arg Asp Ile Gln Asp Lys
 625 630 635 640

Val Thr Thr Leu Tyr Lys Gly Ser Gln Leu His Asp Thr Phe Arg Phe
 645 650 655
 Cys Leu Val Thr Asn Leu Thr Met Asp Ser Val Leu Val Thr Val Lys
 660 665 670
 Ala Leu Phe Ser Ser Asn Leu Asp Pro Ser Leu Val Glu Gln Val Phe
 675 680 685
 Leu Asp Lys Thr Leu Asn Ala Ser Phe His Trp Leu Gly Ser Thr Tyr
 690 695 700
 Gln Leu Val Asp Ile His Val Thr Glu Met Glu Ser Ser Val Tyr Gln
 705 710 715 720
 Pro Thr Ser Ser Ser Ser Thr Gln His Phe Tyr Leu Asn Phe Thr Ile
 725 730 735
 Thr Asn Leu Pro Tyr Ser Gln Asp Lys Ala Gln Pro Gly Thr Thr Asn
 740 745 750
 Tyr Gln Arg Asn Lys Arg Asn Ile Glu Asp Ala Leu Asn Gln Leu Phe
 755 760 765
 Arg Asn Ser Ser Ile Lys Ser Tyr Phe Ser Asp Cys Gln Val Ser Thr
 770 775 780
 Phe Arg Ser Val Pro Asn Arg His His Thr Gly Val Asp Ser Leu Cys
 785 790 795 800
 Asn Phe Ser Pro Leu Ala Arg Arg Val Asp Arg Val Ala Ile Tyr Glu
 805 810 815
 Glu Phe Leu Arg Met Thr Arg Asn Gly Thr Gln Leu Gln Asn Phe Thr
 820 825 830
 Leu Asp Arg Ser Ser Val Leu Val Asp Gly Tyr Phe Pro Asn Arg Asn
 835 840 845
 Glu Pro Leu Thr Gly Asn Ser Asp Leu Pro Phe Trp Ala Val Ile Leu
 850 855 860
 Ile Gly Leu Ala Gly Leu Leu Gly Leu Ile Thr Cys Leu Ile Cys Gly
 865 870 875 880
 Val Leu Val Thr Thr Arg Arg Arg Lys Lys Glu Gly Glu Tyr Asn Val
 885 890 895
 Gln Gln Gln Cys Pro Gly Tyr Tyr Gln Ser His Leu Asp Leu Glu Asp
 900 905 910
 Leu Gln

<210> 479

<211> 1148

<212> PRT

<213> Homo sapiens

<400> 479

Met Pro Leu Phe Lys Asn Thr Ser Val Ser Ser Leu Tyr Ser Gly Cys
 1 5 10 15
 Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Arg Val
 20 25 30
 Asp Ala Val Cys Thr His Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp
 35 40 45
 Arg Glu Arg Leu Tyr Trp Lys Leu Ser Gln Leu Thr His Gly Ile Thr
 50 55 60
 Glu Leu Gly Pro Tyr Thr Leu Asp Arg His Ser Leu Tyr Val Asn Gly
 65 70 75 80
 Phe Thr His Gln Ser Ser Met Thr Thr Thr Arg Thr Pro Asp Thr Ser
 85 90 95
 Thr Met His Leu Ala Thr Ser Arg Thr Pro Ala Ser Leu Ser Gly Pro
 100 105 110

Thr	Thr	Ala	Ser	Pro	Leu	Leu	Val	Leu	Phe	Thr	Ile	Asn	Phe	Thr	Ile
		115					120					125			
Thr	Asn	Leu	Arg	Tyr	Glu	Glu	Asn	Met	His	His	Pro	Gly	Ser	Arg	Lys
	130					135					140				
Phe	Asn	Thr	Thr	Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu	Arg	Pro	Val	Phe
145					150					155					160
Lys	Asn	Thr	Ser	Val	Gly	Pro	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Thr	Leu
			165						170					175	
Leu	Arg	Pro	Lys	Lys	Asp	Gly	Ala	Ala	Thr	Lys	Val	Asp	Ala	Ile	Cys
			180					185					190		
Thr	Tyr	Arg	Pro	Asp	Pro	Lys	Ser	Pro	Gly	Leu	Asp	Arg	Glu	Gln	Leu
	195						200					205			
Tyr	Trp	Glu	Leu	Ser	Gln	Leu	Thr	His	Ser	Ile	Thr	Glu	Leu	Gly	Pro
	210					215					220				
Tyr	Thr	Leu	Asp	Arg	Asp	Ser	Leu	Tyr	Val	Asn	Gly	Phe	Thr	Gln	Arg
225					230					235					240
Ser	Ser	Val	Pro	Thr	Thr	Ser	Ile	Pro	Gly	Thr	Pro	Thr	Val	Asp	Leu
				245						250				255	
Gly	Thr	Ser	Gly	Thr	Pro	Val	Ser	Lys	Pro	Gly	Pro	Ser	Ala	Ala	Ser
		260						265					270		
Pro	Leu	Leu	Val	Leu	Phe	Thr	Leu	Asn	Phe	Thr	Ile	Thr	Asn	Leu	Arg
	275						280					285			
Tyr	Glu	Asn	Met	Gln	His	Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr	Thr	
290					295					300					
Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu	Arg	Ser	Leu	Phe	Lys	Ser	Thr	Ser
305					310					315					320
Val	Gly	Pro	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Thr	Leu	Leu	Arg	Pro	Glu
			325						330					335	
Lys	Asp	Gly	Thr	Ala	Thr	Gly	Val	Asp	Ala	Ile	Cys	Thr	His	His	Pro
		340						345					350		
Asp	Pro	Lys	Ser	Pro	Arg	Leu	Asp	Arg	Glu	Gln	Leu	Tyr	Trp	Glu	Leu
	355						360					365			
Ser	Gln	Leu	Thr	His	Asn	Ile	Thr	Glu	Leu	Gly	His	Tyr	Ala	Leu	Asp
	370				375						380				
Asn	Asp	Ser	Leu	Phe	Val	Asn	Gly	Phe	Thr	His	Arg	Ser	Ser	Val	Ser
385					390					395					400
Thr	Thr	Ser	Thr	Pro	Gly	Thr	Pro	Thr	Val	Tyr	Leu	Gly	Ala	Ser	Lys
			405						410					415	
Thr	Pro	Ala	Ser	Ile	Phe	Gly	Pro	Ser	Ala	Ala	Ser	His	Leu	Leu	Ile
		420					425						430		
Leu	Phe	Thr	Leu	Asn	Phe	Thr	Ile	Thr	Asn	Leu	Arg	Tyr	Glu	Glu	Asn
	435						440					445			
Met	Trp	Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr	Thr	Glu	Arg	Val	Leu	Gln
	450					455					460				
Gly	Leu	Leu	Arg	Pro	Leu	Phe	Lys	Asn	Thr	Ser	Val	Gly	Pro	Leu	Tyr
465					470					475				480	
Ser	Gly	Ser	Arg	Leu	Thr	Leu	Leu	Arg	Pro	Glu	Lys	Asp	Gly	Glu	Ala
			485						490					495	
Thr	Gly	Val	Asp	Ala	Ile	Cys	Thr	His	Arg	Pro	Asp	Pro	Thr	Gly	Pro
		500						505					510		
Gly	Leu	Asp	Arg	Glu	Gln	Leu	Tyr	Leu	Glu	Leu	Ser	Gln	Leu	Thr	His
	515						520					525			
Ser	Ile	Thr	Glu	Leu	Gly	Pro	Tyr	Thr	Leu	Asp	Arg	Asp	Ser	Leu	Tyr
	530				535						540				
Val	Asn	Gly	Phe	Thr	His	Arg	Ser	Ser	Val	Pro	Thr	Thr	Ser	Thr	Gly
545					550					555					560
Val	Val	Ser	Glu	Glu	Pro	Phe	Thr	Leu	Asn	Phe	Thr	Ile	Asn	Asn	Leu
				565					570					575	

Arg Tyr Met Ala Asp Met Gly Gln Pro Gly Ser Leu Lys Phe Asn Ile
 580 585 590
 Thr Asp Asn Val Met Lys His Leu Leu Ser Pro Leu Phe Gln Arg Ser
 595 600 605
 Ser Leu Gly Ala Arg Tyr Thr Gly Cys Arg Val Ile Ala Leu Arg Ser
 610 615 620
 Val Lys Asn Gly Ala Glu Thr Arg Val Asp Leu Leu Cys Thr Tyr Leu
 625 630 635 640
 Gln Pro Leu Ser Gly Pro Gly Leu Pro Ile Lys Gln Val Phe His Glu
 645 650 655
 Leu Ser Gln Gln Thr His Gly Ile Thr Arg Leu Gly Pro Tyr Ser Leu
 660 665 670
 Asp Lys Asp Ser Leu Tyr Leu Asn Gly Tyr Asn Glu Pro Gly Leu Asp
 675 680 685
 Glu Pro Pro Thr Thr Pro Lys Pro Ala Thr Thr Phe Leu Pro Pro Leu
 690 695 700
 Ser Glu Ala Thr Thr Ala Met Gly Tyr His Leu Lys Thr Leu Thr Leu
 705 710 715 720
 Asn Phe Thr Ile Ser Asn Leu Gln Tyr Ser Pro Asp Met Gly Lys Gly
 725 730 735
 Ser Ala Thr Phe Asn Ser Thr Glu Gly Val Leu Gln His Leu Leu Arg
 740 745 750
 Pro Leu Phe Gln Lys Ser Ser Met Gly Pro Phe Tyr Leu Gly Cys Gln
 755 760 765
 Leu Ile Ser Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Gly Val Asp
 770 775 780
 Thr Thr Cys Thr Tyr His Pro Asp Pro Val Gly Pro Gly Leu Asp Ile
 785 790 795 800
 Gln Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Gly Val Thr Gln
 805 810 815
 Leu Gly Phe Tyr Val Leu Asp Arg Asp Ser Leu Phe Ile Asn Gly Tyr
 820 825 830
 Ala Pro Gln Asn Leu Ser Ile Arg Gly Glu Tyr Gln Ile Asn Phe His
 835 840 845
 Ile Val Asn Trp Asn Leu Ser Asn Pro Asp Pro Thr Ser Ser Glu Tyr
 850 855 860
 Ile Thr Leu Leu Arg Asp Ile Gln Asp Lys Val Thr Thr Leu Tyr Lys
 865 870 875 880
 Gly Ser Gln Leu His Asp Thr Phe Arg Phe Cys Leu Val Thr Asn Leu
 885 890 895
 Thr Met Asp Ser Val Leu Val Thr Val Lys Ala Leu Phe Ser Ser Asn
 900 905 910
 Leu Asp Pro Ser Leu Val Glu Gln Val Phe Leu Asp Lys Thr Leu Asn
 915 920 925
 Ala Ser Phe His Trp Leu Gly Ser Thr Tyr Gln Leu Val Asp Ile His
 930 935 940
 Val Thr Glu Met Glu Ser Ser Val Tyr Gln Pro Thr Ser Ser Ser Ser
 945 950 955 960
 Thr Gln His Phe Tyr Pro Asn Phe Thr Ile Thr Asn Leu Pro Tyr Ser
 965 970 975
 Gln Asp Lys Ala Gln Pro Gly Thr Thr Asn Tyr Gln Arg Asn Lys Arg
 980 985 990
 Asn Ile Glu Asp Ala Leu Asn Gln Leu Phe Arg Asn Ser Ser Ile Lys
 995 1000 1005
 Ser Tyr Phe Ser Asp Cys Gln Val Ser Thr Phe Arg Ser Val Pro Asn
 1010 1015 1020
 Arg His His Thr Gly Val Asp Ser Leu Cys Asn Phe Ser Pro Leu Ala
 1025 1030 1035 1040

Arg Arg Val Asp Arg Val Ala Ile Tyr Glu Glu Phe Leu Arg Met Thr
 1045 1050 1055
 Arg Asn Gly Thr Gln Leu Gln Asn Phe Thr Leu Asp Arg Ser Ser Val
 1060 1065 1070
 Leu Val Asp Gly Tyr Ser Pro Asn Arg Asn Glu Pro Leu Thr Gly Asn
 1075 1080 1085
 Ser Asp Leu Pro Phe Trp Ala Val Ile Phe Ile Gly Leu Ala Gly Leu
 1090 1095 1100
 Leu Gly Leu Ile Thr Cys Leu Ile Cys Gly Val Leu Val Thr Thr Arg
 1105 1110 1115 1120
 Arg Arg Lys Lys Glu Gly Glu Tyr Asn Val Gln Gln Gln Cys Pro Gly
 1125 1130 1135
 Tyr Tyr Gln Ser His Leu Asp Leu Glu Asp Leu Gln
 1140 1145

<210> 480
 <211> 230
 <212> PRT
 <213> Homo sapiens

<400> 480
 Met His Arg Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
 1 5 10 15
 Gln Thr Leu Leu Gly Pro Met Phe Lys Asn Thr Ser Val Gly Leu Leu
 20 25 30
 Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Ser Glu Lys Asp Gly Ala
 35 40 45
 Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser
 50 55 60
 Pro Gly Val Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr
 65 70 75 80
 Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu
 85 90 95
 Tyr Val Asn Gly Phe Thr His Trp Ile Pro Val Pro Thr Ser Ser Thr
 100 105 110
 Pro Gly Thr Ser Thr Val Asp Leu Gly Ser Gly Thr Pro Ser Ser Leu
 115 120 125
 Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn
 130 135 140
 Phe Thr Ile Thr Asn Leu Lys Tyr Glu Glu Asp Met His Cys Pro Gly
 145 150 155 160
 Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Ser Leu Leu Gly
 165 170 175
 Pro Met Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg
 180 185 190
 Leu Thr Leu Leu Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp
 195 200 205
 Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser Leu Glu Trp Thr Gly
 210 215 220
 Ser Ser Tyr Thr Gly Ser
 225 230

<210> 481
 <211> 210
 <212> PRT
 <213> Homo sapiens

<400> 481

```

Met Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
 1          5          10          15
Gln Gly Leu Leu Arg Ser Leu Phe Lys Ser Thr Ser Val Gly Pro Leu
          20          25          30
Tyr Ser Gly Cys Arg Leu Thr Leu Arg Pro Glu Lys Asp Gly Thr
 35          40          45
Ala Thr Gly Val Asp Ala Ile Cys Thr His His Pro Asp Pro Lys Ser
 50          55          60
Pro Arg Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr
 65          70          75          80
His Asn Ile Thr Glu Leu Gly Pro Tyr Ala Leu Asp Asn Asp Ser Leu
          85          90          95
Phe Val Asn Gly Phe Thr His Arg Ser Ser Val Ser Thr Thr Ser Thr
          100          105          110
Pro Gly Thr Pro Thr Val Tyr Leu Gly Ala Ser Lys Thr Pro Ala Ser
 115          120          125
Ile Phe Gly Pro Ser Ala Ala Ser His Leu Leu Ile Leu Phe Thr Leu
 130          135          140
Asn Phe Thr Ile Thr Asn Leu Arg Tyr Glu Glu Asn Met Trp Pro Gly
 145          150          155          160
Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg
          165          170          175
Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg
          180          185          190
Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Glu Ala Thr Gly Val Asp
          195          200          205
Ala Ile
 210

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<210> 482

<211> 97

<212> PRT

<213> Homo sapiens

<400> 482

```

Met Ser Met Val Ser His Ser Gly Ala Leu Cys Pro Pro Leu Ala Phe
 1          5          10          15
Leu Gly Pro Pro Gln Trp Thr Trp Glu His Leu Gly Leu Gln Phe Leu
          20          25          30
Asn Leu Val Pro Arg Leu Pro Ala Leu Ser Trp Cys Tyr Ser Leu Ser
 35          40          45
Thr Ser Pro Ser Pro Thr Cys Gly Met Arg Arg Thr Cys Ser Thr Leu
 50          55          60
Ala Pro Gly Ser Ser Thr Pro Arg Arg Gly Ser Phe Arg Ala Cys Ser
 65          70          75          80
Gly Pro Cys Ser Arg Ala Pro Val Leu Ala Leu Cys Thr Leu Ala Ala
          85          90          95
Asp

```

<210> 483

<211> 438

<212> PRT

<213> Homo sapiens

<400> 483

```

Met Gly Tyr His Leu Lys Thr Leu Thr Leu Asn Phe Thr Ile Ser Asn
 1           5           10           15
Leu Gln Tyr Ser Pro Asp Met Gly Lys Gly Ser Ala Thr Phe Asn Ser
      20           25           30
Thr Glu Gly Val Leu Gln His Leu Leu Arg Pro Leu Phe Gln Lys Ser
      35           40           45
Ser Met Gly Pro Phe Tyr Leu Gly Cys Gln Leu Ile Ser Leu Arg Pro
      50           55           60
Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Thr Thr Cys Thr Tyr His
      65           70           75           80
Pro Asp Pro Val Gly Pro Gly Leu Asp Ile Gln Gln Leu Tyr Trp Glu
      85           90           95
Leu Ser Gln Leu Thr His Gly Val Thr Gln Leu Gly Phe Tyr Val Leu
      100          105          110
Asp Arg Asp Ser Leu Phe Ile Asn Gly Tyr Ala Pro Gln Asn Leu Ser
      115          120          125
Ile Arg Gly Glu Tyr Gln Ile Asn Phe His Ile Val Asn Trp Asn Leu
      130          135          140
Ser Asn Pro Asp Pro Thr Ser Ser Glu Tyr Ile Thr Leu Leu Arg Asp
      145          150          155          160
Ile Gln Asp Lys Val Thr Thr Leu Tyr Lys Gly Ser Gln Leu His Asp
      165          170          175
Thr Phe Arg Phe Cys Leu Val Thr Asn Leu Thr Met Asp Ser Val Leu
      180          185          190
Val Thr Val Lys Ala Leu Phe Ser Ser Asn Leu Asp Pro Ser Leu Val
      195          200          205
Glu Gln Val Phe Leu Asp Lys Thr Leu Asn Ala Ser Phe His Trp Leu
      210          215          220
Gly Ser Thr Tyr Gln Leu Val Asp Ile His Val Thr Glu Met Glu Ser
      225          230          235          240
Ser Val Tyr Gln Pro Thr Ser Ser Ser Ser Thr Gln His Phe Tyr Leu
      245          250          255
Asn Phe Thr Ile Thr Asn Leu Pro Tyr Ser Gln Asp Lys Ala Gln Pro
      260          265          270
Gly Thr Thr Asn Tyr Gln Arg Asn Lys Arg Asn Ile Glu Asp Ala Leu
      275          280          285
Asn Gln Leu Phe Arg Asn Ser Ser Ile Lys Ser Tyr Phe Ser Asp Cys
      290          295          300
Gln Val Ser Thr Phe Arg Ser Val Pro Asn Arg His His Thr Gly Val
      305          310          315          320
Asp Ser Leu Cys Asn Phe Ser Pro Leu Ala Arg Arg Val Asp Arg Val
      325          330          335
Ala Ile Tyr Glu Glu Phe Leu Arg Met Thr Arg Asn Gly Thr Gln Leu
      340          345          350
Gln Asn Phe Thr Leu Asp Arg Ser Ser Val Leu Val Asp Gly Tyr Ser
      355          360          365
Pro Asn Arg Asn Glu Pro Leu Thr Gly Asn Ser Asp Leu Pro Phe Trp
      370          375          380
Ala Val Ile Leu Ile Gly Leu Ala Gly Leu Leu Gly Leu Ile Thr Cys
      385          390          395          400
Leu Ile Cys Gly Val Leu Val Thr Thr Arg Arg Arg Lys Lys Glu Gly
      405          410          415
Glu Tyr Asn Val Gln Gln Gln Cys Pro Gly Tyr Tyr Gln Ser His Leu
      420          425          430
Asp Leu Glu Asp Leu Gln
      435

```

<210> 484
 <211> 216
 <212> PRT
 <213> Homo sapiens

<400> 484
 Met Thr Leu Lys Ser Trp Ala Pro Thr Pro Trp Thr Gly Thr Val Ser
 1 5 10 15
 Met Ser Met Val Ser Pro Ile Arg Ala Leu Cys Pro Pro Pro Ala Leu
 20 25 30
 Leu Gly Pro Pro Gln Trp Ile Ser Glu Pro Gln Trp Thr Pro Ser Ser
 35 40 45
 Leu Ser Ser Pro Thr Ile Met Ala Ala Gly Pro Leu Leu Val Pro Phe
 50 55 60
 Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Gly Glu Asp Met Gly
 65 70 75 80
 His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly
 85 90 95
 Leu Leu Gly Pro Ile Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser
 100 105 110
 Gly Cys Arg Leu Thr Ser Leu Arg Ser Lys Lys Asp Gly Ala Ala Thr
 115 120 125
 Gly Val Asp Ala Ile Cys Ile His His Leu Asp Pro Lys Ser Pro Gly
 130 135 140
 Leu Asn Arg Glu Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Gly
 145 150 155 160
 Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val
 165 170 175
 Asn Gly Phe Thr His Arg Thr Ser Val Pro Thr Thr Ser Thr Pro Gly
 180 185 190
 Thr Ser Thr Val Tyr Trp Ala Thr Thr Gly Thr Pro Ser Ser Leu Pro
 195 200 205
 Ala Thr Gln Ser Leu Ala Leu Ser
 210 215

<210> 485
 <211> 268
 <212> PRT
 <213> Homo sapiens

<400> 485
 Met Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Val Gly Thr
 1 5 10 15
 Ser Gly Thr Pro Ser Ser Ser Pro Ser Pro Thr Thr Ala Gly Pro Leu
 20 25 30
 Leu Met Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu
 35 40 45
 Glu Asp Met Arg Arg Thr Gly Ser Arg Lys Phe Asn Thr Met Glu Ser
 50 55 60
 Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr Ser Val Gly
 65 70 75 80
 Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Lys Lys Asp
 85 90 95
 Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu Asp Pro
 100 105 110

```
<210> 486
<211> 304
<212> PRT
<213> Homo sapiens
```

<400> 486

Met 1	Gln	His	Pro	Gly 5	Ser	Arg	Lys	Phe	Asn 10	Thr	Thr	Glu	Arg	Val 15	Leu
Gln	Gly	Leu	Leu	Arg 20	Pro	Leu	Phe	Lys 25	Asn	Thr	Ser	Val	Gly 30	Pro	Leu
Tyr	Ser	Gly	Cys	Arg 35	Leu	Thr	Leu	Leu 40	Arg	Pro	Glu	Lys 45	Asp	Gly	Glu
Ala	Thr	Gly	Val	Asp 50	Ala	Ile	Cys	Thr 55	His	Arg	Pro	Asp 60	Pro	Thr	Gly
Pro 65	Gly	Leu	Asp	Arg 70	Glu	Gln	Leu	Tyr 75	Leu	Glu	Leu	Ser 80	Gln	Leu	Thr
His	Ser	Ile	Thr	Glu 85	Leu	Gly	Pro	Tyr 90	Thr	Leu	Asp	Arg 95	Asp	Ser	Leu
Tyr	Val	Asn	Gly	Phe 100	Thr	His	Arg	Ser 105	Ser	Val	Pro	Thr 110	Thr	Ser	Thr
Gly	Val	Val	Ser	Glu 115	Glu	Pro	Phe 120	Thr	Leu	Asn	Phe	Thr 125	Ile	Asn	Asn
Leu	Arg	Tyr	Met	Ala 130	Asp	Met	Gly 135	Gln	Pro	Gly	Ser 140	Leu	Lys	Phe	Asn
Ile 145	Thr	Asp	Asn	Val 150	Met	Lys	His	Leu	Leu	Ser 155	Pro	Leu 160	Phe	Gln	Arg
Ser	Ser	Leu	Gly	Ala 165	Arg	Tyr	Thr	Gly	Cys 170	Arg	Val	Ile 175	Ala	Leu	Arg
Ser	Val	Lys	Asn	Gly 180	Ala	Glu	Thr	Arg 185	Val	Asp	Leu	Leu 190	Cys	Thr	Tyr
Leu	Gln	Pro	Leu	Ser 195	Gly	Pro	Gly 200	Leu	Pro	Ile	Lys	Gln 205	Val	Phe	His
Glu	Leu	Ser	Gln	Gln 210	Thr	His	Gly 215	Ile	Thr	Arg	Leu 220	Gly	Pro	Tyr	Ser
Leu 225	Asp	Lys	Asp	Ser 230	Leu	Tyr	Leu	Asn	Gly	Tyr 235	Asn	Glu	Pro	Gly	Pro

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<210> 487
<211> 294
<212> PRT
<213> Homo sapiens
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[illegible]

$\langle 210 \rangle$	488
$\langle 211 \rangle$	233

<212> PRT

<213> Homo sapiens

<400> 488

```

Ser Leu Val Glu Gln Val Phe Leu Asp Lys Thr Leu Asn Ala Ser Phe
 1           5           10          15
His Trp Leu Gly Ser Thr Tyr Gln Leu Val Asp Ile His Val Thr Glu
 20          25          30
Met Glu Ser Ser Val Tyr Gln Pro Thr Ser Ser Ser Ser Thr Gln His
 35          40          45
Phe Tyr Leu Asn Phe Thr Ile Thr Asn Leu Pro Tyr Ser Gln Asp Lys
 50          55          60
Ala Gln Pro Gly Thr Thr Asn Tyr Gln Arg Asn Lys Arg Asn Ile Glu
 65          70          75          80
Asp Ala Leu Asn Gln Leu Phe Arg Asn Ser Ser Ile Lys Ser Tyr Phe
 85          90          95
Ser Asp Cys Gln Val Ser Thr Phe Arg Ser Val Pro Asn Arg His His
100         105         110
Thr Gly Val Asp Ser Leu Cys Asn Phe Ser Pro Leu Ala Arg Arg Val
115         120         125
Asp Arg Val Ala Ile Tyr Glu Glu Phe Leu Arg Met Thr Arg Asn Gly
130         135         140
Thr Gln Leu Gln Asn Phe Thr Leu Asp Arg Ser Ser Val Leu Val Asp
145         150         155         160
Gly Tyr Phe Pro Asn Arg Asn Glu Pro Leu Thr Gly Asn Ser Asp Leu
165         170         175
Pro Phe Trp Ala Val Ile Leu Ile Gly Leu Ala Gly Leu Leu Gly Leu
180         185         190
Ile Thr Cys Leu Ile Cys Gly Val Leu Val Thr Thr Arg Arg Arg Lys
195         200         205
Lys Glu Gly Glu Tyr Asn Val Gln Gln Gln Cys Pro Gly Tyr Tyr Gln
210         215         220
Ser His Leu Asp Leu Glu Asp Leu Gln
225         230

```

<210> 489

<211> 178

<212> PRT

<213> Homo sapiens

<400> 489

```

Ser Leu Val Glu Gln Val Phe Leu Asp Lys Thr Leu Asn Ala Ser Phe
 1           5           10          15
His Trp Leu Gly Ser Thr Tyr Gln Leu Val Asp Ile His Val Thr Glu
 20          25          30
Met Glu Ser Ser Val Tyr Gln Pro Thr Ser Ser Ser Ser Thr Gln His
 35          40          45
Phe Tyr Leu Asn Phe Thr Ile Thr Asn Leu Pro Tyr Ser Gln Asp Lys
 50          55          60
Ala Gln Pro Gly Thr Thr Asn Tyr Gln Arg Asn Lys Arg Asn Ile Glu
 65          70          75          80
Asp Ala Leu Asn Gln Leu Phe Arg Asn Ser Ser Ile Lys Ser Tyr Phe
 85          90          95
Ser Asp Cys Gln Val Ser Thr Phe Arg Ser Val Pro Asn Arg His His
100         105         110
Thr Gly Val Asp Ser Leu Cys Asn Phe Ser Pro Leu Ala Arg Arg Val
115         120         125

```

```
<210> 490
<211> 15
<212> PRT
<213> Homo sapiens
```

<400> 490
Thr Cys Gly Met Arg Arg Thr Cys Ser Thr Leu Ala Pro Gly Ser
1 5 10 15

```
<210> 491
<211> 15
<212> PRT
<213> Homo sapiens
```

<400> 491
Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Thr Ala Thr
1 5 10 15

```
<210> 492
<211> 15
<212> PRT
<213> Homo sapiens
```

<400> 492
Asp Gly Thr Ala Thr Gly Val Asp Ala Ile Cys Thr His His Pro
1 5 10 15

```
<210> 493
<211> 15
<212> PRT
<213> Homo sapiens
```

<400> 493
Cys Thr His His Pro Asp Pro Lys Ser Pro Arg Leu Asp Arg Glu
1 5 10 15

```
<210> 494
<211> 15
<212> PRT
<213> Homo sapiens
```

<400> 494
Arg Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr
1 5 10 15

<210> 495
<211> 15
<212> PRT
<213> Homo sapiens

<400> 495
Leu Gly Pro Tyr Ala Leu Asp Asn Asp Ser Leu Phe Val Asn Gly
1 5 10 15

<210> 496
<211> 15
<212> PRT
<213> Homo sapiens

<400> 496
Ser Val Ser Thr Thr Ser Thr Pro Gly Thr Pro Thr Tyr Val Leu
1 5 10 15

<210> 497
<211> 15
<212> PRT
<213> Homo sapiens

<400> 497
Leu Arg Pro Glu Lys Asp Gly Glu Ala Thr Gly Val Asp Ala Ile
1 5 10 15

<210> 498
<211> 15
<212> PRT
<213> Homo sapiens

<400> 498
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<213> Homo sapiens

<400> 501

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<213> Homo sapiens

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<213> Homo sapiens

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<213> Homo sapiens

<400> 504

Gly Ala Ala Thr Gly Val Asp Thr Thr Cys Thr Tyr His Pro Asp
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<210> 505

<211> 15

<212> PRT

<213> Homo sapiens

<400> 505

Thr Tyr His Pro Asp Pro Val Gly Pro Gly Leu Asp Ile Gln Gln
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<211> 15

<212> PRT

<213> Homo sapiens

<400> 506

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<400> 507

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<212> PRT

<213> Homo sapiens

<400> 508

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<210> 509

<211> 15

<212> PRT

<213> Homo sapiens

<400> 509

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<210> 510

<211> 15

<212> PRT

<213> Homo sapiens

<400> 510

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<210> 511

<211> 15

<212> PRT

<213> Homo sapiens

<400> 511

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<212> DNA

<213> Homo sapiens

<400> 512

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<210> 513

<211> 402

<212> DNA

<213> Homo sapiens

<400> 513

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ccctcaagtt caacatcaca gacaacgtca tgaagcacct gctcagtcct ttgttccaga 180
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gtctgcctat caagcaggtg ttccatgagc tgagccagca gacccatggc atcaccgggc 360
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<210> 514

<211> 465

<212> DNA

<213> Homo sapiens

<400> 514

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tactattcac cctcaacttc accatcacta acctgcggta tgaggagaac atgtggcctg 180
gctccaggaa gttcaacact acagagaggg tccttcaggg cctgctaagg cccttggtca 240
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<210> 515

<211> 463

<212> DNA

<213> Homo sapiens

<400> 515

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<211> 156
<212> DNA
<213> Homo sapiens

<400> 516
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cctacaccct ggacagggac agtctctatg tcaatg 156

<210> 517
<211> 450
<212> DNA
<213> Homo sapiens

<400> 517
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<210> 518
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<212> DNA
<213> Homo sapiens

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<210> 519
<211> 465
<212> DNA
<213> Homo sapiens

<400> 519
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agctgggccc ctacacactg gacagggaca gtctctatgt caatg 465

<210> 520
<211> 468
<212> DNA
<213> Homo sapiens

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tgctattcac tctcaacttc accatcacca acctgcggtg tgaggagaac atgcagcacc 180
ctggctccag gaagtccaac accacggaga gggtccttca gggcctgctc aggtccctgt 240
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<210> 521
<211> 468
<212> DNA
<213> Homo sapiens

<400> 521
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<210> 522
<211> 262
<212> DNA
<213> Homo sapiens

<400> 522
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gatgtgtct gcacccatcg tcttgacccc aaaagccctg gactggacag agagcggctg 180
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<210> 523
<211> 302
<212> DNA
<213> Homo sapiens

<400> 523
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tctctctcag gtctgagaag gatggggcag ccactggagt ggatgccatc tgcacccacc 180
accttaaccc tcaaagcctg gactggacag ggagcagctg tactggcagc tgagccagat 240
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tg 302

<210> 524
<211> 468
<212> DNA
<213> Homo sapiens

<400> 524
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agaaggatgg ggcagcaact ggaatggatg ctgtctgcct ctaccaccct aatcccaaaa 360
gacctgggct ggacagagag cagctgtact gggagctaag ccagctgacc cacaacatca 420
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<210> 525

<211> 470

<212> DNA

<213> Homo sapiens

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ggacctgggc tggacagaga gcagctgtac tgggagctga gccagctgac ccacgacatc 420
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<210> 526

<211> 467

<212> DNA

<213> Homo sapiens

<400> 526

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gaagcaggag gcagccactg gagtggacac catctgcaact caccgccttg accctctaaa 360
ccctggactg gacagagagc agctatactg ggagctgagc aaactgacct gtggcatcat 420
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<210> 527

<211> 468

<212> DNA

<213> Homo sapiens

<400> 527

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agaaggacaa ggcagccacc agagtggatg ccactgttac ccaccacct gacctcaaaa 360
gccctggact gaacagagag cagctgtact gggagctgag ccagctgacc caccggcatca 420
ctgagctggg cccctacacc ctggacaggg acagtctcta tgtcaatg 468

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<210> 528

<211> 537

<212> DNA

<213> Homo sapiens

<400> 528

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tgctattcac aattaacttc accatcacta acctgcggta tgaggagaac atgcatcacc 180
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ggcggctcatg ggtccagaca gggagcctgg agttctcgag gttgccaggt gcatgtc 537

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<210> 529

<211> 231

<212> DNA

<213> Homo sapiens

<400> 529

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ctgtgaagaa cgggtgctgag acacgggtgg acctcctctg cacctacctg cagccctca 120
gcggccaggg tctgcctatc aagcagggtg tccatgagct gagccagcag acccatggca 180
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<210> 530

<211> 376

<212> DNA

<213> Homo sapiens

<400> 530

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<210> 531

<211> 75

<212> DNA

<213> Homo sapiens

<400> 531

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<210> 532

<211> 906

<212> DNA

<213> Homo sapiens

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gtgcatcaaa gatgctgacc tcaactggta tcagttctgg gacagacagc actacaactt 540
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<210> 533

<211> 404

<212> DNA

<213> Homo sapiens

<400> 533

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tgccgttcac cctcaacttt accatcacca atctgcagta tggggaggac atgcgtcacc 180
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agaaggatgg ggcagccact ggagtggatg ccactctgcac ccaccacctt aaccctcaa 360
gccctggact ggacagggag cagctgtact ggcagctgag ccag                                     404

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<210> 534

<211> 157

<212> DNA

<213> Homo sapiens

<400> 534

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gacagagagc agctatactg ggagctgagc cagctaacc acagcatcac tgagctgggc 120
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<210> 535

<211> 468

<212> DNA

<213> Homo sapiens

<400> 535

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tgctattcac tctcaacttc accatcacca acctgcggta tgaggagaac atgcagcacc 180
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gccctaggct ggacagagag cagctgtatt gggagctgag ccagctgacc cacaatatca 420
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<210> 536

<211> 334

<212> DNA

<213> Homo sapiens

<400> 536

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tactattcac cctcaacttc accatcacta acctgcggta tgaggagaac atgtggcctg 180
gctccaggaa gttcaacact acagagaggg tccttcaggg cctgctaagg cccttgttca 240

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agaacaccag tgttgccct ctgtactctg gctgcaggct gaccttgctc aggccagaga 300
aagatgggga agccaccgga gtggatgcca tctg 334

<210> 537
<211> 127
<212> DNA
<213> Homo sapiens

<400> 537
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ccagctgacc aatggcatca aagagctggg cccctacacc tggacaggaa cagtctctat 120
gtcaatg 127

<210> 538
<211> 468
<212> DNA
<213> Homo sapiens

<400> 538
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ctggctccag gaagttcaac accactgaga gggctcctgca gactctgctt ggtcctatgt 240
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<210> 539
<211> 465
<212> DNA
<213> Homo sapiens

<400> 539
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aggatggagc agccactgga gtggatgcca tctgcaccca ccgtcttgac cccaaaagcc 360
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gctgggtccc tacaccctgg acagcaacag tcttctatgt caatg 465

<210> 540
<211> 255
<212> DNA
<213> Homo sapiens

<400> 540
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tgccattcac cctcaacttc accatcacca acctgcagta cgaggaggac atgcatcacc 180
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<210> 541
<211> 390
<212> DNA

<213> Homo sapiens

<400> 541

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gcgcacagag agagaactgc agggctcgtgc tcaaacccta gatcaggaat agcagtctgg 180
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<210> 542

<211> 468

<212> DNA

<213> Homo sapiens

<400> 542

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gccctggact caacagggag cagctgtact gggagctaag caaactgacc aatgacattg 420
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<210> 543

<211> 475

<212> DNA

<213> Homo sapiens

<400> 543

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cccaaaagcc ctggactcaa cagagagcgg ctgtactggg agctgagcca actgaccaat 420
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<210> 544

<211> 485

<212> DNA

<213> Homo sapiens

<400> 544

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<210> 546
<211> 142
<212> DNA
<213> Homo sapiens

<400> 546
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<210> 547
<211> 185
<212> DNA
<213> Homo sapiens

<400> 547
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tctgacaaat ggcattcagg agctggggcc ctacaccctg gaccggaaca gtctctatgt 180
caatg 185

<210> 548
<211> 462
<212> DNA
<213> Homo sapiens

<400> 548
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gactcaacag ggagcagctg tactgggagc taagcaaaact gaccaatgac attgaagagc 420
tgggccccta caccctggac aggaacagtc tctatgtcaa tg 462

<210> 549
<211> 400
<212> DNA
<213> Homo sapiens

<400> 549
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<210> 550
 <211> 468
 <212> DNA
 <213> Homo sapiens

<400> 550
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<210> 551
 <211> 366
 <212> DNA
 <213> Homo sapiens

<400> 551
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<210> 552
 <211> 465
 <212> DNA
 <213> Homo sapiens

<400> 552
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<210> 553
 <211> 401
 <212> DNA
 <213> Homo sapiens

<400> 553
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 atactgggag ctgagccagc tgaccaatgg catcaaagaa a 401

<210> 554
<211> 385
<212> DNA
<213> Homo sapiens

<400> 554
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tacatctgct ggccctctcc tgggtgccatt caccctcaac ttcacccatca ccaacctgca 120
gtacgaggag gacatgcatc acccaggctc caggaagtgc aacaccacgg agcgggtcct 180
gcagggtctg cttgggtcca tgttcaagaa caccagtgtc ggccttctgt actctggctg 240
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<210> 555
<211> 173
<212> DNA
<213> Homo sapiens

<400> 555
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catcaaagag ctggggcccct acaccctgga ccggaacagt ctctacgtca atg 173

<210> 556
<211> 468
<212> DNA
<213> Homo sapiens

<400> 556
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<210> 557
<211> 468
<212> DNA
<213> Homo sapiens

<400> 557
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gacctggact ggacagagag cggctatact gggagctgag ccagctgacc aacagcatca 420
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<210> 558
<211> 468
<212> DNA

<213> Homo sapiens

<400> 558

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gtcctggact ggacagagag cggctatact gggagctgag ccagctgacc aacagcgta 420
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<210> 559

<211> 468

<212> DNA

<213> Homo sapiens

<400> 559

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accctggact ggacagagag cagctatact gggagctgag caaactgacc tgtggcatca 420
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<210> 560

<211> 468

<212> DNA

<213> Homo sapiens

<400> 560

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gccctggact gaacagagag cagctgtact gggagctgag ccagctgacc cacggcatca 420
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<210> 561

<211> 468

<212> DNA

<213> Homo sapiens

<400> 561

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<210> 562

<211> 407
<212> DNA
<213> Homo sapiens

<400> 562
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<210> 563
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<212> DNA
<213> Homo sapiens .

<400> 563
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<211> 468
<212> DNA
<213> Homo sapiens

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<213> Homo sapiens

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<210> 566
<211> 402
<212> DNA
<213> Homo sapiens

<400> 566
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<210> 567
<211> 450
<212> DNA
<213> Homo sapiens

<400> 567
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<211> 1060
<212> DNA
<213> Homo sapiens

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<222> 406,742,801
<223> n = A,T,C or G

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 115 120 125

Ser Met
 130

<210> 572
 <211> 130
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> 1,58,78,92,94
 <223> Xaa = Any amino acid

<400> 572
 Xaa Ile Pro Ser Ser Asn Ser Ser His Ser Pro Ile His Gly Ala Ile
 5 10 15

His Pro Gln Leu Gln Leu Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met
 20 25 30

Arg His Leu Val Pro Gly Ser Ser Thr Arg Thr Glu Arg Glu Leu Gln
 35 40 45

Gly Arg Ala Gln Thr Leu Asp Gln Glu Xaa Gln Ser Gly Ile Pro Leu
 50 55 60

Phe Arg Leu Gln Thr Ser Leu Thr Gln Ala Arg Glu Gly Xaa Leu Ser
 65 70 75 80

His Gly Ser Gly Cys His Leu His Thr Ser Pro Xaa Pro Xaa Arg Pro
 85 90 95

Arg Thr Gly Gln Arg Ala Thr Val Leu Gly Ala Glu Gln Ser Asp Lys
 100 105 110

Trp His Pro Gly Ala Gly Pro Leu His Pro Gly Pro Glu Gln Ser Leu
 115 120 125

Cys Gln

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<400> 573
Xaa Ser Pro Ala Arg Thr Ala Ala Thr Val Pro Phe Met Val Pro Phe
      5                                10                                15

Thr Leu Asn Phe Asn Ser Ser Pro Thr Cys Ser Thr Arg Arg Thr Cys
      20                                25                                30

Gly Thr Trp Phe Gln Glu Val Gln Arg Ala Gln Arg Glu Asn Cys Arg
      35                                40                                45

Val Val Leu Lys Pro Xaa Ile Arg Asn Ser Ser Leu Glu Tyr Leu Tyr
      50                                55                                60

Ser Gly Cys Arg Leu Ala Ser Leu Arg Pro Glu Lys Asp Ser Ser Ala
      65                                70                                75                                80

Thr Ala Val Asp Ala Ile Cys Thr His Arg Pro Asp Pro Glu Asp Leu
      85                                90                                95

Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu Ser Asn Leu Thr Asn
      100                                105                                110

Gly Ile Gln Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr
      115                                120                                125

Val Asn
      130

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<400> 574
Gly Phe Thr His Arg Ser Ser Met Pro Thr Thr Ser Thr Pro Gly Thr
 5 10 15

Ser Thr Val Asp Val Gly Thr Ser Gly Thr Pro Ser Ser Ser Pro Ser
 20 25 30

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<220>  
<221> variant  
<222> 103  
<223> Xaa = Any amino acid
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<400> 575
Gly Phe Thr His Gln Ser Ser Val Ser Thr Thr Ser Thr Pro Gly Thr
      5                      10                      15

Ser Thr Val Asp Leu Arg Thr Ser Val Thr Pro Ser Ser Leu Ser Ser
      20                      25                      30

Pro Thr Ile Met Ala Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn
      35                      40                      45

Phe Thr Ile Thr Asn Leu Gln Tyr Gly Glu Asp Met Gly His Pro Gly
      50                      55                      60

Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Gly
      65                      70                      75                      80

Pro Ile Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg
      85                      90                      95

Leu Thr Ser Leu Arg Ser Xaa Lys Asp Gly Ala Ala Thr Gly Val Asp
      100                      105                      110

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Ala Ile Cys Ile His His Leu Asp Pro Lys Ser Pro Gly Leu Asn Arg
 115 120 125
 Glu Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu
 130 135 140
 Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn
 145 150 155

<210> 576
 <211> 122
 <212> PRT
 <213> Homo sapiens

<400> 576
 Ala Ala Gly Pro Leu Leu Val Leu Phe Thr Leu Asn Phe Thr Ile Thr
 5 10 15
 Asn Leu Lys Tyr Glu Glu Asp Met His Arg Pro Gly Ser Arg Lys Phe
 20 25 30
 Asn Thr Thr Glu Arg Val Leu Gln Thr Leu Arg Gly Pro Met Phe Lys
 35 40 45
 Asn Thr Ser Gly Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu
 50 55 60
 Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr
 65 70 75 80
 His Arg Leu Asp Pro Lys Ser Pro Gly Val Asp Arg Glu Gln Leu Tyr
 85 90 95
 Trp Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr
 100 105 110
 Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn
 115 120

<210> 577
 <211> 156
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> 11,106,151
 <223> Xaa = Any amino acid

<400> 577
 Gly Phe Thr His Arg Thr Ser Val Pro Thr Xaa Ser Thr Pro Gly Thr
 5 10 15
 Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Phe Ser Leu Pro Ser
 20 25 30

```
<210> 578
<211> 155
<212> PRT
<213> Homo sapiens
```

```
<400> 578
Gly Phe Thr His Trp Ile Pro Val Pro Thr Ser Ser Thr Pro Gly Thr
      5                      10                    15

Ser Thr Val Asp Leu Gly Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro
      20                      25                    30

Thr Thr Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile
      35                      40                    45

Thr Asn Leu Gln Tyr Glu Glu Asp Met His His Pro Gly Ser Arg Lys
      50                      55                    60

Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Met Phe
      65                      70                    75                    80

Lys Asn Thr Ser Val Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr Leu
      85                      90                    95

Leu Arg Pro Glu Lys Asn Gly Ala Ala Thr Gly Met Asp Ala Ile Cys
     100                      105                   110

Ser His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asn Arg Glu Gln Leu
     115                      120                   125

Tyr Trp Glu Leu Ser Gln Leu Thr His Gly Ile Lys Glu Leu Gly Pro
     130                      135                   140
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195

Tyr Thr Leu Asp Arg His Ser Leu Tyr Val Asn
145 150 155

<210> 579
<211> 155
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> 52,138
<223> Xaa = Any amino acid

<400> 579
Gly Phe Thr His Trp Ile Pro Val Pro Thr Ser Ser Thr Pro Gly Thr
5 10 15

Ser Thr Val Asp Leu Gly Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro
20 25 30

Thr Thr Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile
35 40 45

Thr Asn Leu Xaa Tyr Glu Glu Asp Met His Cys Pro Gly Ser Arg Lys
50 55 60

Phe Asn Thr Thr Glu Arg Val Leu Gln Ser Leu Leu Gly Pro Met Phe
65 70 75 80

Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu
85 90 95

Leu Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys
100 105 110

Thr His Arg Leu Asp Pro Lys Ser Pro Gly Val Asp Arg Glu Gln Leu
115 120 125

Tyr Trp Glu Leu Ser Gln Leu Thr Asn Xaa Ile Lys Glu Leu Gly Pro
130 135 140

Tyr Thr Leu Asp Ser Asn Ser Leu Tyr Val Asn
145 150 155

<210> 580
<211> 156
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> 23
<223> Xaa = Any amino acid

<400> 580
Gly Phe Thr His Gln Thr Ser Ala Pro Asn Thr Ser Thr Pro Gly Thr

```

<210> 581
<211> 156
<212> PRT
<213> Homo sapiens

<400> 581
Gly Phe Thr His Arg Ser Ser Val Ala Pro Thr Ser Thr Pro Gly Thr
      5                      10                      15
Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Ser Leu Pro Ser
      20                      25                      30
Pro Thr Thr Ala Val Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr
      35                      40                      45
Ile Thr Asn Leu Gln Tyr Gly Glu Asp Met Arg His Pro Gly Ser Arg
      50                      55                      60
Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Leu
      65                      70                      75                      80
Phe Lys Asn Ser Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Ile
      85                      90                      95
Ser Leu Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile
      100                      105                      110
Cys Thr His His Leu Asn Pro Gln Ser Pro Gly Leu Asp Arg Glu Gln

```

115 120 125
 Leu Tyr Trp Gln Leu Ser Gln Met Thr Asn Gly Ile Lys Glu Leu Gly
 130 135 140
 Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn
 145 150 155

<210> 582
 <211> 156
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> 151
 <223> Xaa = Any amino acid

<400> 582
 Gly Phe Thr His Arg Ser Ser Gly Leu Thr Thr Ser Thr Pro Trp Thr
 5 10 15
 Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Pro Val Pro Ser
 20 25 30
 Pro Thr Thr Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr
 35 40 45
 Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met His Arg Pro Gly Ser Arg
 50 55 60
 Lys Phe Asn Ala Thr Glu Arg Val Leu Gln Gly Leu Leu Ser Pro Ile
 65 70 75 80
 Phe Lys Asn Ser Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr
 85 90 95
 Ser Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Gly Met Asp Ala Val
 100 105 110
 Cys Leu Tyr His Pro Asn Pro Lys Arg Pro Gly Leu Asp Arg Glu Gln
 115 120 125
 Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly
 130 135 140
 Pro Tyr Ser Leu Asp Arg Xaa Ser Leu Tyr Val Asn
 145 150 155

<210> 583
 <211> 156
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant

<223> Xaa = Any amino acid

Gly Phe Thr His Gln Asn Ser Val Pro Thr Thr Ser Thr Pro Gly Thr
5 10 15

Ser Thr Val Tyr Trp Ala Thr Thr Gly Thr Pro Ser Ser Phe Pro Gly
20 25 30

His Thr Glu Pro Gly Pro Leu Leu Ile Pro Phe Thr Phe Asn Phe Thr
35 40 45

Ile Thr Asn Leu His Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg
50 55 60

Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Thr Pro Leu
65 70 75 80

Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr
85 90 95

Leu Leu Arg Pro Glu Lys Gln Glu Ala Ala Thr Gly Xaa Asp Thr Ile
100 105 110

Cys Xaa His Arg Xaa Asp Pro Ile Gly Pro Gly Leu Asp Arg Glu Xaa
115 120 125

Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Xaa Ile Thr Glu Leu Gly
130 135 140

Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn
145 150 155

<211> 156

<212> PRT

<213> Homo sapiens

Gly Phe Asn Pro Trp Ser Ser Val Pro Thr Thr Ser Thr Pro Gly Thr
5 10 15

Ser Thr Val His Leu Ala Thr Ser Gly Thr Pro Ser Ser Leu Pro Gly
20 25 30

His Thr Ala Pro Val Pro Leu Leu Ile Pro Phe Thr Leu Asn Phe Thr
35 40 45

Ile Thr Asn Leu His Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg
50 55 60

Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu
65 70 75 80

Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr
85 90 95

Leu Leu Arg Pro Glu Lys His Gly Ala Ala Thr Gly Val Asp Ala Ile
100 105 110

Cys Thr Leu Arg Leu Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Arg
115 120 125

Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Ser Val Thr Glu Leu Gly
130 135 140

Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn
145 150 155

<210> 585

<211> 156

<212> PRT

<213> Homo sapiens

<400> 585

Gly Phe Thr His Arg Ser Ser Val Pro Thr Thr Ser Ile Pro Gly Thr
5 10 15

Ser Ala Val His Leu Glu Thr Ser Gly Thr Pro Ala Ser Leu Pro Gly
20 25 30

His Thr Ala Pro Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr
35 40 45

Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met Arg His Pro Gly Ser Arg
50 55 60

Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu
65 70 75 80

Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr
85 90 95

Leu Leu Arg Pro Glu Lys Arg Gly Ala Ala Thr Gly Val Asp Thr Ile
100 105 110

Cys Thr His Arg Leu Asp Pro Leu Asn Pro Gly Leu Asp Arg Glu Gln
115 120 125

Leu Tyr Trp Glu Leu Ser Lys Leu Thr Cys Gly Ile Ile Glu Leu Gly
130 135 140

Pro Tyr Leu Leu Asp Arg Gly Ser Leu Tyr Val Asn
145 150 155

<210> 586

<211> 156

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> 151,156

<223> Xaa = Any amino acid

<400> 586

Gly Phe Thr His Arg Asn Phe Val Pro Ile Thr Ser Thr Pro Gly Thr
 5 10 15
 Ser Thr Val His Leu Gly Thr Ser Glu Thr Pro Ser Ser Leu Pro Arg
 20 25 30
 Pro Ile Val Pro Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr
 35 40 45
 Ile Thr Asn Leu Gln Tyr Glu Glu Ala Met Arg His Pro Gly Ser Arg
 50 55 60
 Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Leu
 65 70 75 80
 Phe Lys Asn Thr Ser Ile Gly Pro Leu Tyr Ser Ser Cys Arg Leu Thr
 85 90 95
 Leu Leu Arg Pro Glu Lys Asp Lys Ala Ala Thr Arg Val Asp Ala Ile
 100 105 110
 Cys Thr His His Pro Asp Pro Gln Ser Pro Gly Leu Asn Arg Glu Gln
 115 120 125
 Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Gly Ile Thr Glu Leu Gly
 130 135 140
 Pro Tyr Thr Leu Asp Arg Xaa Ser Leu Tyr Val Xaa
 145 150 155

<210> 587

<211> 156

<212> PRT

<213> Homo sapiens

<400> 587

Gly Phe Thr His Trp Ser Pro Ile Pro Thr Thr Ser Thr Pro Gly Thr
 5 10 15
 Ser Ile Val Asn Leu Gly Thr Ser Gly Ile Pro Pro Ser Leu Pro Glu
 20 25 30
 Thr Thr Ala Thr Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr
 35 40 45
 Ile Thr Asn Leu Gln Tyr Glu Glu Asn Met Gly His Pro Gly Ser Arg
 50 55 60
 Lys Phe Asn Ile Thr Glu Ser Val Leu Gln Gly Leu Leu Lys Pro Leu
 65 70 75 80
 Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr
 85 90 95

Leu Leu Arg Pro Glu Lys Asp Gly Val Ala Thr Arg Val Asp Ala Ile
 100 105 110

Cys Thr His Arg Pro Asp Pro Lys Ile Pro Gly Leu Asp Arg Gln Gln
 115 120 125

Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly
 130 135 140

Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn
 145 150 155

<210> 588

<211> 156

<212> PRT

<213> Homo sapiens

<400> 588

Gly Phe Thr Gln Arg Ser Ser Val Pro Thr Thr Ser Thr Pro Gly Thr
 5 10 15

Phe Thr Val Gln Pro Glu Thr Ser Glu Thr Pro Ser Ser Leu Pro Gly
 20 25 30

Pro Thr Ala Thr Gly Pro Val Leu Leu Pro Phe Thr Leu Asn Phe Thr
 35 40 45

Ile Ile Asn Leu Gln Tyr Glu Glu Asp Met His Arg Pro Gly Ser Arg
 50 55 60

Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Met Pro Leu
 65 70 75 80

Phe Lys Asn Thr Ser Val Ser Ser Leu Tyr Ser Gly Cys Arg Leu Thr
 85 90 95

Leu Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Arg Val Asp Ala Val
 100 105 110

Cys Thr His Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Arg
 115 120 125

Leu Tyr Trp Lys Leu Ser Gln Leu Thr His Gly Ile Thr Glu Leu Gly
 130 135 140

Pro Tyr Thr Leu Asp Arg His Ser Leu Tyr Val Asn
 145 150 155

<210> 589

<211> 156

<212> PRT

<213> Homo sapiens

<400> 589

Gly Phe Thr His Gln Ser Ser Met Thr Thr Thr Arg Thr Pro Asp Thr

	5		10		15
Ser Thr Met His Leu Ala Thr Ser Arg Thr Pro Ala Ser Leu Ser Gly					
	20		25		30
Pro Thr Thr Ala Ser Pro Leu Leu Val Leu Phe Thr Ile Asn Phe Thr					
	35		40		45
Ile Thr Asn Leu Arg Tyr Glu Glu Asn Met His His Pro Gly Ser Arg					
	50		55		60
Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Val					
	65		70		75
Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr					
		85		90	95
Leu Leu Arg Pro Lys Lys Asp Gly Ala Ala Thr Lys Val Asp Ala Ile					
		100		105	110
Cys Thr Tyr Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln					
		115		120	125
Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly					
	130		135		140
Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn					
	145		150		155

<210> 590

<211> 156

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> 145

<223> Xaa = Any amino acid

<400> 590

Gly Phe Thr Gln Arg Ser Ser Val Pro Thr Thr Ser Ile Pro Gly Thr					
		5		10	15
Pro Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Val Ser Lys Pro Gly					
	20		25		30
Pro Ser Ala Ala Ser Pro Leu Leu Val Leu Phe Thr Leu Asn Phe Thr					
	35		40		45
Ile Thr Asn Leu Arg Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg					
	50		55		60
Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Ser Leu					
	65		70		75
Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr					
		85		90	95

Leu Leu Arg Pro Glu Lys Asp Gly Thr Ala Thr Gly Val Asp Ala Ile
100 105 110

Cys Thr His His Pro Asp Pro Lys Ser Pro Arg Leu Asp Arg Glu Gln
115 120 125

Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly
130 135 140

Xaa Tyr Ala Leu Asp Asn Asp Ser Leu Phe Val Asn
145 150 155

<210> 591

<211> 155

<212> PRT

<213> Homo sapiens

<400> 591

Gly Phe Thr His Arg Ser Ser Val Ser Thr Thr Ser Thr Pro Gly Thr
5 10 15

Pro Thr Val Tyr Leu Gly Ala Ser Lys Thr Pro Ala Ser Ile Phe Gly
20 25 30

Pro Ser Ala Ala Ser His Leu Leu Ile Leu Phe Thr Leu Asn Phe Thr
35 40 45

Ile Thr Asn Leu Arg Tyr Glu Glu Asn Met Trp Pro Gly Ser Arg Lys
50 55 60

Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Leu Phe
65 70 75 80

Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu
85 90 95

Leu Arg Pro Glu Lys Asp Gly Glu Ala Thr Gly Val Asp Ala Ile Cys
100 105 110

Thr His Arg Pro Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Gln Leu
115 120 125

Tyr Leu Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro
130 135 140

Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn
145 150 155

<210> 592

<211> 134

<212> PRT

<213> Homo sapiens

<400> 592

Gly Phe Thr His Arg Ser Ser Val Pro Thr Thr Ser Thr Gly Val Val

204

5 10 15
 Ser Glu Glu Pro Phe Thr Leu Asn Phe Thr Ile Asn Asn Leu Arg Tyr
 20 25 30
 Met Ala Asp Met Gly Gln Pro Gly Ser Leu Lys Phe Asn Ile Thr Asp
 35 40 45
 Asn Val Met Lys His Leu Leu Ser Pro Leu Phe Gln Arg Ser Ser Leu
 50 55 60
 Gly Ala Arg Tyr Thr Gly Cys Arg Val Ile Ala Leu Arg Ser Val Lys
 65 70 75 80
 Asn Gly Ala Glu Thr Arg Val Asp Leu Leu Cys Thr Tyr Leu Gln Pro
 85 90 95
 Leu Ser Gly Pro Gly Leu Pro Ile Lys Gln Val Phe His Glu Leu Ser
 100 105 110
 Gln Gln Thr His Gly Ile Thr Arg Leu Gly Pro Tyr Ser Leu Asp Lys
 115 120 125
 Asp Ser Leu Tyr Leu Asn
 130

<210> 593
 <211> 150
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> 7
 <223> Xaa = Any amino acid

<400> 593
 Gly Tyr Asn Glu Pro Gly Xaa Asp Glu Pro Pro Thr Thr Pro Lys Pro
 5 10 15
 Ala Thr Thr Phe Leu Pro Pro Leu Ser Glu Ala Thr Thr Ala Met Gly
 20 25 30
 Tyr His Leu Lys Thr Leu Thr Leu Asn Phe Thr Ile Ser Asn Leu Gln
 35 40 45
 Tyr Ser Pro Asp Met Gly Lys Gly Ser Ala Thr Phe Asn Ser Thr Glu
 50 55 60
 Gly Val Leu Gln His Leu Leu Arg Pro Leu Phe Gln Lys Ser Ser Met
 65 70 75 80
 Gly Pro Phe Tyr Leu Gly Cys Gln Leu Ile Ser Leu Arg Pro Glu Lys
 85 90 95
 Asp Gly Ala Ala Thr Gly Val Asp Thr Thr Cys Thr Tyr His Pro Asp
 100 105 110

Pro Val Gly Pro Gly Leu Asp Ile Gln Gln Leu Tyr Trp Glu Leu Ser
 115 120 125
 Gln Leu Thr His Gly Val Thr Gln Leu Gly Phe Tyr Val Leu Asp Arg
 130 135 140
 Asp Ser Leu Phe Ile Asn
 145 150

<210> 594
 <211> 318
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> variant
 <222> 136,248,268
 <223> Xaa = Any amino acid

<400> 594
 Gly Tyr Ala Pro Gln Asn Leu Ser Ile Arg Gly Glu Tyr Gln Ile Asn
 5 10 15
 Phe His Ile Val Asn Trp Asn Leu Ser Asn Pro Asp Pro Thr Ser Ser
 20 25 30
 Glu Tyr Ile Thr Leu Leu Arg Asp Ile Gln Asp Lys Val Thr Thr Leu
 35 40 45
 Tyr Lys Gly Ser Gln Leu His Asp Thr Phe Arg Phe Cys Leu Val Thr
 50 55 60
 Asn Leu Thr Met Asp Ser Val Leu Val Thr Val Lys Ala Leu Phe Ser
 65 70 75 80
 Ser Asn Leu Asp Pro Ser Leu Val Glu Gln Val Phe Leu Asp Lys Thr
 85 90 95
 Leu Asn Ala Ser Phe His Trp Leu Gly Ser Thr Tyr Gln Leu Val Asp
 100 105 110
 Ile His Val Thr Glu Met Glu Ser Ser Val Tyr Gln Pro Thr Ser Ser
 115 120 125
 Ser Ser Thr Gln His Phe Tyr Xaa Asn Phe Thr Ile Thr Asn Leu Pro
 130 135 140
 Tyr Ser Gln Asp Lys Ala Gln Pro Gly Thr Thr Asn Tyr Gln Arg Asn
 145 150 155 160
 Lys Arg Asn Ile Glu Asp Ala Leu Asn Gln Leu Phe Arg Asn Ser Ser
 165 170 175
 Ile Lys Ser Tyr Phe Ser Asp Cys Gln Val Ser Thr Phe Arg Ser Val
 180 185 190

Pro Asn Arg His His Thr Gly Val Asp Ser Leu Cys Asn Phe Ser Pro
 195 200 205
 Leu Ala Arg Arg Val Asp Arg Val Ala Ile Tyr Glu Glu Phe Leu Arg
 210 215 220
 Met Thr Arg Asn Gly Thr Gln Leu Gln Asn Phe Thr Leu Asp Arg Ser
 225 230 235 240
 Ser Val Leu Val Asp Gly Tyr Xaa Pro Asn Arg Asn Glu Pro Leu Thr
 245 250 255
 Gly Asn Ser Asp Leu Pro Phe Trp Ala Val Ile Xaa Ile Gly Leu Ala
 260 265 270
 Gly Leu Leu Gly Leu Ile Thr Cys Leu Ile Cys Gly Val Leu Val Thr
 275 280 285
 Thr Arg Arg Arg Lys Lys Glu Gly Glu Tyr Asn Val Gln Gln Gln Cys
 290 295 300
 Pro Gly Tyr Tyr Gln Ser His Leu Asp Leu Glu Asp Leu Gln
 305 310 315

<210> 595

<211> 3451

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> 177, 335, 523, 618, 663, 875, 961, 1001, 1441, 1555, 1560,
 1563, 1574, 1585, 2065, 2070, 2683, 2990, 3269, 3381, 3401
 <223> Xaa = Any Amino Acid

<400> 595

Ile Arg Asn Ser Ser Leu Glu Tyr Leu Tyr Ser Gly Cys Arg Leu Ala
 1 5 10 15
 Ser Leu Arg Pro Glu Lys Asp Ser Ser Ala Thr Ala Val Asp Ala Ile
 20 25 30
 Cys Thr His Arg Pro Asp Pro Glu Asp Leu Gly Leu Asp Arg Glu Arg
 35 40 45
 Leu Tyr Trp Glu Leu Ser Asn Leu Thr Asn Gly Ile Gln Glu Leu Gly
 50 55 60
 Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His
 65 70 75 80
 Arg Ser Ser Met Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Asp
 85 90 95
 Val Gly Thr Ser Gly Thr Pro Ser Ser Ser Pro Ser Pro Thr Thr Ala
 100 105 110
 Gly Pro Leu Leu Met Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu
 115 120 125
 Gln Tyr Glu Glu Asp Met Arg Arg Thr Gly Ser Arg Lys Phe Asn Thr
 130 135 140
 Met Glu Ser Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr
 145 150 155 160
 Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro

625		630		635		640
Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly						
	645			650		655
Pro Tyr Thr Leu Asp Arg Xaa Ser Leu Tyr Val Asn Gly Phe Thr His						
	660			665		670
Trp Ile Pro Val Pro Thr Ser Ser Thr Pro Gly Thr Ser Thr Val Asp						
	675			680		685
Leu Gly Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro Thr Thr Ala Gly						
	690			695		700
Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln						
705		710		715		720
Tyr Glu Glu Asp Met His His Pro Gly Ser Arg Lys Phe Asn Thr Thr						
	725			730		735
Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Met Phe Lys Asn Thr Ser						
	740			745		750
Val Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu						
	755			760		765
Lys Asn Gly Ala Ala Thr Gly Met Asp Ala Ile Cys Ser His Arg Leu						
	770			775		780
Asp Pro Lys Ser Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp Glu Leu						
785		790		795		800
Ser Gln Leu Thr His Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp						
	805			810		815
Arg His Ser Leu Tyr Val Asn Gly Phe Thr His Trp Ile Pro Val Pro						
	820			825		830
Thr Ser Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Gly Ser Gly Thr						
	835			840		845
Pro Ser Ser Leu Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Val Pro						
	850			855		860
Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Xaa Tyr Glu Glu Asp Met						
865		870		875		880
His Cys Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln						
	885			890		895
Ser Leu Leu Gly Pro Met Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr						
	900			905		910
Ser Gly Cys Arg Leu Thr Leu Leu Arg Ser Glu Lys Asp Gly Ala Ala						
	915			920		925
Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser Pro						
	930			935		940
Gly Val Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn						
945		950		955		960
Xaa Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Ser Asn Ser Leu Tyr						
	965			970		975
Val Asn Gly Phe Thr His Gln Thr Ser Ala Pro Asn Thr Ser Thr Pro						
	980			985		990
Gly Thr Ser Thr Val Asp Leu Gly Xaa Ser Gly Thr Pro Ser Ser Leu						
	995			1000		1005
Pro Ser Pro Thr Ser Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn						
	1010			1015		1020
Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met His His Pro Gly						
1025		1030		1035		1040
Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Gly						
	1045			1050		1055
Pro Met Phe Lys Asn Thr Ser Val Gly Leu Leu Tyr Ser Gly Cys Arg						
	1060			1065		1070
Leu Thr Leu Leu Arg Pro Glu Lys Asn Gly Ala Ala Thr Gly Met Asp						
	1075			1080		1085
Ala Ile Cys Ser His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asn Arg						

1090	1095	1100
Glu Gln Leu Tyr Trp	Glu Leu Ser Gln Leu Thr	His Gly Ile Lys Glu
1105	1110	1115
Leu Gly Pro Tyr Thr	Leu Asp Arg Asn Ser	Leu Tyr Val Asn Gly Phe
1125	1130	1135
Thr His Arg Ser Ser	Val Ala Pro Thr Ser Thr	Pro Gly Thr Ser Thr
1140	1145	1150
Val Asp Leu Gly Thr	Ser Gly Thr Pro Ser Ser	Leu Pro Ser Pro Thr
1155	1160	1165
Thr Ala Val Pro Leu	Leu Val Pro Phe Thr	Leu Asn Phe Thr Ile Thr
1170	1175	1180
Asn Leu Gln Tyr Gly	Glu Asp Met Arg His	Pro Gly Ser Arg Lys Phe
1185	1190	1195
Asn Thr Thr Glu Arg	Val Leu Gln Gly	Leu Leu Gly Pro Leu Phe Lys
1205	1210	1215
Asn Ser Ser Val Gly	Pro Leu Tyr Ser Gly	Cys Arg Leu Ile Ser Leu
1220	1225	1230
Arg Ser Glu Lys Asp	Gly Ala Ala Thr Gly	Val Asp Ala Ile Cys Thr
1235	1240	1245
His His Leu Asn Pro	Gln Ser Pro Gly Leu	Asp Arg Glu Gln Leu Tyr
1250	1255	1260
Trp Gln Leu Ser Gln	Met Thr Asn Gly Ile	Lys Glu Leu Gly Pro Tyr
1265	1270	1275
Thr Leu Asp Arg Asn	Ser Leu Tyr Val Asn	Gly Phe Thr His Arg Ser
1285	1290	1295
Ser Gly Leu Thr Thr	Ser Thr Pro Trp Thr	Ser Thr Val Asp Leu Gly
1300	1305	1310
Thr Ser Gly Thr Pro	Ser Pro Val Pro Ser	Pro Thr Thr Ala Gly Pro
1315	1320	1325
Leu Leu Val Pro Phe	Thr Leu Asn Phe Thr	Ile Thr Asn Leu Gln Tyr
1330	1335	1340
Glu Glu Asp Met His	Arg Pro Gly Ser Arg	Lys Phe Asn Ala Thr Glu
1345	1350	1355
Arg Val Leu Gln Gly	Leu Leu Ser Pro Ile	Phe Lys Asn Ser Ser Val
1365	1370	1375
Gly Pro Leu Tyr Ser	Gly Cys Arg Leu Thr	Ser Leu Arg Pro Glu Lys
1380	1385	1390
Asp Gly Ala Ala Thr	Gly Met Asp Ala Val	Cys Leu Tyr His Pro Asn
1395	1400	1405
Pro Lys Arg Pro Gly	Leu Asp Arg Glu Gln	Leu Tyr Trp Glu Leu Ser
1410	1415	1420
Gln Leu Thr His Asn	Ile Thr Glu Leu Gly	Pro Tyr Ser Leu Asp Arg
1425	1430	1435
Xaa Ser Leu Tyr Val	Asn Gly Phe Thr His	Gln Asn Ser Val Pro Thr
1445	1450	1455
Thr Ser Thr Pro Gly	Thr Ser Thr Val Tyr	Trp Ala Thr Thr Gly Thr
1460	1465	1470
Pro Ser Ser Phe Pro	Gly His Thr Glu Pro	Gly Pro Leu Leu Ile Pro
1475	1480	1485
Phe Thr Phe Asn Phe	Thr Ile Thr Asn Leu	His Tyr Glu Glu Asn Met
1490	1495	1500
Gln His Pro Gly Ser	Arg Lys Phe Asn Thr	Thr Glu Arg Val Leu Gln
1505	1510	1515
Gly Leu Leu Thr Pro	Leu Phe Lys Asn Thr	Ser Val Gly Pro Leu Tyr
1525	1530	1535
Ser Gly Cys Arg Leu	Thr Leu Leu Arg Pro	Glu Lys Gln Glu Ala Ala
1540	1545	1550
Thr Gly Xaa Asp Thr	Ile Cys Xaa His Arg	Xaa Asp Pro Ile Gly Pro

1555	1560	1565
Gly Leu Asp Arg Glu Xaa Leu Tyr Trp Glu Leu Ser Gln Leu Thr His		
1570	1575	1580
Xaa Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr		
1585	1590	1595
Val Asn Gly Phe Asn Pro Trp Ser Ser Val Pro Thr Thr Ser Thr Pro		
1605	1610	1615
Gly Thr Ser Thr Val His Leu Ala Thr Ser Gly Thr Pro Ser Ser Leu		
1620	1625	1630
Pro Gly His Thr Ala Pro Val Pro Leu Leu Ile Pro Phe Thr Leu Asn		
1635	1640	1645
Phe Thr Ile Thr Asn Leu His Tyr Glu Glu Asn Met Gln His Pro Gly		
1650	1655	1660
Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys		
1665	1670	1675
Pro Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg		
1685	1690	1695
Leu Thr Leu Leu Arg Pro Glu Lys His Gly Ala Ala Thr Gly Val Asp		
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Ala Ile Cys Thr Leu Arg Leu Asp Pro Thr Gly Pro Gly Leu Asp Arg		
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Glu Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Ser Val Thr Glu		
1730	1735	1740
Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe		
1745	1750	1755
Thr His Arg Ser Ser Val Pro Thr Thr Ser Ile Pro Gly Thr Ser Ala		
1765	1770	1775
Val His Leu Glu Thr Ser Gly Thr Pro Ala Ser Leu Pro Gly His Thr		
1780	1785	1790
Ala Pro Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr		
1795	1800	1805
Asn Leu Gln Tyr Glu Glu Asp Met Arg His Pro Gly Ser Arg Lys Phe		
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Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys		
1825	1830	1835
Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu		
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Arg Pro Glu Lys Arg Gly Ala Ala Thr Gly Val Asp Thr Ile Cys Thr		
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His Arg Leu Asp Pro Leu Asn Pro Gly Leu Asp Arg Glu Gln Leu Tyr		
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Trp Glu Leu Ser Lys Leu Thr Cys Gly Ile Ile Glu Leu Gly Pro Tyr		
1890	1895	1900
Leu Leu Asp Arg Gly Ser Leu Tyr Val Asn Gly Phe Thr His Arg Asn		
1905	1910	1915
Phe Val Pro Ile Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Gly		
1925	1930	1935
Thr Ser Glu Thr Pro Ser Ser Leu Pro Arg Pro Ile Val Pro Gly Pro		
1940	1945	1950
Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr		
1955	1960	1965
Glu Glu Ala Met Arg His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu		
1970	1975	1980
Arg Val Leu Gln Gly Leu Leu Arg Pro Leu Phe Lys Asn Thr Ser Ile		
1985	1990	1995
Gly Pro Leu Tyr Ser Ser Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys		
2005	2010	2015
Asp Lys Ala Ala Thr Arg Val Asp Ala Ile Cys Thr His His Pro Asp		

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Tyr Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr					
	2500		2505		2510
Trp Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr					
	2515		2520		2525
Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr Gln Arg Ser					
	2530		2535		2540
Ser Val Pro Thr Thr Ser Ile Pro Gly Thr Pro Thr Val Asp Leu Gly					
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Thr Ser Gly Thr Pro Val Ser Lys Pro Gly Pro Ser Ala Ala Ser Pro					
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Leu Leu Val Leu Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Arg Tyr					
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Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu					
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Arg Val Leu Gln Gly Leu Leu Arg Ser Leu Phe Lys Ser Thr Ser Val					
	2610		2615		2620
Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys					
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Asp Gly Thr Ala Thr Gly Val Asp Ala Ile Cys Thr His His Pro Asp					
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Pro Lys Ser Pro Arg Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser					
	2660		2665		2670
Gln Leu Thr His Asn Ile Thr Glu Leu Gly Xaa Tyr Ala Leu Asp Asn					
	2675		2680		2685
Asp Ser Leu Phe Val Asn Gly Phe Thr His Arg Ser Ser Val Ser Thr					
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Thr Ser Thr Pro Gly Thr Pro Thr Val Tyr Leu Gly Ala Ser Lys Thr					
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Pro Ala Ser Ile Phe Gly Pro Ser Ala Ala Ser His Leu Leu Ile Leu					
	2725		2730		2735
Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Arg Tyr Glu Glu Asn Met					
	2740		2745		2750
Trp Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly					
	2755		2760		2765
Leu Leu Arg Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser					
	2770		2775		2780
Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Glu Ala Thr					
2785	2790		2795		2800
Gly Val Asp Ala Ile Cys Thr His Arg Pro Asp Pro Thr Gly Pro Gly					
	2805		2810		2815
Leu Asp Arg Glu Gln Leu Tyr Leu Glu Leu Ser Gln Leu Thr His Ser					
	2820		2825		2830
Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val					
	2835		2840		2845
Asn Gly Phe Thr His Arg Ser Ser Val Pro Thr Thr Ser Thr Gly Val					
	2850		2855		2860
Val Ser Glu Glu Pro Phe Thr Leu Asn Phe Thr Ile Asn Asn Leu Arg					
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Tyr Met Ala Asp Met Gly Gln Pro Gly Ser Leu Lys Phe Asn Ile Thr					
	2885		2890		2895
Asp Asn Val Met Lys His Leu Leu Ser Pro Leu Phe Gln Arg Ser Ser					
	2900		2905		2910
Leu Gly Ala Arg Tyr Thr Gly Cys Arg Val Ile Ala Leu Arg Ser Val					
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Lys Asn Gly Ala Glu Thr Arg Val Asp Leu Leu Cys Thr Tyr Leu Gln					
	2930		2935		2940
Pro Leu Ser Gly Pro Gly Leu Pro Ile Lys Gln Val Phe His Glu Leu					

2945 2950 2955 2960
 Ser Gln Gln Thr His Gly Ile Thr Arg Leu Gly Pro Tyr Ser Leu Asp
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 Lys Asp Ser Leu Tyr Leu Asn Gly Tyr Asn Glu Pro Gly Xaa Asp Glu
 2980 2985 2990
 Pro Pro Thr Thr Pro Lys Pro Ala Thr Thr Phe Leu Pro Pro Leu Ser
 2995 3000 3005
 Glu Ala Thr Thr Ala Met Gly Tyr His Leu Lys Thr Leu Thr Leu Asn
 3010 3015 3020
 Phe Thr Ile Ser Asn Leu Gln Tyr Ser Pro Asp Met Gly Lys Gly Ser
 3025 3030 3035 3040
 Ala Thr Phe Asn Ser Thr Glu Gly Val Leu Gln His Leu Leu Arg Pro
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 Leu Phe Gln Lys Ser Ser Met Gly Pro Phe Tyr Leu Gly Cys Gln Leu
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 Ile Ser Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Thr
 3075 3080 3085
 Thr Cys Thr Tyr His Pro Asp Pro Val Gly Pro Gly Leu Asp Ile Gln
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 Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Gly Val Thr Gln Leu
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 Gly Phe Tyr Val Leu Asp Arg Asp Ser Leu Phe Ile Asn Gly Tyr Ala
 3125 3130 3135
 Pro Gln Asn Leu Ser Ile Arg Gly Glu Tyr Gln Ile Asn Phe His Ile
 3140 3145 3150
 Val Asn Trp Asn Leu Ser Asn Pro Asp Pro Thr Ser Ser Glu Tyr Ile
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 Thr Leu Leu Arg Asp Ile Gln Asp Lys Val Thr Thr Leu Tyr Lys Gly
 3170 3175 3180
 Ser Gln Leu His Asp Thr Phe Arg Phe Cys Leu Val Thr Asn Leu Thr
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 Met Asp Ser Val Leu Val Thr Val Lys Ala Leu Phe Ser Ser Asn Leu
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 Asp Pro Ser Leu Val Glu Gln Val Phe Leu Asp Lys Thr Leu Asn Ala
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 Ser Phe His Trp Leu Gly Ser Thr Tyr Gln Leu Val Asp Ile His Val
 3235 3240 3245
 Thr Glu Met Glu Ser Ser Val Tyr Gln Pro Thr Ser Ser Ser Thr
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 Gln His Phe Tyr Xaa Asn Phe Thr Ile Thr Asn Leu Pro Tyr Ser Gln
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 Asp Lys Ala Gln Pro Gly Thr Thr Asn Tyr Gln Arg Asn Lys Arg Asn
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 Ile Glu Asp Ala Leu Asn Gln Leu Phe Arg Asn Ser Ser Ile Lys Ser
 3300 3305 3310
 Tyr Phe Ser Asp Cys Gln Val Ser Thr Phe Arg Ser Val Pro Asn Arg
 3315 3320 3325
 His His Thr Gly Val Asp Ser Leu Cys Asn Phe Ser Pro Leu Ala Arg
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 Arg Val Asp Arg Val Ala Ile Tyr Glu Glu Phe Leu Arg Met Thr Arg
 3345 3350 3355 3360
 Asn Gly Thr Gln Leu Gln Asn Phe Thr Leu Asp Arg Ser Ser Val Leu
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 Val Asp Gly Tyr Xaa Pro Asn Arg Asn Glu Pro Leu Thr Gly Asn Ser
 3380 3385 3390
 Asp Leu Pro Phe Trp Ala Val Ile Xaa Ile Gly Leu Ala Gly Leu Leu
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 Gly Leu Ile Thr Cys Leu Ile Cys Gly Val Leu Val Thr Thr Arg Arg

3410 3415 3420
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 Pro Thr Ala Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr
 35 40 45
 Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met His His Pro Gly Ser Arg
 50 55 60
 Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Leu
 65 70 75 80
 Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr
 85 90 95
 Leu Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile
 100 105 110
 Cys Thr His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln
 115 120 125
 Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Gly Ile Thr Glu Leu Gly
 130 135 140
 Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn
 145 150 155